



Segon set #4



# SEQUENCE LISTING

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Tomb, Jean-Francois  
Oomen, Raymond P.

<120> Identification of Polynucleotides  
Encoding Novel Helicobacter Polypeptides in the Helicobacter  
Genome

<130> 06132/041002

<140> US 09/881,752

<141> 2001-06-15

<150> US 08/833,457

<151> 1997-04-01

<160> 370

<170> FastSEQ for Windows Version 4.0

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<211> 265

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(212)

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ttt ttg gga ctg att tta agt ctg gcc gct att ttg ata gcg ttt aaa 104  
Phe Leu Gly Leu Ile Leu Ser Leu Ala Ala Ile Leu Ile Ala Phe Lys  
5 10 15

aag cct gaa aaa gaa aat tgg gcg ttt ggg att ttg atg gtg gtg tgg 152  
Lys Pro Glu Lys Glu Asn Trp Ala Phe Gly Ile Leu Met Val Val Trp  
20 25 30

tta gtg gag ctt att att ttt ata gcc cac agc tct agc gtt ttg cct 200  
Leu Val Glu Leu Ile Ile Phe Ile Ala His Ser Ser Ser Val Leu Pro  
35 40 45 50

aac atg aat cta taaggggat gcatggataa agaaacccga ttttacaacc 252  
Asn Met Asn Leu

ttttttctttt ggc

265

<210> 2

<211> 54

<212> PRT

<213> Helicobacter pylori

<400> 2

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Phe	Lys	Lys	Pro	Glu	Lys	Glu	Asn	Trp	Ala	Phe	Gly	Ile	Leu	Met	Val
			20				25					30			
Val	Trp	Leu	Val	Glu	Leu	Ile	Ile	Phe	Ile	Ala	His	Ser	Ser	Ser	Val
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Leu	Pro	Asn	Met	Asn	Leu										
	50														

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<213> Helicobacter pylori

<220>

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<222> (51)...(617)

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aaa	att	gct	ttc	att	ttg	gct	tta
Lys	Ile	Ala	Phe	Ile	Leu	Ala	Leu
	5				10		15
gag	cct	aaa	aaa	agt	cat	att	tat
Glu	Pro	Lys	Lys	Ser	His	Ile	Tyr
	20				25		30
cct	att	aaa	ata	acc	cca	aaa	ccg
Pro	Ile	Lys	Ile	Thr	Pro	Lys	Pro
	35				40		45
ttt	tta	tgg	ggg	gct	aaa	gga	ggg
Phe	Leu	Trp	Gly	Ala	Lys	Gly	Gly
			55			60	
cta	gcg	tta	agg	ggg	gaa	ttt	tcc
Leu	Ala	Leu	Arg	Gly	Glu	Phe	Ser
		70				75	
gca	ctg	cac	acg	att	aac	act	tct
Ala	Leu	His	Thr	Ile	Asn	Thr	Ser
	85					90	

tta agc gat ttt tac act tac aaa aaa tac agc ttt ggg gtg tat ggg 392  
 Leu Ser Asp Phe Tyr Thr Tyr Lys Lys Tyr Ser Phe Gly Val Tyr Gly  
           100                                  105                                  110

ggg ctt ggg ata ggg tat ttt tat caa agc aac cat tta ggc atg aaa 440  
 Gly Leu Gly Ile Gly Tyr Phe Tyr Gln Ser Asn His Leu Gly Met Lys  
           115                                  120                                  125                                  130

aat agt tcg ttt atg ggt tat aac ggc ttg ttt aat gtg ggg ctt ggc 488  
 Asn Ser Ser Phe Met Gly Tyr Asn Gly Leu Phe Asn Val Gly Leu Gly  
                                   135                                  140                                  145

agc acg atc gat cgc cac cac cgc ata gag ctt ggg gct aaa atc cct 536  
 Ser Thr Ile Asp Arg His His Arg Ile Glu Leu Gly Ala Lys Ile Pro  
                                   150                                  155                                  160

ttt tca aag act aga aat tct ttt aaa aat cct tat ttt tta gag agc 584  
 Phe Ser Lys Thr Arg Asn Ser Phe Lys Asn Pro Tyr Phe Leu Glu Ser  
                                   165                                  170                                  175

gtt ttt atc cat gcg act tat agc tat atg ttt taagagagaa tagcctatta 637  
 Val Phe Ile His Ala Thr Tyr Ser Tyr Met Phe  
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gtggtcgtta tcaataagat aagatcctta atg 670

<210> 4

<211> 189

<212> PRT

<213> Helicobacter pylori

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 Ala Phe Glu Pro Lys Lys Ser His Ile Tyr Phe Gly Ala Met Val Gly  
                                   20                                  25                                  30  
 Leu Ala Pro Ile Lys Ile Thr Pro Lys Pro Ala Ser Asp Ser Ser Tyr  
                                   35                                  40                                  45  
 Thr Ala Phe Leu Trp Gly Ala Lys Gly Gly Tyr Gln Phe Ala Phe Phe  
                                   50                                  55                                  60  
 Lys Ala Leu Ala Leu Arg Gly Glu Phe Ser Tyr Leu Met Ala Ile Lys  
   65                                  70                                  75                                  80  
 Pro Thr Ala Leu His Thr Ile Asn Thr Ser Leu Leu Ser Leu Asn Ile  
                                   85                                  90                                  95  
 Asp Val Leu Ser Asp Phe Tyr Thr Tyr Lys Lys Tyr Ser Phe Gly Val  
                                   100                                  105                                  110  
 Tyr Gly Gly Leu Gly Ile Gly Tyr Phe Tyr Gln Ser Asn His Leu Gly  
                                   115                                  120                                  125  
 Met Lys Asn Ser Ser Phe Met Gly Tyr Asn Gly Leu Phe Asn Val Gly  
   130                                  135                                  140  
 Leu Gly Ser Thr Ile Asp Arg His His Arg Ile Glu Leu Gly Ala Lys  
   145                                  150                                  155                                  160  
 Ile Pro Phe Ser Lys Thr Arg Asn Ser Phe Lys Asn Pro Tyr Phe Leu  
                                   165                                  170                                  175

Glu Ser Val Phe Ile His Ala Thr Tyr Ser Tyr Met Phe  
 180 185

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(380)

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 Met Leu  
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 aaa aaa agt ttg tta ttg ctt gtt ttt tta gtc tta cag ctt agc ggc 104  
 Lys Lys Ser Leu Leu Leu Leu Val Phe Leu Val Leu Gln Leu Ser Gly  
 5 10 15  
 gct gaa gaa aac aat caa gcc cca aaa aac acg ccc cct gaa tta aac 152  
 Ala Glu Glu Asn Asn Gln Ala Pro Lys Asn Thr Pro Pro Glu Leu Asn  
 20 25 30  
 ccc gct aac gct aag ggc gcg cca aac tct aac acc cag atc acc cct 200  
 Pro Ala Asn Ala Lys Gly Ala Pro Asn Ser Asn Thr Gln Ile Thr Pro  
 35 40 45 50  
 aaa aac gat aac tct aac ctg tta gac aaa tta ggt tcg cct gaa aac 248  
 Lys Asn Asp Asn Ser Asn Leu Leu Asp Lys Leu Gly Ser Pro Glu Asn  
 55 60 65  
 gct caa acc gag ctt tct gcc ggt att gat ttg gct aaa aag ggc gat 296  
 Ala Gln Thr Glu Leu Ser Ala Gly Ile Asp Leu Ala Lys Lys Gly Asp  
 70 75 80  
 tat caa ggg gct ttc aag ctt ttt tcc caa tcg tgc gat aat ggt aat 344  
 Tyr Gln Gly Ala Phe Lys Leu Phe Ser Gln Ser Cys Asp Asn Gly Asn  
 85 90 95  
 gcg gcc ggg tgt ttt gca agt ggg ggc gat gta tgc taatggggta 390  
 Ala Ala Gly Cys Phe Ala Ser Gly Gly Asp Val Cys  
 100 105 110  
 gggatccaaa ccaacagatt aaaagccgct cgctattatg aatg 434

<210> 6  
 <211> 110  
 <212> PRT  
 <213> Helicobacter pylori

<400> 6  
 Met Leu Lys Lys Ser Leu Leu Leu Leu Val Phe Leu Val Leu Gln Leu



1				5					10					15			
Ser	Gly	Ala	Glu	Glu	Asn	Asn	Gln	Ala	Pro	Lys	Asn	Thr	Pro	Pro	Glu		
			20					25					30				
Leu	Asn	Pro	Ala	Asn	Ala	Lys	Gly	Ala	Pro	Asn	Ser	Asn	Thr	Gln	Ile		
		35					40					45					
Thr	Pro	Lys	Asn	Asp	Asn	Ser	Asn	Leu	Leu	Asp	Lys	Leu	Gly	Ser	Pro		
	50				55					60							
Glu	Asn	Ala	Gln	Thr	Glu	Leu	Ser	Ala	Gly	Ile	Asp	Leu	Ala	Lys	Lys		
65				70				75						80			
Gly	Asp	Tyr	Gln	Gly	Ala	Phe	Lys	Leu	Phe	Ser	Gln	Ser	Cys	Asp	Asn		
			85					90					95				
Gly	Asn	Ala	Ala	Gly	Cys	Phe	Ala	Ser	Gly	Gly	Asp	Val	Cys				
		100					105					110					

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 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (73)...(522)

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 Met His Gln Asn Asn Lys Thr Phe Leu Pro Ser Gln Ser  
 1 5 10

gct cac ctc tct aaa atc att ctt ttt tta aac acc ggc ttt tta gcc 159  
 Ala His Leu Ser Lys Ile Ile Leu Phe Leu Asn Thr Gly Phe Leu Ala  
 15 20 25

tat ctg tta agc gct tgt ggg gcg aat gtg cct ata gaa gaa gtg ttg 207  
 Tyr Leu Leu Ser Ala Cys Gly Ala Asn Val Pro Ile Glu Glu Val Leu  
 30 35 40 45

ggt aaa gat cct aaa gag acc aaa gcc caa gaa gtc gcc aga gaa gaa 255  
 Val Lys Asp Pro Lys Glu Thr Lys Ala Gln Glu Val Ala Arg Glu Glu  
 50 55 60

aag gct atc cag caa gaa aac gcc act att gat gcg cgc acc acg cct 303  
 Lys Ala Ile Gln Gln Glu Asn Ala Thr Ile Asp Ala Arg Thr Thr Pro  
 65 70 75

tta atc aat cgt ttc act aat tat agc gct tat ggc tct tta aac ggc 351  
 Leu Ile Asn Arg Phe Thr Asn Tyr Ser Ala Tyr Gly Ser Leu Asn Gly  
 80 85 90

ttt tac aat tca gtg gat aat ctc aat tcg ccc atg caa aac ggg atg 399  
 Phe Tyr Asn Ser Val Asp Asn Leu Asn Ser Pro Met Gln Asn Gly Met  
 95 100 105

tat gga ggc tat tac atg cct tat tat tac atg ccc tat ggt ttc atg 447

Tyr Gly Gly Tyr Tyr Met Pro Tyr Tyr Tyr Met Pro Tyr Gly Phe Met  
 110 115 120 125  
 cct tat ggg tca ggt ctt atg cct tat ggg cct tat ggg tat gga gcg 495  
 Pro Tyr Gly Ser Gly Leu Met Pro Tyr Gly Pro Tyr Gly Tyr Gly Ala  
 130 135 140  
 cct gga tac ttc cct tac gct ttt tat tgattgagtg gcttttagaaa 542  
 Pro Gly Tyr Phe Pro Tyr Ala Phe Tyr  
 145 150  
 gcgtgggtggg gttggtgttt ttactcaaac acg 575

<210> 8  
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 <212> PRT  
 <213> Helicobacter pylori

<400> 8  
 Met His Gln Asn Asn Lys Thr Phe Leu Pro Ser Gln Ser Ala His Leu  
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 Ser Lys Ile Ile Leu Phe Leu Asn Thr Gly Phe Leu Ala Tyr Leu Leu  
 20 25 30  
 Ser Ala Cys Gly Ala Asn Val Pro Ile Glu Glu Val Leu Val Lys Asp  
 35 40 45  
 Pro Lys Glu Thr Lys Ala Gln Glu Val Ala Arg Glu Glu Lys Ala Ile  
 50 55 60  
 Gln Gln Glu Asn Ala Thr Ile Asp Ala Arg Thr Thr Pro Leu Ile Asn  
 65 70 75 80  
 Arg Phe Thr Asn Tyr Ser Ala Tyr Gly Ser Leu Asn Gly Phe Tyr Asn  
 85 90 95  
 Ser Val Asp Asn Leu Asn Ser Pro Met Gln Asn Gly Met Tyr Gly Gly  
 100 105 110  
 Tyr Tyr Met Pro Tyr Tyr Tyr Met Pro Tyr Gly Phe Met Pro Tyr Gly  
 115 120 125  
 Ser Gly Leu Met Pro Tyr Gly Pro Tyr Gly Tyr Gly Ala Pro Gly Tyr  
 130 135 140  
 Phe Pro Tyr Ala Phe Tyr  
 145 150

<210> 9  
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> (51)...(860)

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aag ttt gta gtg ttt aaa acg ctc tgt tta tcg gta gtg tta ggt aat	104
Lys Phe Val Val Phe Lys Thr Leu Cys Leu Ser Val Val Leu Gly Asn	
5 10 15	
agt ctt gtg gca gca gaa ggc agc aca gaa gtg caa aag caa ttg gaa	152
Ser Leu Val Ala Ala Glu Gly Ser Thr Glu Val Gln Lys Gln Leu Glu	
20 25 30	
aag cca aaa gag tat aaa gca gtg aaa ggc gag aaa aac gct tgg tat	200
Lys Pro Lys Glu Tyr Lys Ala Val Lys Gly Glu Lys Asn Ala Trp Tyr	
35 40 45 50	
ttg ggg att agc tat caa gtc ggt cag gct tcg caa agc gtt aaa aac	248
Leu Gly Ile Ser Tyr Gln Val Gly Gln Ala Ser Gln Ser Val Lys Asn	
55 60 65	
ccc ccc aaa agc agt gaa ttt aac tac cct aag ttc cct gtg ggt aaa	296
Pro Pro Lys Ser Ser Glu Phe Asn Tyr Pro Lys Phe Pro Val Gly Lys	
70 75 80	
acc gac tat ctg gcc gtt atg caa ggc tta ggg ctt act gtg ggt tat	344
Thr Asp Tyr Leu Ala Val Met Gln Gly Leu Gly Leu Thr Val Gly Tyr	
85 90 95	
aag cag ttt ttc ggg gaa aag aga tgg ttt ggt gca cgc tat tac ggc	392
Lys Gln Phe Phe Gly Glu Lys Arg Trp Phe Gly Ala Arg Tyr Tyr Gly	
100 105 110	
ttc atg gat tat ggg cat gcc gta ttt gga gcg aac gct tta aca tcg	440
Phe Met Asp Tyr Gly His Ala Val Phe Gly Ala Asn Ala Leu Thr Ser	
115 120 125 130	
gat aat ggt ggg gtg tgt gag ctt cac caa cca tgt gcg acc aaa gta	488
Asp Asn Gly Gly Val Cys Glu Leu His Gln Pro Cys Ala Thr Lys Val	
135 140 145	
ggg aca atg ggc aat ctg tct gac atg ttc act tat ggt gtg ggt att	536
Gly Thr Met Gly Asn Leu Ser Asp Met Phe Thr Tyr Gly Val Gly Ile	
150 155 160	
gac act tta tac aat gtc atc aat aaa gaa gat gcg agt ttt ggt ttc	584
Asp Thr Leu Tyr Asn Val Ile Asn Lys Glu Asp Ala Ser Phe Gly Phe	
165 170 175	
ttt ttt ggg gct caa atc gcg ggt aac tct tgg ggt aat acg aca ggg	632
Phe Phe Gly Ala Gln Ile Ala Gly Asn Ser Trp Gly Asn Thr Thr Gly	
180 185 190	
gcc ttt ttg gaa act aaa agc cct tat aag cac act tcc tat agc ctt	680
Ala Phe Leu Glu Thr Lys Ser Pro Tyr Lys His Thr Ser Tyr Ser Leu	
195 200 205 210	
gat ccg gcg att ttc cag ttc ctt ttt aat tta ggg atc cgc acc cat	728
Asp Pro Ala Ile Phe Gln Phe Leu Phe Asn Leu Gly Ile Arg Thr His	
215 220 225	

att ggc cgg cat caa gaa ttt gac ttt ggc gtg aag att ccc act atc 776  
 Ile Gly Arg His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro Thr Ile  
                   230                  235                  240

aat gtt tat tat ttt aac cat ggg aat ttg agc ttc act tac cgc cgt 824  
 Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr Arg Arg  
                   245                  250                  255

caa tac agc ctt tat gtg ggg tat cgt tac aat ttc tgatttaaaa 870  
 Gln Tyr Ser Leu Tyr Val Gly Tyr Arg Tyr Asn Phe  
                   260                  265                  270

cgcttggtttt tctctaattg aattttcaat tagagttttc 910

<210> 10  
 <211> 270  
 <212> PRT  
 <213> Helicobacter pylori

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 Gly Asn Ser Leu Val Ala Ala Glu Gly Ser Thr Glu Val Gln Lys Gln  
                   20                  25                  30  
 Leu Glu Lys Pro Lys Glu Tyr Lys Ala Val Lys Gly Glu Lys Asn Ala  
                   35                  40                  45  
 Trp Tyr Leu Gly Ile Ser Tyr Gln Val Gly Gln Ala Ser Gln Ser Val  
   50                  55                  60  
 Lys Asn Pro Pro Lys Ser Ser Glu Phe Asn Tyr Pro Lys Phe Pro Val  
  65                  70                  75                  80  
 Gly Lys Thr Asp Tyr Leu Ala Val Met Gln Gly Leu Gly Leu Thr Val  
                   85                  90                  95  
 Gly Tyr Lys Gln Phe Phe Gly Glu Lys Arg Trp Phe Gly Ala Arg Tyr  
                   100                  105                  110  
 Tyr Gly Phe Met Asp Tyr Gly His Ala Val Phe Gly Ala Asn Ala Leu  
                   115                  120                  125  
 Thr Ser Asp Asn Gly Gly Val Cys Glu Leu His Gln Pro Cys Ala Thr  
  130                  135                  140  
 Lys Val Gly Thr Met Gly Asn Leu Ser Asp Met Phe Thr Tyr Gly Val  
  145                  150                  155                  160  
 Gly Ile Asp Thr Leu Tyr Asn Val Ile Asn Lys Glu Asp Ala Ser Phe  
                   165                  170                  175  
 Gly Phe Phe Phe Gly Ala Gln Ile Ala Gly Asn Ser Trp Gly Asn Thr  
                   180                  185                  190  
 Thr Gly Ala Phe Leu Glu Thr Lys Ser Pro Tyr Lys His Thr Ser Tyr  
  195                  200                  205  
 Ser Leu Asp Pro Ala Ile Phe Gln Phe Leu Phe Asn Leu Gly Ile Arg  
  210                  215                  220  
 Thr His Ile Gly Arg His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro  
  225                  230                  235                  240  
 Thr Ile Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr  
                   245                  250                  255  
 Arg Arg Gln Tyr Ser Leu Tyr Val Gly Tyr Arg Tyr Asn Phe  
                   260                  265                  270

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<220>  
 <221> CDS  
 <222> (58)...(1305)

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 Gln Tyr Lys Lys Asn Lys Lys Arg Tyr Tyr Tyr Leu Ala Leu Gly Ile  
51015

ttt ttt tta aat ggt ctg tct ttg aaa gct tta gaa atc gcc gtc aaa 156  
 Phe Phe Leu Asn Gly Leu Ser Leu Lys Ala Leu Glu Ile Ala Val Lys  
202530

cct ttt ggc tat ctg ggg cta tta tat aat caa ggg gcg caa aaa aac 204  
 Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Asn Gln Gly Ala Gln Lys Asn  
354045

cct cac agc tat gtg ggg gct tta gcg cgt ctt ggg gtg gat ttt tct 252  
 Pro His Ser Tyr Val Gly Ala Leu Ala Arg Leu Gly Val Asp Phe Ser  
50556065

tat agc aac ggg tgg tcc ttt ggt att gga gcg att ggg gct tgg aat 300  
 Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp Asn  
707580

att tat aac aaa cag cgt ttg gct aac ctt tat atc agt cta ggg aat 348  
 Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly Asn  
859095

ttt ttt ggt agt tct aaa aat gtt aaa cct tat ttg agc gct ggc gat 396  
 Phe Phe Gly Ser Ser Lys Asn Val Lys Pro Tyr Leu Ser Ala Gly Asp  
100105110

gtt tct gat gcg tat gtt caa tac act aac cag cgt ttt aaa atc gct 444  
 Val Ser Asp Ala Tyr Val Gln Tyr Thr Asn Gln Arg Phe Lys Ile Ala  
115120125

tta ggg cgt ttc aat acc gat ttt gtg gat ttt gat tgg ata ggg ggc 492  
 Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly Gly  
130135140145

aat att caa ggg gtt tct gta gct ttt aag caa aat tcc atg cgt tat 540  
 Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg Tyr  
150155160

ttt ggg att ttt atg gat agc atg ctt tat aat ggg cat caa atc aac	588
Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile Asn	
165 170 175	
aaa gag caa ggg aat cgg atc gct act tcc cta aac gct cta gcg tct	636
Lys Glu Gln Gly Asn Arg Ile Ala Thr Ser Leu Asn Ala Leu Ala Ser	
180 185 190	
tat gac cct gtg tct aaa cgc ttg tat gtg ggg ggg gaa gtg ttt gtt	684
Tyr Asp Pro Val Ser Lys Arg Leu Tyr Val Gly Gly Glu Val Phe Val	
195 200 205	
tta ggt gca gaa tac agg cat gaa aat ctt aaa gtg gtg cct ttt att	732
Leu Gly Ala Glu Tyr Arg His Glu Asn Leu Lys Val Val Pro Phe Ile	
210 215 220 225	
tta acg gac acc cgc ttg cct tta tcc acc caa aat gtt tta gtg caa	780
Leu Thr Asp Thr Arg Leu Pro Leu Ser Thr Gln Asn Val Leu Val Gln	
230 235 240	
gtg ggg ggt aag ttg gag tat gac gct tct tta gct aag ggt ttc act	828
Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe Thr	
245 250 255	
tcg cac act cta gtg cat ggc atg tat caa tac ggc aac act gat gcg	876
Ser His Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp Ala	
260 265 270	
gct aca agc gtt aaa aat gcc ggc ttg ttt ttg atc gat caa act ttt	924
Ala Thr Ser Val Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr Phe	
275 280 285	
aaa tac aaa att ttt aat ttt gga acg ggt ttt tat atc gtt ccg gca	972
Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro Ala	
290 295 300 305	
aga aac aat aag ggc tat cta tgg act ttt aat gac agg act aaa ttc	1020
Arg Asn Asn Lys Gly Tyr Leu Trp Thr Phe Asn Asp Arg Thr Lys Phe	
310 315 320	
tat ggc cgt ggg atc aat gcg ccc ggc gtg cca gcg att tat ttt gca	1068
Tyr Gly Arg Gly Ile Asn Ala Pro Gly Val Pro Ala Ile Tyr Phe Ala	
325 330 335	
aac tct agc att tca ggc tat gtt ttt tta ggg ctt aag act aaa agg	1116
Asn Ser Ser Ile Ser Gly Tyr Val Phe Leu Gly Leu Lys Thr Lys Arg	
340 345 350	
gtg cgt tta gac gcg atg gtg gct ttt ggg gat tac caa gaa tat tct	1164
Val Arg Leu Asp Ala Met Val Ala Phe Gly Asp Tyr Gln Glu Tyr Ser	
355 360 365	
tta atg agc agt ttt agg gtt tgg act tat agg agt ttg tct ttt gat	1212
Leu Met Ser Ser Phe Arg Val Trp Thr Tyr Arg Ser Leu Ser Phe Asp	
370 375 380 385	

atg ggt ggg ggg tat gtg tat gct tac aat tct aaa gcc acg aga aaa 1260  
 Met Gly Gly Gly Tyr Val Tyr Ala Tyr Asn Ser Lys Ala Thr Arg Lys  
                   390                  395                  400

agt ctt gga aat agt tct ttt gtc ttt ttt ggg aag ttt ttg ttt 1305  
 Ser Leu Gly Asn Ser Ser Phe Val Phe Phe Gly Lys Phe Leu Phe  
                   405                  410                  415

taaaaaatac catttctaca atcaatagtg aagagtttgc aataaagtaa gc 1357

<210> 12  
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<400> 12  
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   1                  5                  10                  15  
 Ile Phe Phe Leu Asn Gly Leu Ser Leu Lys Ala Leu Glu Ile Ala Val  
                   20                  25                  30  
 Lys Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Asn Gln Gly Ala Gln Lys  
                   35                  40                  45  
 Asn Pro His Ser Tyr Val Gly Ala Leu Ala Arg Leu Gly Val Asp Phe  
   50                  55                  60  
 Ser Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp  
  65                  70                  75                  80  
 Asn Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly  
                   85                  90                  95  
 Asn Phe Phe Gly Ser Ser Lys Asn Val Lys Pro Tyr Leu Ser Ala Gly  
                  100                 105                 110  
 Asp Val Ser Asp Ala Tyr Val Gln Tyr Thr Asn Gln Arg Phe Lys Ile  
                  115                 120                 125  
 Ala Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly  
  130                 135                 140  
 Gly Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg  
  145                 150                 155                 160  
 Tyr Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile  
                  165                 170                 175  
 Asn Lys Glu Gln Gly Asn Arg Ile Ala Thr Ser Leu Asn Ala Leu Ala  
                  180                 185                 190  
 Ser Tyr Asp Pro Val Ser Lys Arg Leu Tyr Val Gly Gly Glu Val Phe  
                  195                 200                 205  
 Val Leu Gly Ala Glu Tyr Arg His Glu Asn Leu Lys Val Val Pro Phe  
  210                 215                 220  
 Ile Leu Thr Asp Thr Arg Leu Pro Leu Ser Thr Gln Asn Val Leu Val  
  225                 230                 235                 240  
 Gln Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe  
                  245                 250                 255  
 Thr Ser His Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp  
                  260                 265                 270  
 Ala Ala Thr Ser Val Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr  
                  275                 280                 285  
 Phe Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro  
  290                 295                 300

Ala	Arg	Asn	Asn	Lys	Gly	Tyr	Leu	Trp	Thr	Phe	Asn	Asp	Arg	Thr	Lys
305					310					315					320
Phe	Tyr	Gly	Arg	Gly	Ile	Asn	Ala	Pro	Gly	Val	Pro	Ala	Ile	Tyr	Phe
				325					330						335
Ala	Asn	Ser	Ser	Ile	Ser	Gly	Tyr	Val	Phe	Leu	Gly	Leu	Lys	Thr	Lys
				340				345					350		
Arg	Val	Arg	Leu	Asp	Ala	Met	Val	Ala	Phe	Gly	Asp	Tyr	Gln	Glu	Tyr
		355					360					365			
Ser	Leu	Met	Ser	Ser	Phe	Arg	Val	Trp	Thr	Tyr	Arg	Ser	Leu	Ser	Phe
	370					375					380				
Asp	Met	Gly	Gly	Gly	Tyr	Val	Tyr	Ala	Tyr	Asn	Ser	Lys	Ala	Thr	Arg
385					390					395					400
Lys	Ser	Leu	Gly	Asn	Ser	Ser	Phe	Val	Phe	Phe	Gly	Lys	Phe	Leu	Phe
				405					410						415

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 <213> Helicobacter pylori

<220>  
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 aaaaggaaaa aa atg aaa aat agc acg cct tta aag aat caa gtt ttt tgt 111  
                   Met Lys Asn Ser Thr Pro Leu Lys Asn Gln Val Phe Cys  
                   1                  5                  10

ggg tta tat gtt tta agt ttg agc gct tct ttg caa gcg ttt gat tat 159  
 Gly Leu Tyr Val Leu Ser Leu Ser Ala Ser Leu Gln Ala Phe Asp Tyr  
           15                  20                  25

aaa att gaa gtt tca gcg gag tcc ttt tct aaa gtt ggc ttt aat aaa 207  
 Lys Ile Glu Val Ser Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Lys  
           30                  35                  40                  45

aaa aag att gat ata gct agg ggg att tat cct aca gag act ttt gta 255  
 Lys Lys Ile Asp Ile Ala Arg Gly Ile Tyr Pro Thr Glu Thr Phe Val  
                   50                  55                  60

acc gct gta ggg cag ggc aat atc tat gcg gat ttt tta ccc aaa ggc 303  
 Thr Ala Val Gly Gln Gly Asn Ile Tyr Ala Asp Phe Leu Pro Lys Gly  
                   65                  70                  75

ctt aaa gat caa ggg cat gtt tta gag gga aaa atc ggt ggc acg cta 351  
 Leu Lys Asp Gln Gly His Val Leu Glu Gly Lys Ile Gly Gly Thr Leu  
           80                  85                  90

gga ggg gtc gct tat gat agc acg aaa ttc aat caa ggc gga tcg gtt 399  
 Gly Gly Val Ala Tyr Asp Ser Thr Lys Phe Asn Gln Gly Gly Ser Val  
           95                  100                  105



att tat aac tac atc ggt tat tgg gat ggc tat tta ggg ggt aaa aga	447
Ile Tyr Asn Tyr Ile Gly Tyr Trp Asp Gly Tyr Leu Gly Gly Lys Arg	
110 115 120 125	
gcc ttg ctt gat ggc acg agt atc cat gag tgc gcg ctt gga tct gat	495
Ala Leu Leu Asp Gly Thr Ser Ile His Glu Cys Ala Leu Gly Ser Asp	
130 135 140	
ggc aag gtg att gat tct ata gcg tgc ggg aac gct agg gcc aat aaa	543
Gly Lys Val Ile Asp Ser Ile Ala Cys Gly Asn Ala Arg Ala Asn Lys	
145 150 155	
atc cgc cgt aat tac ttg atg aat aac gct ttt tta gaa tac cgc tat	591
Ile Arg Arg Asn Tyr Leu Met Asn Asn Ala Phe Leu Glu Tyr Arg Tyr	
160 165 170	
aaa gat att ttt tta gct aag gga ggg cgt tat caa tcc aat gct cct	639
Lys Asp Ile Phe Leu Ala Lys Gly Gly Arg Tyr Gln Ser Asn Ala Pro	
175 180 185	
tat atg agc ggt tac acg caa ggc ttt gaa atc agc gct aaa gtc aag	687
Tyr Met Ser Gly Tyr Thr Gln Gly Phe Glu Ile Ser Ala Lys Val Lys	
190 195 200 205	
gat aaa aat gaa gga atc cac aaa tta tgg tgg ttt agc tca tgg ggt	735
Asp Lys Asn Glu Gly Ile His Lys Leu Trp Trp Phe Ser Ser Trp Gly	
210 215 220	
agg gcg ttc gct tat ggg gag tgg att tat gat ttt tat tct cca aga	783
Arg Ala Phe Ala Tyr Gly Glu Trp Ile Tyr Asp Phe Tyr Ser Pro Arg	
225 230 235	
acc gtg gtt aaa aac ggg cgc act ttg aat tat ggt atc cat tta gtg	831
Thr Val Val Lys Asn Gly Arg Thr Leu Asn Tyr Gly Ile His Leu Val	
240 245 250	
aat tat act tat gaa aga aaa ggg gtt agc gtt agc cct ttt ttc caa	879
Asn Tyr Thr Tyr Glu Arg Lys Gly Val Ser Val Ser Pro Phe Phe Gln	
255 260 265	
ttt tcg cct ggg act tat tat agc cct ggg gtg gtt gta ggc tat gat	927
Phe Ser Pro Gly Thr Tyr Tyr Ser Pro Gly Val Val Val Gly Tyr Asp	
270 275 280 285	
agt aac cct aat ttt aac ggc gtt ggc ttt aga tcc gaa aca aaa gct	975
Ser Asn Pro Asn Phe Asn Gly Val Gly Phe Arg Ser Glu Thr Lys Ala	
290 295 300	
tat att ttg ctc cct gtc cat gac ccc tta aga agg gat act tat cgt	1023
Tyr Ile Leu Leu Pro Val His Asp Pro Leu Arg Arg Asp Thr Tyr Arg	
305 310 315	
tac gct ata aag gct ggc act gcc ggg caa agc ttg ctc att agg caa	1071
Tyr Ala Ile Lys Ala Gly Thr Ala Gly Gln Ser Leu Leu Ile Arg Gln	
320 325 330	

cga ttt gat tac aat gaa ttt aat ttt ggg gga gcg ttt tat aaa gta 1119  
Arg Phe Asp Tyr Asn Glu Phe Asn Phe Gly Gly Ala Phe Tyr Lys Val  
335 340 345  
  
tgg aaa aac gca aac gct tac atc ggc acg aca gga aac cct tta ggc 1167  
Trp Lys Asn Ala Asn Ala Tyr Ile Gly Thr Thr Gly Asn Pro Leu Gly  
350 355 360 365  
  
att gat ttt tgg acc aat agc gtt tat gat ata ggg caa gct tta agc 1215  
Ile Asp Phe Trp Thr Asn Ser Val Tyr Asp Ile Gly Gln Ala Leu Ser  
370 375 380  
  
cat gtg gta acc gct gat gcc gtc tct ggt tgg gtt ttt ggt ggg ggc 1263  
His Val Val Thr Ala Asp Ala Val Ser Gly Trp Val Phe Gly Gly Gly  
385 390 395  
  
gtg cat aaa aag tgg ctg tgg ggg act tta tgg cgt tgg act agc ggc 1311  
Val His Lys Lys Trp Leu Trp Gly Thr Leu Trp Arg Trp Thr Ser Gly  
400 405 410  
  
act tta gcc aat gaa gcg agt gcg gct gtt aat gtg ggc tat aag atc 1359  
Thr Leu Ala Asn Glu Ala Ser Ala Ala Val Asn Val Gly Tyr Lys Ile  
415 420 425  
  
agt aag agt ttg aca gcg agc gtg aaa tta gaa tat ttg ggc gtg atg 1407  
Ser Lys Ser Leu Thr Ala Ser Val Lys Leu Glu Tyr Leu Gly Val Met  
430 435 440 445  
  
acg cat gca ggc ttt acg gta ggg agt tac agg ccc acg ccc ggc tct 1455  
Thr His Ala Gly Phe Thr Val Gly Ser Tyr Arg Pro Thr Pro Gly Ser  
450 455 460  
  
aaa gcg ctt tat tca gac agg agt cat ttg atg aca act ctt agc gct 1503  
Lys Ala Leu Tyr Ser Asp Arg Ser His Leu Met Thr Thr Leu Ser Ala  
465 470 475  
  
aaa ttc taaccaatcg cttaaagctg tttattaaag cgtaaataa cccttaataa 1559  
Lys Phe

aaa 1562

<210> 14

<211> 479

<212> PRT

<213> Helicobacter pylori

<400> 14

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Val Leu Ser Leu Ser Ala Ser Leu Gln Ala Phe Asp Tyr Lys Ile Glu  
20 25 30  
Val Ser Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Lys Lys Lys Ile  
35 40 45

Asp	Ile	Ala	Arg	Gly	Ile	Tyr	Pro	Thr	Glu	Thr	Phe	Val	Thr	Ala	Val
50						55					60				
Gly	Gln	Gly	Asn	Ile	Tyr	Ala	Asp	Phe	Leu	Pro	Lys	Gly	Leu	Lys	Asp
65					70					75					80
Gln	Gly	His	Val	Leu	Glu	Gly	Lys	Ile	Gly	Gly	Thr	Leu	Gly	Gly	Val
				85					90					95	
Ala	Tyr	Asp	Ser	Thr	Lys	Phe	Asn	Gln	Gly	Gly	Ser	Val	Ile	Tyr	Asn
			100					105					110		
Tyr	Ile	Gly	Tyr	Trp	Asp	Gly	Tyr	Leu	Gly	Gly	Lys	Arg	Ala	Leu	Leu
		115					120					125			
Asp	Gly	Thr	Ser	Ile	His	Glu	Cys	Ala	Leu	Gly	Ser	Asp	Gly	Lys	Val
130						135					140				
Ile	Asp	Ser	Ile	Ala	Cys	Gly	Asn	Ala	Arg	Ala	Asn	Lys	Ile	Arg	Arg
145					150					155					160
Asn	Tyr	Leu	Met	Asn	Asn	Ala	Phe	Leu	Glu	Tyr	Arg	Tyr	Lys	Asp	Ile
				165					170					175	
Phe	Leu	Ala	Lys	Gly	Gly	Arg	Tyr	Gln	Ser	Asn	Ala	Pro	Tyr	Met	Ser
			180					185					190		
Gly	Tyr	Thr	Gln	Gly	Phe	Glu	Ile	Ser	Ala	Lys	Val	Lys	Asp	Lys	Asn
		195					200					205			
Glu	Gly	Ile	His	Lys	Leu	Trp	Trp	Phe	Ser	Ser	Trp	Gly	Arg	Ala	Phe
210						215					220				
Ala	Tyr	Gly	Glu	Trp	Ile	Tyr	Asp	Phe	Tyr	Ser	Pro	Arg	Thr	Val	Val
225					230					235					240
Lys	Asn	Gly	Arg	Thr	Leu	Asn	Tyr	Gly	Ile	His	Leu	Val	Asn	Tyr	Thr
				245					250					255	
Tyr	Glu	Arg	Lys	Gly	Val	Ser	Val	Ser	Pro	Phe	Phe	Gln	Phe	Ser	Pro
			260					265					270		
Gly	Thr	Tyr	Tyr	Ser	Pro	Gly	Val	Val	Val	Gly	Tyr	Asp	Ser	Asn	Pro
		275				280						285			
Asn	Phe	Asn	Gly	Val	Gly	Phe	Arg	Ser	Glu	Thr	Lys	Ala	Tyr	Ile	Leu
290						295					300				
Leu	Pro	Val	His	Asp	Pro	Leu	Arg	Arg	Asp	Thr	Tyr	Arg	Tyr	Ala	Ile
305					310					315					320
Lys	Ala	Gly	Thr	Ala	Gly	Gln	Ser	Leu	Leu	Ile	Arg	Gln	Arg	Phe	Asp
				325					330					335	
Tyr	Asn	Glu	Phe	Asn	Phe	Gly	Gly	Ala	Phe	Tyr	Lys	Val	Trp	Lys	Asn
			340					345					350		
Ala	Asn	Ala	Tyr	Ile	Gly	Thr	Thr	Gly	Asn	Pro	Leu	Gly	Ile	Asp	Phe
		355					360					365			
Trp	Thr	Asn	Ser	Val	Tyr	Asp	Ile	Gly	Gln	Ala	Leu	Ser	His	Val	Val
370						375					380				
Thr	Ala	Asp	Ala	Val	Ser	Gly	Trp	Val	Phe	Gly	Gly	Gly	Val	His	Lys
385					390					395					400
Lys	Trp	Leu	Trp	Gly	Thr	Leu	Trp	Arg	Trp	Thr	Ser	Gly	Thr	Leu	Ala
			405						410					415	
Asn	Glu	Ala	Ser	Ala	Ala	Val	Asn	Val	Gly	Tyr	Lys	Ile	Ser	Lys	Ser
			420					425					430		
Leu	Thr	Ala	Ser	Val	Lys	Leu	Glu	Tyr	Leu	Gly	Val	Met	Thr	His	Ala
		435					440					445			
Gly	Phe	Thr	Val	Gly	Ser	Tyr	Arg	Pro	Thr	Pro	Gly	Ser	Lys	Ala	Leu
	450					455					460				
Tyr	Ser	Asp	Arg	Ser	His	Leu	Met	Thr	Thr	Leu	Ser	Ala	Lys	Phe	
465					470					475					

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 <211> 810  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (98)...(757)

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 ggcaagtgtg gggcaggata acataaggaa ttgggtt atg aat aaa aca acg gtt 115  
 Met Asn Lys Thr Thr Val  
 1 5

aaa ata tta atg ggc atg gcg tta tta tca tcg ctt caa gcc gca gag 163  
 Lys Ile Leu Met Gly Met Ala Leu Leu Ser Ser Leu Gln Ala Ala Glu  
 10 15 20

gca gag ctt gat gaa aaa tca aaa aaa cct aaa ttt gcg gac agg aat 211  
 Ala Glu Leu Asp Glu Lys Ser Lys Lys Pro Lys Phe Ala Asp Arg Asn  
 25 30 35

aca ttt tat tta ggg gtt ggg tat caa ctt agt gcg atc aac aca tct 259  
 Thr Phe Tyr Leu Gly Val Gly Tyr Gln Leu Ser Ala Ile Asn Thr Ser  
 40 45 50

ttt agc acc gag tct gta gat aaa tcg tat ttt atg acc ggc aat ggc 307  
 Phe Ser Thr Glu Ser Val Asp Lys Ser Tyr Phe Met Thr Gly Asn Gly  
 55 60 65 70

ttt ggt gtg gtg tta ggg ggg aaa ttt gtg gct aaa acg caa gct gta 355  
 Phe Gly Val Val Leu Gly Gly Lys Phe Val Ala Lys Thr Gln Ala Val  
 75 80 85

gag cat gtg ggt ttc cgt tac ggg ttg ttt tat gat cag acc ttt tct 403  
 Glu His Val Gly Phe Arg Tyr Gly Leu Phe Tyr Asp Gln Thr Phe Ser  
 90 95 100

tct cac aaa tcc tat att tct acc tat ggt tta gaa ttt agc ggt ttg 451  
 Ser His Lys Ser Tyr Ile Ser Thr Tyr Gly Leu Glu Phe Ser Gly Leu  
 105 110 115

tgg gac gct ttc aat tcg cca aag atg ttt tta ggg tta gag ttt ggc 499  
 Trp Asp Ala Phe Asn Ser Pro Lys Met Phe Leu Gly Leu Glu Phe Gly  
 120 125 130

tta ggc atc gct ggg gcg act tat atg cca gga ggg gct atg cat ggg 547  
 Leu Gly Ile Ala Gly Ala Thr Tyr Met Pro Gly Gly Ala Met His Gly  
 135 140 145 150

att atc gct caa aat tta ggc aaa gaa aat tcg ctt ttc caa ttg ctt 595  
 Ile Ile Ala Gln Asn Leu Gly Lys Glu Asn Ser Leu Phe Gln Leu Leu  
 155 160 165

gtg aaa gtg ggt ttt cgt ttt ggc ttt ttg cac aat gaa atc act ttc 643  
Val Lys Val Gly Phe Arg Phe Gly Phe Leu His Asn Glu Ile Thr Phe  
170 175 180

ggg ttg aaa ttc cct gtc att cct aac aaa aga acg gaa atc att gat 691  
Gly Leu Lys Phe Pro Val Ile Pro Asn Lys Arg Thr Glu Ile Ile Asp  
185 190 195

ggc ttg agc acg act act tta tgg cac cgc tta ccg gta gct tat ttc 739  
Gly Leu Ser Thr Thr Thr Leu Trp His Arg Leu Pro Val Ala Tyr Phe  
200 205 210

aat tat atc tat aat ttt tagatatggg tatttagagg ttttagattt 787  
Asn Tyr Ile Tyr Asn Phe  
215 220

gacaaaatca atcaactctc gtg 810

<210> 16  
<211> 220  
<212> PRT  
<213> Helicobacter pylori

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1 5 10 15  
Ser Leu Gln Ala Ala Glu Ala Glu Leu Asp Glu Lys Ser Lys Lys Pro  
20 25 30  
Lys Phe Ala Asp Arg Asn Thr Phe Tyr Leu Gly Val Gly Tyr Gln Leu  
35 40 45  
Ser Ala Ile Asn Thr Ser Phe Ser Thr Glu Ser Val Asp Lys Ser Tyr  
50 55 60  
Phe Met Thr Gly Asn Gly Phe Gly Val Val Leu Gly Gly Lys Phe Val  
65 70 75 80  
Ala Lys Thr Gln Ala Val Glu His Val Gly Phe Arg Tyr Gly Leu Phe  
85 90 95  
Tyr Asp Gln Thr Phe Ser Ser His Lys Ser Tyr Ile Ser Thr Tyr Gly  
100 105 110  
Leu Glu Phe Ser Gly Leu Trp Asp Ala Phe Asn Ser Pro Lys Met Phe  
115 120 125  
Leu Gly Leu Glu Phe Gly Leu Gly Ile Ala Gly Ala Thr Tyr Met Pro  
130 135 140  
Gly Gly Ala Met His Gly Ile Ile Ala Gln Asn Leu Gly Lys Glu Asn  
145 150 155 160  
Ser Leu Phe Gln Leu Leu Val Lys Val Gly Phe Arg Phe Gly Phe Leu  
165 170 175  
His Asn Glu Ile Thr Phe Gly Leu Lys Phe Pro Val Ile Pro Asn Lys  
180 185 190  
Arg Thr Glu Ile Ile Asp Gly Leu Ser Thr Thr Thr Leu Trp His Arg  
195 200 205  
Leu Pro Val Ala Tyr Phe Asn Tyr Ile Tyr Asn Phe  
210 215 220

<210> 17

<211> 1516  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1463)

<400> 17  
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Met Lys  
1

aag gca agt cag gtt tta ttc ttt ggg gca ttt tta agc tct tct ttg 104  
 Lys Ala Ser Gln Val Leu Phe Phe Gly Ala Phe Leu Ser Ser Ser Leu  
5 10 15

caa ggt ttt gaa gct aag ctc aac ggc ttt gtg gat caa tcc agc act 152  
 Gln Gly Phe Glu Ala Lys Leu Asn Gly Phe Val Asp Gln Ser Ser Thr  
20 25 30

atc ggt ttt aac cag cat aaa atc aat aaa gaa aga ggt atc tac cct 200  
 Ile Gly Phe Asn Gln His Lys Ile Asn Lys Glu Arg Gly Ile Tyr Pro  
35 40 45 50

atg cag caa ttc gca acg att gcg ggc tat tta ggg ctt ggt ttt agc 248  
 Met Gln Gln Phe Ala Thr Ile Ala Gly Tyr Leu Gly Leu Gly Phe Ser  
55 60 65

ctg tta ccc aaa aag gtt tca gac cat gtt cta aaa ggc aaa ata gga 296  
 Leu Leu Pro Lys Lys Val Ser Asp His Val Leu Lys Gly Lys Ile Gly  
70 75 80

ggc atg gtg gga tct att ttc tat gat ggc acg aag aag ttt gaa gac 344  
 Gly Met Val Gly Ser Ile Phe Tyr Asp Gly Thr Lys Lys Phe Glu Asp  
85 90 95

agc tct gta gct tac aac ctc ttt ggt tat tat gat ggg ttc atg ggg 392  
 Ser Ser Val Ala Tyr Asn Leu Phe Gly Tyr Tyr Asp Gly Phe Met Gly  
100 105 110

ggt tat aca aac atc tta caa agc gat gat tta gcg aca caa aac atg 440  
 Gly Tyr Thr Asn Ile Leu Gln Ser Asp Asp Leu Ala Thr Gln Asn Met  
115 120 125 130

aaa tac aat aaa aat gtc cgc aac tat gtc ttt agc gac gcg tat tta 488  
 Lys Tyr Asn Lys Asn Val Arg Asn Tyr Val Phe Ser Asp Ala Tyr Leu  
135 140 145

gaa tac gct tat aag aat tat ttt gaa ata aaa gcc ggg cgc tat tta 536  
 Glu Tyr Ala Tyr Lys Asn Tyr Phe Glu Ile Lys Ala Gly Arg Tyr Leu  
150 155 160

tcc act atg cct tat aaa agc ggt caa acg caa ggc ttt caa att tct 584  
 Ser Thr Met Pro Tyr Lys Ser Gly Gln Thr Gln Gly Phe Gln Ile Ser

165	170	175	
ggg caa tac aag aaa gcg cgc ttg act tgg ttt agc tct ttt ggg agg			632
Gly Gln Tyr Lys Lys Ala Arg Leu Thr Trp Phe Ser Ser Phe Gly Arg			
180	185	190	
gcg ttc gct tac ggc tcg ttt ttg atg gat tgg ttt gcc gct agg acc			680
Ala Phe Ala Tyr Gly Ser Phe Leu Met Asp Trp Phe Ala Ala Arg Thr			
195	200	205	210
act tat agc gga ggt ttt acc aaa aac gat aag gga ggt tat gat agc			728
Thr Tyr Ser Gly Gly Phe Thr Lys Asn Asp Lys Gly Gly Tyr Asp Ser			
	215	220	225
cat ggg cga aag gtg ctt tat ggc acg cat gcg gtg caa ctc acc tat			776
His Gly Arg Lys Val Leu Tyr Gly Thr His Ala Val Gln Leu Thr Tyr			
	230	235	240
aaa cct cat cgt ttc ctc ata gaa ggc ttt tat tac ctt tcg cct caa			824
Lys Pro His Arg Phe Leu Ile Glu Gly Phe Tyr Tyr Leu Ser Pro Gln			
	245	250	255
atc ttt aac gct ccg ggc gtt aag att ggt tgg gat tct aac cct aat			872
Ile Phe Asn Ala Pro Gly Val Lys Ile Gly Trp Asp Ser Asn Pro Asn			
	260	265	270
ttt agc ggc aca ggc ttt cgc tct gat aca gct atc ata ggg ttt ttc			920
Phe Ser Gly Thr Gly Phe Arg Ser Asp Thr Ala Ile Ile Gly Phe Phe			
275	280	285	290
ccc att tac tac cct tgg atg atc gtt aaa tcc aat gga agc ccg gtc			968
Pro Ile Tyr Tyr Pro Trp Met Ile Val Lys Ser Asn Gly Ser Pro Val			
	295	300	305
tat aaa tac gac acg cct gcc act caa aat ggg caa aac ctc att atc			1016
Tyr Lys Tyr Asp Thr Pro Ala Thr Gln Asn Gly Gln Asn Leu Ile Ile			
	310	315	320
ctc caa cgc ttt gac atc aac aat tac aat gtt tcc atc gct ttt tat			1064
Leu Gln Arg Phe Asp Ile Asn Asn Tyr Asn Val Ser Ile Ala Phe Tyr			
	325	330	335
aaa gtc ttt caa aac gct aat ggt tgg ata ggc aac atg ggg aat cca			1112
Lys Val Phe Gln Asn Ala Asn Gly Trp Ile Gly Asn Met Gly Asn Pro			
	340	345	350
agc ggt gtg atc atg ggg agt aac agc gtc tat gcg ggt ttt aca ggc			1160
Ser Gly Val Ile Met Gly Ser Asn Ser Val Tyr Ala Gly Phe Thr Gly			
355	360	365	370
aca gcc ctt aaa aga gat gcc gct acc att ttc ctt tct tgt ggc ggc			1208
Thr Ala Leu Lys Arg Asp Ala Ala Thr Ile Phe Leu Ser Cys Gly Gly			
	375	380	385
act cat ttt gcc aaa aaa ttc aca tgg aaa ttc gcc acg caa tac tcc			1256

Thr	His	Phe	Ala	Lys	Lys	Phe	Thr	Trp	Lys	Phe	Ala	Thr	Gln	Tyr	Ser		
			390					395					400				
aat	tca	gtg	ggt	tct	tgg	gaa	gcg	aga	gcg	atg	atc	tct	tta	ggg	tat	1304	
Asn	Ser	Val	Val	Ser	Trp	Glu	Ala	Arg	Ala	Met	Ile	Ser	Leu	Gly	Tyr		
		405					410					415					
aaa	ttc	act	gaa	tac	ttg	agc	ggg	agc	gtg	gat	ctt	gca	tat	tat	ggc	1352	
Lys	Phe	Thr	Glu	Tyr	Leu	Ser	Gly	Ser	Val	Asp	Leu	Ala	Tyr	Tyr	Gly		
		420				425					430						
gtg	tat	act	aac	aaa	gga	ttt	aaa	ccg	ggg	gaa	aac	ggg	cct	gtg	cct	1400	
Val	Tyr	Thr	Asn	Lys	Gly	Phe	Lys	Pro	Gly	Glu	Asn	Gly	Pro	Val	Pro		
435					440					445					450		
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Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Ala Leu
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Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys
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Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile
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Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu
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gcg gac aag gtg cgt tat gac act aaa acc aaa gaa gcg tta tta gag 299
Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu
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Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp
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Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe
100 105 110

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Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala
115 120 125

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Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly
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Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser
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Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp	
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Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser	
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Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro	
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Gly Gly Gly Val Gly Gly Ala Val Gly Gly Ala Val Gly Gly Pro Ala  
55 60 65

ggt ggt tgg gct ggc aga tta gtt ggt ggt tct gtg ggg aga gag ttt 296  
Gly Gly Trp Ala Gly Arg Leu Val Gly Gly Ser Val Gly Arg Glu Phe  
70 75 80

ggt cgg gaa ata ggc gat agg gta gaa gat tac atc cgt ggc gtt gat 344  
Gly Arg Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly Val Asp  
85 90 95

aga gag cca caa gcc cca aga gaa ccc acc tat gat cgt cat ttc gtg 392  
Arg Glu Pro Gln Ala Pro Arg Glu Pro Thr Tyr Asp Arg His Phe Val  
100 105 110

tat gac agg tagctttggg cgagaaagga gagagcatga atgtcaaaaa 441  
Tyr Asp Arg  
115

tcgtttgagc gat 454

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<212> PRT  
<213> Helicobacter pylori

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Val Leu Cys Gly Ala Met Ala Asn Thr Ala Ile Ala Gly Pro Lys Ile  
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Glu Ala Arg Gly Glu Phe Gly Arg Phe Trp Gly Gly Ala Val Gly Gly  
35 40 45  
Ala Ile Gly Gly Gly Val Gly Gly Ala Val Gly Gly Ala Val Gly Gly  
50 55 60  
Pro Ala Gly Gly Trp Ala Gly Arg Leu Val Gly Gly Ser Val Gly Arg  
65 70 75 80  
Glu Phe Gly Arg Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly



				85						90					95				
Val	Asp	Arg	Glu	Pro	Gln	Ala	Pro	Arg	Glu	Pro	Thr	Tyr	Asp	Arg	His				
			100					105					110						
Phe	Val	Tyr	Asp	Arg															
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 atg ttg aaa aga atg ata tta tta ggg gct ttg ggt gtt tta gcg agc 106  
 Met Leu Lys Arg Met Ile Leu Leu Gly Ala Leu Gly Val Leu Ala Ser  
 1 5 10 15  
  
 gct gaa gag agt gcg gct ttt gtg gga gtc aat tac cag gtg agc atg 154  
 Ala Glu Glu Ser Ala Ala Phe Val Gly Val Asn Tyr Gln Val Ser Met  
 20 25 30  
  
 ata caa aat cag act aaa atg gtg aat gac aac ggc ttg caa aag cct 202  
 Ile Gln Asn Gln Thr Lys Met Val Asn Asp Asn Gly Leu Gln Lys Pro  
 35 40 45  
  
 ttg ata aag ttt ccg cct tac gca gga gcg ggt ttt gaa gtg ggc tat 250  
 Leu Ile Lys Phe Pro Pro Tyr Ala Gly Ala Gly Phe Glu Val Gly Tyr  
 50 55 60  
  
 aag caa ttt ttt ggt aag aaa aaa tgg ttt ggc atg cgt tat tat ggg 298  
 Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Met Arg Tyr Tyr Gly  
 65 70 75 80  
  
 ttt ttt gac tac gcg cac aac cgc ttt ggc gtg atg aaa aag ggc att 346  
 Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile  
 85 90 95  
  
 ccg gtg ggc gat agt ggg ttt att tac aat agt ttt agt ttt gga ggg 394  
 Pro Val Gly Asp Ser Gly Phe Ile Tyr Asn Ser Phe Ser Phe Gly Gly  
 100 105 110  
  
 aac act tta acg gaa agg gat tcc tat cag ggg caa tac tat gtc aat 442  
 Asn Thr Leu Thr Glu Arg Asp Ser Tyr Gln Gly Gln Tyr Tyr Val Asn  
 115 120 125  
  
 tta ttc act tat ggc gtg ggg tta gat acg ctg tgg aat ttt gtg aat 490  
 Leu Phe Thr Tyr Gly Val Gly Leu Asp Thr Leu Trp Asn Phe Val Asn  
 130 135 140  
  
 aaa gaa aac atg gtt ttt ggt ttt gtg gtg ggg atc caa tta gcg ggg 538

Lys Glu Asn Met Val Phe Gly Phe Val Val Gly Ile Gln Leu Ala Gly  
 145 150 155 160

gat agt tgg gca acg agc atc agt aaa gaa atc gct cat tat gca aaa 586  
 Asp Ser Trp Ala Thr Ser Ile Ser Lys Glu Ile Ala His Tyr Ala Lys  
 165 170 175

cac cac agc aat tcc agt tat agc ccg gcc aat ttc cag ttt tta tgg 634  
 His His Ser Asn Ser Ser Tyr Ser Pro Ala Asn Phe Gln Phe Leu Trp  
 180 185 190

aag ttt ggg gtc cgc acc cat atc gct aaa cac aat agc cta gaa tta 682  
 Lys Phe Gly Val Arg Thr His Ile Ala Lys His Asn Ser Leu Glu Leu  
 195 200 205

ggg att aaa gtg cct acg atc aca cac cag ctt ttc tct ctt acc aac 730  
 Gly Ile Lys Val Pro Thr Ile Thr His Gln Leu Phe Ser Leu Thr Asn  
 210 215 220

gaa aag gga tac acc tta cag gct gat gtg cgt aga gtt tat gcg ttt 778  
 Glu Lys Gly Tyr Thr Leu Gln Ala Asp Val Arg Arg Val Tyr Ala Phe  
 225 230 235 240

caa atc agt tac ttg agg gat ttt taacccttt ttagatacaa tcacgcctga 832  
 Gln Ile Ser Tyr Leu Arg Asp Phe  
 245

aactatccat ttaaaggtgt gaaa 856

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 <211> 248  
 <212> PRT  
 <213> Helicobacter pylori

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 Ile Gln Asn Gln Thr Lys Met Val Asn Asp Asn Gly Leu Gln Lys Pro  
 35 40 45  
 Leu Ile Lys Phe Pro Pro Tyr Ala Gly Ala Gly Phe Glu Val Gly Tyr  
 50 55 60  
 Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Met Arg Tyr Tyr Gly  
 65 70 75 80  
 Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile  
 85 90 95  
 Pro Val Gly Asp Ser Gly Phe Ile Tyr Asn Ser Phe Ser Phe Gly Gly  
 100 105 110  
 Asn Thr Leu Thr Glu Arg Asp Ser Tyr Gln Gly Gln Tyr Tyr Val Asn  
 115 120 125  
 Leu Phe Thr Tyr Gly Val Gly Leu Asp Thr Leu Trp Asn Phe Val Asn  
 130 135 140  
 Lys Glu Asn Met Val Phe Gly Phe Val Val Gly Ile Gln Leu Ala Gly  
 145 150 155 160

Asp	Ser	Trp	Ala	Thr	Ser	Ile	Ser	Lys	Glu	Ile	Ala	His	Tyr	Ala	Lys
				165					170					175	
His	His	Ser	Asn	Ser	Ser	Tyr	Ser	Pro	Ala	Asn	Phe	Gln	Phe	Leu	Trp
			180					185					190		
Lys	Phe	Gly	Val	Arg	Thr	His	Ile	Ala	Lys	His	Asn	Ser	Leu	Glu	Leu
		195					200				205				
Gly	Ile	Lys	Val	Pro	Thr	Ile	Thr	His	Gln	Leu	Phe	Ser	Leu	Thr	Asn
	210					215					220				
Glu	Lys	Gly	Tyr	Thr	Leu	Gln	Ala	Asp	Val	Arg	Arg	Val	Tyr	Ala	Phe
225					230					235					240
Gln	Ile	Ser	Tyr	Leu	Arg	Asp	Phe								
				245											

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<211> 2750

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (69)...(2699)

<400> 27

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Met	Leu	Arg	Asn	Gln	Phe	Arg	Ile	Val	Phe	Val	Ser	Cys	Ile
1				5					10				

gtc	gct	agc	aat	ttg	caa	gct	caa	gaa	aca	acc	cac	act	ttg	ggt	aag	158
Val	Ala	Ser	Asn	Leu	Gln	Ala	Gln	Glu	Thr	Thr	His	Thr	Leu	Gly	Lys	
15					20				25					30		

gta	acc	act	aag	ggt	gaa	agg	act	ttt	gaa	tac	aac	aat	aaa	atg	tat	206
Val	Thr	Thr	Lys	Gly	Glu	Arg	Thr	Phe	Glu	Tyr	Asn	Asn	Lys	Met	Tyr	
				35					40					45		

att	gac	aga	aaa	gag	ctc	caa	caa	cgc	caa	agt	aac	caa	atc	cgt	gat	254
Ile	Asp	Arg	Lys	Glu	Leu	Gln	Gln	Arg	Gln	Ser	Asn	Gln	Ile	Arg	Asp	
			50					55					60			

att	ttt	agg	act	aga	gcg	gat	gtg	aat	gtg	gcc	agt	ggg	ggc	ttg	atg	302
Ile	Phe	Arg	Thr	Arg	Ala	Asp	Val	Asn	Val	Ala	Ser	Gly	Gly	Leu	Met	
			65				70					75				

gcg	caa	aag	atc	tat	gtt	agg	ggg	att	gag	agc	cgt	ctc	tta	agg	gta	350
Ala	Gln	Lys	Ile	Tyr	Val	Arg	Gly	Ile	Glu	Ser	Arg	Leu	Leu	Arg	Val	
	80					85					90					

aca	ata	gat	ggc	gtc	gcc	caa	aat	ggt	aac	att	ttc	cac	cat	gac	gct	398
Thr	Ile	Asp	Gly	Val	Ala	Gln	Asn	Gly	Asn	Ile	Phe	His	His	Asp	Ala	
	95				100				105						110	

aac	acc	gtg	atc	gat	cct	aac	atg	att	aaa	gaa	gtg	gaa	gtg	atc	aag	446
Asn	Thr	Val	Ile	Asp	Pro	Asn	Met	Ile	Lys	Glu	Val	Glu	Val	Ile	Lys	

115										120					125					
ggg	gcg	gcg	aac	gct	tca	gca	ggc	cca	ggg	gcg	gtg	gcg	ggg	aaa	ttg	494				
Gly	Ala	Ala	Asn	Ala	Ser	Ala	Gly	Pro	Gly	Ala	Val	Ala	Gly	Lys	Leu					
			130				135						140							
tct	ttc	acc	acg	att	gac	gct	aac	gac	ttc	tta	aga	aag	aat	caa	act	542				
Ser	Phe	Thr	Thr	Ile	Asp	Ala	Asn	Asp	Phe	Leu	Arg	Lys	Asn	Gln	Thr					
			145				150						155							
tat	ggc	gct	aaa	gcg	gaa	gcg	gcc	ttt	tat	acc	aac	ttc	ggg	tat	cgc	590				
Tyr	Gly	Ala	Lys	Ala	Glu	Ala	Ala	Phe	Tyr	Thr	Asn	Phe	Gly	Tyr	Arg					
			160				165						170							
atg	aac	gcc	act	gcg	gct	tac	cgg	ggg	aaa	aac	tgg	gac	atc	cta	gcc	638				
Met	Asn	Ala	Thr	Ala	Ala	Tyr	Arg	Gly	Lys	Asn	Trp	Asp	Ile	Leu	Ala					
			175				180						185							
tat	tac	aac	cat	caa	aat	att	ttt	tac	tac	aga	gac	ggg	aac	aac	gct	686				
Tyr	Tyr	Asn	His	Gln	Asn	Ile	Phe	Tyr	Tyr	Arg	Asp	Gly	Asn	Asn	Ala					
			195				200						205							
ttt	agg	aat	gtc	ttc	cac	cct	aac	tac	gat	tta	caa	gat	cca	agc	aat	734				
Phe	Arg	Asn	Val	Phe	His	Pro	Asn	Tyr	Asp	Leu	Gln	Asp	Pro	Ser	Asn					
			210				215						220							
agc	gat	atg	agc	gta	ggg	act	ccc	agt	gaa	gtc	aat	agc	gtt	tta	gct	782				
Ser	Asp	Met	Ser	Val	Gly	Thr	Pro	Ser	Glu	Val	Asn	Ser	Val	Leu	Ala					
			225				230						235							
aaa	att	aat	ggc	tat	atc	aac	gaa	aca	gac	agc	att	agc	gtg	agc	tac	830				
Lys	Ile	Asn	Gly	Tyr	Ile	Asn	Glu	Thr	Asp	Ser	Ile	Ser	Val	Ser	Tyr					
			240				245						250							
aac	ctc	aca	cga	gac	aat	tct	aca	agg	ctt	tta	cgc	cct	aac	acc	act	878				
Asn	Leu	Thr	Arg	Asp	Asn	Ser	Thr	Arg	Leu	Leu	Arg	Pro	Asn	Thr	Thr					
			255				260						270							
tca	gcc	ctc	tct	aaa	gcc	aat	gac	cca	gga	agc	cag	cca	gcc	ccc	ttt	926				
Ser	Ala	Leu	Ser	Lys	Ala	Asn	Asp	Pro	Gly	Ser	Gln	Pro	Ala	Pro	Phe					
			275				280						285							
gtg	att	gac	ttt	ggg	aaa	gaa	tta	gcc	cat	acg	atc	aac	ttc	aac	cac	974				
Val	Ile	Asp	Phe	Gly	Lys	Glu	Leu	Ala	His	Thr	Ile	Asn	Phe	Asn	His					
			290				295						300							
aat	ttg	agc	ttg	aaa	tac	aag	cat	gaa	ggc	ggc	cct	aat	ttt	aac	cag	1022				
Asn	Leu	Ser	Leu	Lys	Tyr	Lys	His	Glu	Gly	Gly	Pro	Asn	Phe	Asn	Gln					
			305				310						315							
ccg	cgc	gtt	gaa	tcc	acc	gcc	ttt	tta	ggg	gta	agg	ggg	ggc	aat	tat	1070				
Pro	Arg	Val	Glu	Ser	Thr	Ala	Phe	Leu	Gly	Val	Arg	Gly	Gly	Asn	Tyr					
			320				325						330							
aac	cct	gtg	gtg	aat	cct	ttc	gct	tac	aat	tct	aac	gag	ccg	gct	aac	1118				

Asn	Pro	Val	Val	Asn	Pro	Phe	Ala	Tyr	Asn	Ser	Asn	Glu	Pro	Ala	Asn	
335					340					345					350	
cca	gat	tat	atc	cct	gaa	gtg	aaa	gag	tgg	tgt	aat	aac	cca	gat	aat	1166
Pro	Asp	Tyr	Ile	Pro	Glu	Val	Lys	Glu	Trp	Cys	Asn	Asn	Pro	Asp	Asn	
				355					360					365		
atc	agc	cag	tgc	acg	caa	ggg	gct	atc	agg	cct	tct	aat	gga	ggc	tat	1214
Ile	Ser	Gln	Cys	Thr	Gln	Gly	Ala	Ile	Arg	Pro	Ser	Asn	Gly	Gly	Tyr	
			370					375					380			
caa	ata	ggc	tat	ggc	acg	cct	aat	tct	att	aat	tgg	caa	ggg	act	agc	1262
Gln	Ile	Gly	Tyr	Gly	Thr	Pro	Asn	Ser	Ile	Asn	Trp	Gln	Gly	Thr	Ser	
		385					390					395				
gat	tct	agt	gga	ggg	gcg	caa	gca	ggg	tat	ggg	cag	ctt	aac	gct	att	1310
Asp	Ser	Ser	Gly	Gly	Ala	Gln	Ala	Gly	Tyr	Gly	Gln	Leu	Asn	Ala	Ile	
	400					405					410					
tct	aca	agc	gcg	aac	gtt	tat	cat	ggg	ctt	gtc	cct	aaa	aat	cct	gat	1358
Ser	Thr	Ser	Ala	Asn	Val	Tyr	His	Gly	Leu	Val	Pro	Lys	Asn	Pro	Asp	
415					420					425					430	
tat	gac	atg	acc	ccc	cct	aac	gct	caa	aac	cct	agc	gca	aac	gat	tgg	1406
Tyr	Asp	Met	Thr	Pro	Pro	Asn	Ala	Gln	Asn	Pro	Ser	Ala	Asn	Asp	Trp	
				435					440					445		
act	tta	ggg	aat	gcg	gac	gct	gag	ggg	act	tta	gcc	aga	agg	att	ttt	1454
Thr	Leu	Gly	Asn	Ala	Asp	Ala	Glu	Gly	Thr	Leu	Ala	Arg	Arg	Ile	Phe	
			450					455					460			
tta	atc	aac	tcg	ggc	gtt	aat	ttt	aaa	gta	acc	cac	ccc	att	agc	gaa	1502
Leu	Ile	Asn	Ser	Gly	Val	Asn	Phe	Lys	Val	Thr	His	Pro	Ile	Ser	Glu	
		465					470					475				
gat	tat	ggg	aat	gtg	ttt	gaa	tac	ggc	atg	att	tat	caa	aac	ctg	agc	1550
Asp	Tyr	Gly	Asn	Val	Phe	Glu	Tyr	Gly	Met	Ile	Tyr	Gln	Asn	Leu	Ser	
	480					485					490					
gtt	ttc	tct	gga	ttg	gat	aaa	ggc	aaa	aac	ggc	tat	tat	aaa	aac	aac	1598
Val	Phe	Ser	Gly	Leu	Asp	Lys	Gly	Lys	Asn	Gly	Tyr	Tyr	Lys	Asn	Asn	
495					500					505					510	
att	gat	cct	aac	gac	cct	aac	ggg	ccg	ggc	ttg	cct	tac	cgc	cat	tac	1646
Ile	Asp	Pro	Asn	Asp	Pro	Asn	Gly	Pro	Gly	Leu	Pro	Tyr	Arg	His	Tyr	
				515					520					525		
tac	acc	gat	caa	agc	tcc	caa	tac	ccc	caa	aat	ctc	aac	acc	cct	aac	1694
Tyr	Thr	Asp	Gln	Ser	Ser	Gln	Tyr	Pro	Gln	Asn	Leu	Asn	Thr	Pro	Asn	
			530					535					540			
ccg	ctc	tat	cgt	aac	atg	ccc	caa	aat	tcg	cat	gcg	atc	ggc	aat	atc	1742
Pro	Leu	Tyr	Arg	Asn	Met	Pro	Gln	Asn	Ser	His	Ala	Ile	Gly	Asn	Ile	
		545					550					555				

atc gga ggg ttt atg caa gca aac tac aac att tta agc aat gtg atc	1790
Ile Gly Gly Phe Met Gln Ala Asn Tyr Asn Ile Leu Ser Asn Val Ile	
560 565 570	
gtg ggt gcg gga act cgt tat gat att tac acc ttg cta gac aaa aac	1838
Val Gly Ala Gly Thr Arg Tyr Asp Ile Tyr Thr Leu Leu Asp Lys Asn	
575 580 585 590	
ggc cgc acg cat gta act tct ggt ttc tcg cct tct gca acc gtg ctt	1886
Gly Arg Thr His Val Thr Ser Gly Phe Ser Pro Ser Ala Thr Val Leu	
595 600 605	
tat aac ccc att gaa agc att ggc ttg aaa gtg agt tat gcg tat gta	1934
Tyr Asn Pro Ile Glu Ser Ile Gly Leu Lys Val Ser Tyr Ala Tyr Val	
610 615 620	
act aag ggg gct ttg cct ggc gat ggc gtt ttg atg cgc gat cct acg	1982
Thr Lys Gly Ala Leu Pro Gly Asp Gly Val Leu Met Arg Asp Pro Thr	
625 630 635	
gtg att tat caa agg aat ttg cgc cct gcg atc ggt caa aat gtg gaa	2030
Val Ile Tyr Gln Arg Asn Leu Arg Pro Ala Ile Gly Gln Asn Val Glu	
640 645 650	
ttt aat gtg gat ttc aac agc aag tat ttc aat gtg cgc ggg gca gcg	2078
Phe Asn Val Asp Phe Asn Ser Lys Tyr Phe Asn Val Arg Gly Ala Ala	
655 660 665 670	
ttc tat caa gtc atc aat aat ttc atc aac agc tac ggg caa gac act	2126
Phe Tyr Gln Val Ile Asn Asn Phe Ile Asn Ser Tyr Gly Gln Asp Thr	
675 680 685	
tct aaa aat gga ggg ggt aac gca acc gca aaa aac atg tca ggg aat	2174
Ser Lys Asn Gly Gly Gly Asn Ala Thr Ala Lys Asn Met Ser Gly Asn	
690 695 700	
tta ccc gaa acc att aac att tat ggt tat gaa gtt tca ggg aat gtg	2222
Leu Pro Glu Thr Ile Asn Ile Tyr Gly Tyr Glu Val Ser Gly Asn Val	
705 710 715	
agg tat aag aat ttc tta ggg act ttc tca gtg gct cgc tct tgg cca	2270
Arg Tyr Lys Asn Phe Leu Gly Thr Phe Ser Val Ala Arg Ser Trp Pro	
720 725 730	
acg gct agg ggg cat tta tta gcg gac act tac gct cta gct gca acg	2318
Thr Ala Arg Gly His Leu Leu Ala Asp Thr Tyr Ala Leu Ala Ala Thr	
735 740 745 750	
act ggg aat gtg ttt att tta aaa gcc gat tat gat gtt cgc agg tgg	2366
Thr Gly Asn Val Phe Ile Leu Lys Ala Asp Tyr Asp Val Arg Arg Trp	
755 760 765	
ggg ctt act tta acc tgg ctc tcg cgc ttt gta act aac atg tat tat	2414
Gly Leu Thr Leu Thr Trp Leu Ser Arg Phe Val Thr Asn Met Tyr Tyr	
770 775 780	

gag ggc tat tct atc tat tac ccg caa tac ggc ttg atc aaa atc cat	2462
Glu Gly Tyr Ser Ile Tyr Tyr Pro Gln Tyr Gly Leu Ile Lys Ile His	
785 790 795	
aaa ccc ggg tat ggc gtg cat aat gtc ttt atc aac tgg act ccg cct	2510
Lys Pro Gly Tyr Gly Val His Asn Val Phe Ile Asn Trp Thr Pro Pro	
800 805 810	
tct aaa aaa tgg cag ggt tta agg att tca gcc gtg ttt aat aat atc	2558
Ser Lys Lys Trp Gln Gly Leu Arg Ile Ser Ala Val Phe Asn Asn Ile	
815 820 825 830	
tta aac aag caa tat gtg gat caa act tct gtg ttt caa gcg agc gcg	2606
Leu Asn Lys Gln Tyr Val Asp Gln Thr Ser Val Phe Gln Ala Ser Ala	
835 840 845	
gac gct cca gcg agc gat atg atc cct aaa ggt aag cgc atg gcg ctc	2654
Asp Ala Pro Ala Ser Asp Met Ile Pro Lys Gly Lys Arg Met Ala Leu	
850 855 860	
ccg gct cct gga ttt aac gcg cgt ttt gag gta tcc tat cag ttc	2699
Pro Ala Pro Gly Phe Asn Ala Arg Phe Glu Val Ser Tyr Gln Phe	
865 870 875	
taaaatgaaa ggaatccttag gatttctttt tgaattttga acatggaaac a	2750

<210> 28  
 <211> 877  
 <212> PRT  
 <213> Helicobacter pylori

<400> 28

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Thr Lys Gly Glu Arg Thr Phe Glu Tyr Asn Asn Lys Met Tyr Ile Asp	
35 40 45	
Arg Lys Glu Leu Gln Gln Arg Gln Ser Asn Gln Ile Arg Asp Ile Phe	
50 55 60	
Arg Thr Arg Ala Asp Val Asn Val Ala Ser Gly Gly Leu Met Ala Gln	
65 70 75 80	
Lys Ile Tyr Val Arg Gly Ile Glu Ser Arg Leu Leu Arg Val Thr Ile	
85 90 95	
Asp Gly Val Ala Gln Asn Gly Asn Ile Phe His His Asp Ala Asn Thr	
100 105 110	
Val Ile Asp Pro Asn Met Ile Lys Glu Val Glu Val Ile Lys Gly Ala	
115 120 125	
Ala Asn Ala Ser Ala Gly Pro Gly Ala Val Ala Gly Lys Leu Ser Phe	
130 135 140	
Thr Thr Ile Asp Ala Asn Asp Phe Leu Arg Lys Asn Gln Thr Tyr Gly	
145 150 155 160	
Ala Lys Ala Glu Ala Ala Phe Tyr Thr Asn Phe Gly Tyr Arg Met Asn	
165 170 175	

Ala	Thr	Ala	Ala	Tyr	Arg	Gly	Lys	Asn	Trp	Asp	Ile	Leu	Ala	Tyr	Tyr		
			180					185					190				
Asn	His	Gln	Asn	Ile	Phe	Tyr	Tyr	Arg	Asp	Gly	Asn	Asn	Ala	Phe	Arg		
		195					200					205					
Asn	Val	Phe	His	Pro	Asn	Tyr	Asp	Leu	Gln	Asp	Pro	Ser	Asn	Ser	Asp		
	210					215					220						
Met	Ser	Val	Gly	Thr	Pro	Ser	Glu	Val	Asn	Ser	Val	Leu	Ala	Lys	Ile		
225					230					235					240		
Asn	Gly	Tyr	Ile	Asn	Glu	Thr	Asp	Ser	Ile	Ser	Val	Ser	Tyr	Asn	Leu		
				245					250					255			
Thr	Arg	Asp	Asn	Ser	Thr	Arg	Leu	Leu	Arg	Pro	Asn	Thr	Thr	Ser	Ala		
			260				265						270				
Leu	Ser	Lys	Ala	Asn	Asp	Pro	Gly	Ser	Gln	Pro	Ala	Pro	Phe	Val	Ile		
		275					280					285					
Asp	Phe	Gly	Lys	Glu	Leu	Ala	His	Thr	Ile	Asn	Phe	Asn	His	Asn	Leu		
	290					295					300						
Ser	Leu	Lys	Tyr	Lys	His	Glu	Gly	Gly	Pro	Asn	Phe	Asn	Gln	Pro	Arg		
305					310					315					320		
Val	Glu	Ser	Thr	Ala	Phe	Leu	Gly	Val	Arg	Gly	Gly	Asn	Tyr	Asn	Pro		
				325					330					335			
Val	Val	Asn	Pro	Phe	Ala	Tyr	Asn	Ser	Asn	Glu	Pro	Ala	Asn	Pro	Asp		
			340				345						350				
Tyr	Ile	Pro	Glu	Val	Lys	Glu	Trp	Cys	Asn	Asn	Pro	Asp	Asn	Ile	Ser		
		355					360					365					
Gln	Cys	Thr	Gln	Gly	Ala	Ile	Arg	Pro	Ser	Asn	Gly	Gly	Tyr	Gln	Ile		
	370					375					380						
Gly	Tyr	Gly	Thr	Pro	Asn	Ser	Ile	Asn	Trp	Gln	Gly	Thr	Ser	Asp	Ser		
385					390					395					400		
Ser	Gly	Gly	Ala	Gln	Ala	Gly	Tyr	Gly	Gln	Leu	Asn	Ala	Ile	Ser	Thr		
			405						410					415			
Ser	Ala	Asn	Val	Tyr	His	Gly	Leu	Val	Pro	Lys	Asn	Pro	Asp	Tyr	Asp		
			420				425						430				
Met	Thr	Pro	Pro	Asn	Ala	Gln	Asn	Pro	Ser	Ala	Asn	Asp	Trp	Thr	Leu		
		435					440					445					
Gly	Asn	Ala	Asp	Ala	Glu	Gly	Thr	Leu	Ala	Arg	Arg	Ile	Phe	Leu	Ile		
	450					455					460						
Asn	Ser	Gly	Val	Asn	Phe	Lys	Val	Thr	His	Pro	Ile	Ser	Glu	Asp	Tyr		
465					470					475					480		
Gly	Asn	Val	Phe	Glu	Tyr	Gly	Met	Ile	Tyr	Gln	Asn	Leu	Ser	Val	Phe		
			485						490					495			
Ser	Gly	Leu	Asp	Lys	Gly	Lys	Asn	Gly	Tyr	Tyr	Lys	Asn	Asn	Ile	Asp		
			500					505					510				
Pro	Asn	Asp	Pro	Asn	Gly	Pro	Gly	Leu	Pro	Tyr	Arg	His	Tyr	Tyr	Thr		
		515					520					525					
Asp	Gln	Ser	Ser	Gln	Tyr	Pro	Gln	Asn	Leu	Asn	Thr	Pro	Asn	Pro	Leu		
	530					535					540						
Tyr	Arg	Asn	Met	Pro	Gln	Asn	Ser	His	Ala	Ile	Gly	Asn	Ile	Ile	Gly		
545					550					555					560		
Gly	Phe	Met	Gln	Ala	Asn	Tyr	Asn	Ile	Leu	Ser	Asn	Val	Ile	Val	Gly		
			565						570					575			
Ala	Gly	Thr	Arg	Tyr	Asp	Ile	Tyr	Thr	Leu	Leu	Asp	Lys	Asn	Gly	Arg		
			580					585					590				
Thr	His	Val	Thr	Ser	Gly	Phe	Ser	Pro	Ser	Ala	Thr	Val	Leu	Tyr	Asn		
		595					600					605					
Pro	Ile	Glu	Ser	Ile	Gly	Leu	Lys	Val	Ser	Tyr	Ala	Tyr	Val	Thr	Lys		



610		615		620
Gly Ala Leu Pro Gly Asp	Gly Val Leu Met Arg Asp	Pro Thr Val Ile		
625	630	635	640	
Tyr Gln Arg Asn Leu Arg	Pro Ala Ile Gly Gln Asn Val	Glu Phe Asn		
	645	650	655	
Val Asp Phe Asn Ser Lys Tyr	Phe Asn Val Arg Gly Ala	Ala Phe Tyr		
	660	665	670	
Gln Val Ile Asn Asn Phe Ile	Asn Ser Tyr Gly Gln Asp	Thr Ser Lys		
	675	680	685	
Asn Gly Gly Gly Asn Ala Thr	Ala Lys Asn Met Ser Gly	Asn Leu Pro		
	690	695	700	
Glu Thr Ile Asn Ile Tyr Gly	Tyr Glu Val Ser Gly	Asn Val Arg Tyr		
705	710	715	720	
Lys Asn Phe Leu Gly Thr Phe	Ser Val Ala Arg Ser Trp	Pro Thr Ala		
	725	730	735	
Arg Gly His Leu Leu Ala Asp	Thr Tyr Ala Leu Ala	Ala Thr Thr Gly		
	740	745	750	
Asn Val Phe Ile Leu Lys Ala	Asp Tyr Asp Val Arg Arg	Trp Gly Leu		
	755	760	765	
Thr Leu Thr Trp Leu Ser Arg	Phe Val Thr Asn Met Tyr	Tyr Tyr Glu Gly		
	770	775	780	
Tyr Ser Ile Tyr Tyr Pro Gln	Tyr Gly Leu Ile Lys	Ile His Lys Pro		
785	790	795	800	
Gly Tyr Gly Val His Asn Val	Phe Ile Asn Trp Thr Pro	Pro Ser Lys		
	805	810	815	
Lys Trp Gln Gly Leu Arg Ile	Ser Ala Val Phe Asn Asn	Ile Leu Asn		
	820	825	830	
Lys Gln Tyr Val Asp Gln Thr	Ser Val Phe Gln Ala Ser	Ala Asp Ala		
	835	840	845	
Pro Ala Ser Asp Met Ile Pro	Lys Gly Lys Arg Met Ala	Leu Pro Ala		
	850	855	860	
Pro Gly Phe Asn Ala Arg Phe	Glu Val Ser Tyr Gln Phe			
865	870	875		

<210> 29  
 <211> 370  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(317)

<400> 29	
tttaaaatca cccgttacag catcactgaa atcactaata ggggtgattg atg cgt	56
	Met Arg
	1
aag gtt tta tac gct ctt gtg ggc ttt ttg ttg gct ttt agc gct tta	104
Lys Val Leu Tyr Ala Leu Val Gly Phe Leu Leu Ala Phe Ser Ala Leu	
5 10 15	
aaa gcc gat gat ttt tta gaa gaa gcg aac gaa aca gcc ccg gcg cat	152
Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala Pro Ala His	

20	25	30	
tta aac cac cct atg cag gat tta aac gcc att caa ggg agc ttt ttt			200
Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser Phe Phe			
35	40	45	50
gac aaa aac cgc tca aaa atg tcc aac act ttg aac att gat tac ttt			248
Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp Tyr Phe			
	55	60	65
caa ggg caa act tat aaa atc ccg ctt gcg tta tgc gat ggc gmc ctt			296
Gln Gly Gln Thr Tyr Lys Ile Pro Leu Ala Leu Cys Asp Gly Xaa Leu			
	70	75	80
att gtt ttt ttc aaa acc cat tagcgatttt gttttagggg ataagggtggg			347
Ile Val Phe Phe Lys Thr His			
85			
ttttgatgcg aaaatttttag aaa			370

<210> 30  
 <211> 89  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <221> VARIANT  
 <222> 81  
 <223> Xaa = Any Amino Acid

<400> 30	
Met Arg Lys Val Leu Tyr Ala Leu Val Gly Phe Leu Leu Ala Phe Ser	
1	15
Ala Leu Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala Pro	
20	30
Ala His Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser	
35	45
Phe Phe Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp	
50	60
Tyr Phe Gln Gly Gln Thr Tyr Lys Ile Pro Leu Ala Leu Cys Asp Gly	
65	80
Xaa Leu Ile Val Phe Phe Lys Thr His	
85	

<210> 31  
 <211> 357  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(305)

<400> 31

atgcaataaa aaaagaaatt cttaggattt ctcacattaa ggagtttttaa atg aaa 56  
Met Lys  
1

aag gtt ttt tta ggt atg gca tta gcc ttt agt gtg tcc atg gca gaa 104  
Lys Val Phe Leu Gly Met Ala Leu Ala Phe Ser Val Ser Met Ala Glu  
5 10 15

aaa agt ggc gcg ttt tta gga ggg ggg ttt caa tat tct aat tta gaa 152  
Lys Ser Gly Ala Phe Leu Gly Gly Gly Phe Gln Tyr Ser Asn Leu Glu  
20 25 30

aac caa aac acc acc cgc acc cca ggc gct aac aat aac acc ccg ata 200  
Asn Gln Asn Thr Thr Arg Thr Pro Gly Ala Asn Asn Asn Thr Pro Ile  
35 40 45 50

gac act tca atg ttt ggc agc aac aaa aca gct cca gcc caa gaa acg 248  
Asp Thr Ser Met Phe Gly Ser Asn Lys Thr Ala Pro Ala Gln Glu Thr  
55 60 65

caa agc gct tcc aaa ccg gac act aaa gtc aat cca agc gca agt tgg 296  
Gln Ser Ala Ser Lys Pro Asp Thr Lys Val Asn Pro Ser Ala Ser Trp  
70 75 80

atg aaa aaa taagaaggaa gttatgaaaa agtcattcaa aaaattaggc 345  
Met Lys Lys  
85

tttgtctctt ta 357

<210> 32  
<211> 85  
<212> PRT  
<213> Helicobacter pylori

<400> 32  
Met Lys Lys Val Phe Leu Gly Met Ala Leu Ala Phe Ser Val Ser Met  
1 5 10 15  
Ala Glu Lys Ser Gly Ala Phe Leu Gly Gly Gly Phe Gln Tyr Ser Asn  
20 25 30  
Leu Glu Asn Gln Asn Thr Thr Arg Thr Pro Gly Ala Asn Asn Asn Thr  
35 40 45  
Pro Ile Asp Thr Ser Met Phe Gly Ser Asn Lys Thr Ala Pro Ala Gln  
50 55 60  
Glu Thr Gln Ser Ala Ser Lys Pro Asp Thr Lys Val Asn Pro Ser Ala  
65 70 75 80  
Ser Trp Met Lys Lys  
85

<210> 33  
<211> 961  
<212> DNA  
<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(908)

<400> 33

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gaatgtagca tttagaactc aagtagagaa aatgtagaag gaaggaatac atg aag      56
                                     Met Lys
                                     1

aaa tct gtt ata gta ggt gct atc tct cta gca atg aca agc tta ttg      104
Lys Ser Val Ile Val Gly Ala Ile Ser Leu Ala Met Thr Ser Leu Leu
      5                      10                      15

tca gca gag acc cct aag caa gaa aaa gct att aag act agc cct acc      152
Ser Ala Glu Thr Pro Lys Gln Glu Lys Ala Ile Lys Thr Ser Pro Thr
      20                      25                      30

aaa aaa ggt gaa aga aat gct gct ttt ata ggg att gat tac cag ttg      200
Lys Lys Gly Glu Arg Asn Ala Ala Phe Ile Gly Ile Asp Tyr Gln Leu
      35                      40                      45                      50

ggt atg ctc agc act acc gct caa aat tgt tcc cat ggg aat tgc aat      248
Gly Met Leu Ser Thr Thr Ala Gln Asn Cys Ser His Gly Asn Cys Asn
                        55                      60                      65

ggt aat caa agt ggg gct tac ggc tct aat acg cct aac atg cct aca      296
Gly Asn Gln Ser Gly Ala Tyr Gly Ser Asn Thr Pro Asn Met Pro Thr
                        70                      75                      80

gcg tca aac cca aca gga ggg ttt act cat ggc gct cta ggg act cgt      344
Ala Ser Asn Pro Thr Gly Gly Phe Thr His Gly Ala Leu Gly Thr Arg
      85                      90                      95

ggg tat aaa ggc tta agc aac caa caa tac gct atc aat ggt ttt ggt      392
Gly Tyr Lys Gly Leu Ser Asn Gln Gln Tyr Ala Ile Asn Gly Phe Gly
      100                      105                      110

ttt gtt gta ggg tat aag cat ttt ttc aag aaa tcc ccg caa ttt gga      440
Phe Val Val Gly Tyr Lys His Phe Phe Lys Lys Ser Pro Gln Phe Gly
      115                      120                      125                      130

atg cgt tat tac gga ttc ttt gat ttt gca agc tct tat tat aag tat      488
Met Arg Tyr Tyr Gly Phe Phe Asp Phe Ala Ser Ser Tyr Tyr Lys Tyr
                        135                      140                      145

tac act tat aat gat tat ggc atg aga gac gct cgc aag ggt tct caa      536
Tyr Thr Tyr Asn Asp Tyr Gly Met Arg Asp Ala Arg Lys Gly Ser Gln
                        150                      155                      160

agt ttc atg ttt ggc tat ggg gct ggc aca gat gtg ttg ttt aac ccg      584
Ser Phe Met Phe Gly Tyr Gly Ala Gly Thr Asp Val Leu Phe Asn Pro
      165                      170                      175

gct att ttc aat cgt gag aac ttg cat ttt ggg ttt ttc ttg ggc gtt      632
Ala Ile Phe Asn Arg Glu Asn Leu His Phe Gly Phe Phe Leu Gly Val
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180	185	190	
gcg atc ggt ggc acc tct tgg ggt cca aca aac tat tat ttt aag gac			680
Ala Ile Gly Gly Thr Ser Trp Gly Pro Thr Asn Tyr Tyr Phe Lys Asp			
195	200	205	210
ttg gct gat gag tat aga ggg agt ttc cac cca tca aat ttc cag gtc			728
Leu Ala Asp Glu Tyr Arg Gly Ser Phe His Pro Ser Asn Phe Gln Val			
	215	220	225
tta gtt aat ggt ggg att cgc tta ggc act aaa cac caa ggt ttt gaa			776
Leu Val Asn Gly Gly Ile Arg Leu Gly Thr Lys His Gln Gly Phe Glu			
	230	235	240
att ggc ttg aaa atc caa acc atc cgc aac aat tac tac acc gct agt			824
Ile Gly Leu Lys Ile Gln Thr Ile Arg Asn Asn Tyr Tyr Thr Ala Ser			
	245	250	255
gcg gat aat gtg cct gaa ggg act act tat aga ttc act ttc cac cgc			872
Ala Asp Asn Val Pro Glu Gly Thr Thr Tyr Arg Phe Thr Phe His Arg			
	260	265	270
ccc tat gcc ttt tat tgg cgt tac att gta agc ttt taaggtgttt			918
Pro Tyr Ala Phe Tyr Trp Arg Tyr Ile Val Ser Phe			
275	280	285	
tagggctaatt cttatggggg catagaaaag ggcttttgc ttt			961
<210> 34			
<211> 286			
<212> PRT			
<213> Helicobacter pylori			
<400> 34			
Met Lys Lys Ser Val Ile Val Gly Ala Ile Ser Leu Ala Met Thr Ser			
1 5 10 15			
Leu Leu Ser Ala Glu Thr Pro Lys Gln Glu Lys Ala Ile Lys Thr Ser			
20 25 30			
Pro Thr Lys Lys Gly Glu Arg Asn Ala Ala Phe Ile Gly Ile Asp Tyr			
35 40 45			
Gln Leu Gly Met Leu Ser Thr Thr Ala Gln Asn Cys Ser His Gly Asn			
50 55 60			
Cys Asn Gly Asn Gln Ser Gly Ala Tyr Gly Ser Asn Thr Pro Asn Met			
65 70 75 80			
Pro Thr Ala Ser Asn Pro Thr Gly Gly Phe Thr His Gly Ala Leu Gly			
85 90 95			
Thr Arg Gly Tyr Lys Gly Leu Ser Asn Gln Gln Tyr Ala Ile Asn Gly			
100 105 110			
Phe Gly Phe Val Val Gly Tyr Lys His Phe Phe Lys Lys Ser Pro Gln			
115 120 125			
Phe Gly Met Arg Tyr Tyr Gly Phe Phe Asp Phe Ala Ser Ser Tyr Tyr			
130 135 140			
Lys Tyr Tyr Thr Tyr Asn Asp Tyr Gly Met Arg Asp Ala Arg Lys Gly			
145 150 155 160			
Ser Gln Ser Phe Met Phe Gly Tyr Gly Ala Gly Thr Asp Val Leu Phe			

				165					170					175			
Asn	Pro	Ala	Ile	Phe	Asn	Arg	Glu	Asn	Leu	His	Phe	Gly	Phe	Phe	Leu		
			180					185					190				
Gly	Val	Ala	Ile	Gly	Gly	Thr	Ser	Trp	Gly	Pro	Thr	Asn	Tyr	Tyr	Phe		
		195					200					205					
Lys	Asp	Leu	Ala	Asp	Glu	Tyr	Arg	Gly	Ser	Phe	His	Pro	Ser	Asn	Phe		
	210					215					220						
Gln	Val	Leu	Val	Asn	Gly	Gly	Ile	Arg	Leu	Gly	Thr	Lys	His	Gln	Gly		
225					230					235					240		
Phe	Glu	Ile	Gly	Leu	Lys	Ile	Gln	Thr	Ile	Arg	Asn	Asn	Tyr	Tyr	Thr		
			245					250						255			
Ala	Ser	Ala	Asp	Asn	Val	Pro	Glu	Gly	Thr	Thr	Tyr	Arg	Phe	Thr	Phe		
		260					265						270				
His	Arg	Pro	Tyr	Ala	Phe	Tyr	Trp	Arg	Tyr	Ile	Val	Ser	Phe				
	275						280					285					

<210> 35  
 <211> 289  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(236)

<400> 35  
 gggattttat ttcttatagc agaaattatt tttaaagtaa aagacaaatc atg ttt 56  
 Met Phe  
 1

aga gat ata gta gat att tta ata tct gtt gtt att att gga tta gta 104  
 Arg Asp Ile Val Asp Ile Leu Ile Ser Val Val Ile Ile Gly Leu Val  
 5 10 15

tta aca gct att aga gct act ata atg gcg ttt aaa ggc gat act gat 152  
 Leu Thr Ala Ile Arg Ala Thr Ile Met Ala Phe Lys Gly Asp Thr Asp  
 20 25 30

gat gat gaa gtt gag agt gat ggg ttt ttt agt aga ata tgg gat aaa 200  
 Asp Asp Glu Val Glu Ser Asp Gly Phe Phe Ser Arg Ile Trp Asp Lys  
 35 40 45 50

ttc gtt gaa tat ttc ggc tat act cta gtt act ata taatgttttt 246  
 Phe Val Glu Tyr Phe Gly Tyr Thr Leu Val Thr Ile  
 55 60

tccttatata attggaccag ttatcgcttt aatttttata ttt 289

<210> 36  
 <211> 62  
 <212> PRT  
 <213> Helicobacter pylori

<400> 36

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<210> 37
<211> 1544
<212> DNA
<213> Helicobacter pylori
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<400> 37
gacacacatt agttatagtt tctaagagag ttctccccct atctcttaga t atg cct 57
                                     Met Pro
                                     1
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aag aaa tat ttt tct tac tct cta ttt ttt ttg ctt ttt tct agt ctc 153  
Lys Lys Tyr Phe Ser Tyr Ser Leu Phe Phe Leu Leu Phe Ser Ser Leu  
20 25 30

aag gtg agc agc tat acc aag ttt ggc ttt aac aac caa aga tac cag 249  
Lys Val Ser Ser Tyr Thr Lys Phe Gly Phe Asn Asn Gln Arg Tyr Gln  
55 60 65

gaa ttg aat ttg agc atg ggt tta tac aag ggt ttg aga gcg gaa gtg 345  
Glu Leu Asn Leu Ser Met Gly Leu Tyr Lys Gly Leu Arg Ala Glu Val  
85 90 95

aac aat atc cct aac ggc cag ccc ggc tct agg acc gat cct ttt ggg 441  
Asn Asn Ile Pro Asn Gly Gln Pro Gly Ser Arg Thr Asp Pro Phe Gly  
115 120 125 130

gcg ggt atc ttt tgg caa tat att ggt tgg tat gcg ggg cat agt ggt	489
Ala Gly Ile Phe Trp Gln Tyr Ile Gly Trp Tyr Ala Gly His Ser Gly	
135 140 145	
ttg caa gtg caa aaa cct cgt tta gcc atg gtg cat aac gct ttt ttg	537
Leu Gln Val Gln Lys Pro Arg Leu Ala Met Val His Asn Ala Phe Leu	
150 155 160	
agc tac aac tac aaa aaa gac aaa ttc agt ttt ggc gtg aaa ggg ggg	585
Ser Tyr Asn Tyr Lys Lys Asp Lys Phe Ser Phe Gly Val Lys Gly Gly	
165 170 175	
cgc tat gac gct gaa gag tat gat tgg ttc act tct tac act caa ggg	633
Arg Tyr Asp Ala Glu Glu Tyr Asp Trp Phe Thr Ser Tyr Thr Gln Gly	
180 185 190	
gtt gaa ggc ttt gtc aaa tat aaa gac acc aga ttc agg gtg atg tat	681
Val Glu Gly Phe Val Lys Tyr Lys Asp Thr Arg Phe Arg Val Met Tyr	
195 200 205 210	
tca gac gct agg gct tca gcg tca agc gac tgg ttt tgg tat ttt ggg	729
Ser Asp Ala Arg Ala Ser Ala Ser Ser Asp Trp Phe Trp Tyr Phe Gly	
215 220 225	
cgt tac tat aca agc ggt aag gct cta atg gta gct gat ttg aaa tat	777
Arg Tyr Tyr Thr Ser Gly Lys Ala Leu Met Val Ala Asp Leu Lys Tyr	
230 235 240	
gaa aaa gac aac cta aaa atc aac cct tat ttt tat gcg atc ttt caa	825
Glu Lys Asp Asn Leu Lys Ile Asn Pro Tyr Phe Tyr Ala Ile Phe Gln	
245 250 255	
aga atg tat gcg cca ggc att aat atc act tat gac acc aac cct aat	873
Arg Met Tyr Ala Pro Gly Ile Asn Ile Thr Tyr Asp Thr Asn Pro Asn	
260 265 270	
ttc aac aat aag ggt ttt cgt ttt gta ggc act ttc gta ggg ttt ttc	921
Phe Asn Asn Lys Gly Phe Arg Phe Val Gly Thr Phe Val Gly Phe Phe	
275 280 285 290	
ccc att ttt gcc act ccg gct aat caa aat gat att atc ctc ttc caa	969
Pro Ile Phe Ala Thr Pro Ala Asn Gln Asn Asp Ile Ile Leu Phe Gln	
295 300 305	
caa gtg cca tta ggc aag agt ggg caa act tat ttc ttc cgc act cgt	1017
Gln Val Pro Leu Gly Lys Ser Gly Gln Thr Tyr Phe Phe Arg Thr Arg	
310 315 320	
ttt tac tat aat aag tgg caa ttt ggg ggc agc gtc tat aaa aac atc	1065
Phe Tyr Tyr Asn Lys Trp Gln Phe Gly Gly Ser Val Tyr Lys Asn Ile	
325 330 335	
ggg aac gct aat ggt gat ata ggt att tat ggc gac cct ttg ggg tat	1113
Gly Asn Ala Asn Gly Asp Ile Gly Ile Tyr Gly Asp Pro Leu Gly Tyr	



340	345	350	
aac att tgg acg aat agt att tat gac gca gaa att aac aat att gtt			1161
Asn Ile Trp Thr Asn Ser Ile Tyr Asp Ala Glu Ile Asn Asn Ile Val			
355	360	365	370
ggc gct gat gtt att aac ggg ttt ttg tat gta ggc tca caa tat aga			1209
Gly Ala Asp Val Ile Asn Gly Phe Leu Tyr Val Gly Ser Gln Tyr Arg			
	375	380	385
ggg ttt agt tgg aaa att tta ggc cgt tgg acg gat agc cca agg gct			1257
Gly Phe Ser Trp Lys Ile Leu Gly Arg Trp Thr Asp Ser Pro Arg Ala			
	390	395	400
gat gaa agg agt ctc gcg ctc ttt ttg agt tat ttt tct aat aag tat			1305
Asp Glu Arg Ser Leu Ala Leu Phe Leu Ser Tyr Phe Ser Asn Lys Tyr			
	405	410	415
aat att aga atg gat tta aaa cta gaa tat tat ggc aat atc acc aaa			1353
Asn Ile Arg Met Asp Leu Lys Leu Glu Tyr Tyr Gly Asn Ile Thr Lys			
	420	425	430
aaa ggc tat tgt att ggg tat tgt ggc atg tat gtt cca gtc gat cct			1401
Lys Gly Tyr Cys Ile Gly Tyr Cys Gly Met Tyr Val Pro Val Asp Pro			
	435	440	445
aac ggc cct ggc aca cag cct tta acg cac aat gtg tat tct gac agg			1449
Asn Gly Pro Gly Thr Gln Pro Leu Thr His Asn Val Tyr Ser Asp Arg			
	455	460	465
agc cat ata atg ttt aac att gct tac ggt ttt agg att tac			1491
Ser His Ile Met Phe Asn Ile Ala Tyr Gly Phe Arg Ile Tyr			
	470	475	480
tagcatttta tccttaatgg atatttttga ttagcctttt taaaatattg aaa			1544
<210> 38			
<211> 480			
<212> PRT			
<213> Helicobacter pylori			
<400> 38			
Met Pro Phe Cys Ile Phe Ile Leu Ile Ser Leu Gly Val Arg Val Leu			
1	5	10	15
Glu Ile Lys Lys Tyr Phe Ser Tyr Ser Leu Phe Phe Leu Leu Phe Ser			
	20	25	30
Ser Leu Phe Leu Ser Lys Leu Gln Ala Tyr Lys Phe Asn Met Ser Ile			
	35	40	45
Val Gly Lys Val Ser Ser Tyr Thr Lys Phe Gly Phe Asn Asn Gln Arg			
	50	55	60
Tyr Gln Pro Ser Lys Asp Ile Tyr Pro Thr Gly Ser Tyr Thr Ser Leu			
	65	70	75
Leu Gly Glu Leu Asn Leu Ser Met Gly Leu Tyr Lys Gly Leu Arg Ala			
	85	90	95
Glu Val Gly Ala Met Met Ala Ala Leu Pro Tyr Asp Ser Thr Ala Tyr			



<221> CDS  
 <222> (51)...(605)

<400> 39

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aatttttaggt tattagttac cattttatta ttcttaagga tgtgtttata atg aga      56
                                     Met Arg
                                     1

att aag gct tat ttt ttg cgt ttt atc gcg ctg gtt ttg att gtt ttg      104
Ile Lys Ala Tyr Phe Leu Arg Phe Ile Ala Leu Val Leu Ile Val Leu
      5                      10                      15

tta ggt ttt agt gct tgt aaa aat tct caa aaa tct caa gat tct caa      152
Leu Gly Phe Ser Ala Cys Lys Asn Ser Gln Lys Ser Gln Asp Ser Gln
      20                      25                      30

aac aat acc ccc caa caa gat agc cct aaa acc tac acc gct atg gat      200
Asn Asn Thr Pro Gln Gln Asp Ser Pro Lys Thr Tyr Thr Ala Met Asp
      35                      40                      45                      50

ttg aat aac caa gaa tac acc atc aca ggc gat tta gat tct ctc aat      248
Leu Asn Asn Gln Glu Tyr Thr Ile Thr Gly Asp Leu Asp Ser Leu Asn
      55                      60                      65

atc agc ccg gat tcc aac acc cct acc cta tta gtt tta agc gct tta      296
Ile Ser Pro Asp Ser Asn Thr Pro Thr Leu Leu Val Leu Ser Ala Leu
      70                      75                      80

gat aat tct tta aaa gat tac gcc ccc agc ttt aac atc tta aaa aaa      344
Asp Asn Ser Leu Lys Asp Tyr Ala Pro Ser Phe Asn Ile Leu Lys Lys
      85                      90                      95

act ttt aaa gat cgt ttg agg gtg ctt att tta ctc aat aaa ccc tat      392
Thr Phe Lys Asp Arg Leu Arg Val Leu Ile Leu Leu Asn Lys Pro Tyr
      100                      105                      110

tca agc gat gca atc aaa gac ttt agc gcg cat ttt caa gct gat ttg      440
Ser Ser Asp Ala Ile Lys Asp Phe Ser Ala His Phe Gln Ala Asp Leu
      115                      120                      125                      130

atg att tta aac cct aaa gat acc gct ctt ttt gat cat tta aag tat      488
Met Ile Leu Asn Pro Lys Asp Thr Ala Leu Phe Asp His Leu Lys Tyr
      135                      140                      145

gac gct tta aac cat tct ttt aac atg ctc tta tac cac aaa cac caa      536
Asp Ala Leu Asn His Ser Phe Asn Met Leu Leu Tyr His Lys His Gln
      150                      155                      160

ttg atc aaa atg tat caa ggg atc gtg cca ata gaa atg ctc caa ttt      584
Leu Ile Lys Met Tyr Gln Gly Ile Val Pro Ile Glu Met Leu Gln Phe
      165                      170                      175

gat att tcc aat tta aag gat taaaaaaaaac catgtttaat tttttcaaaa      635
Asp Ile Ser Asn Leu Lys Asp
      180                      185

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aaattgtcaa taaaattaag ggt

658

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 <213> Helicobacter pylori

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 20 25 30  
 Ser Gln Asn Asn Thr Pro Gln Gln Asp Ser Pro Lys Thr Tyr Thr Ala  
 35 40 45  
 Met Asp Leu Asn Asn Gln Glu Tyr Thr Ile Thr Gly Asp Leu Asp Ser  
 50 55 60  
 Leu Asn Ile Ser Pro Asp Ser Asn Thr Pro Thr Leu Leu Val Leu Ser  
 65 70 75 80  
 Ala Leu Asp Asn Ser Leu Lys Asp Tyr Ala Pro Ser Phe Asn Ile Leu  
 85 90 95  
 Lys Lys Thr Phe Lys Asp Arg Leu Arg Val Leu Ile Leu Leu Asn Lys  
 100 105 110  
 Pro Tyr Ser Ser Asp Ala Ile Lys Asp Phe Ser Ala His Phe Gln Ala  
 115 120 125  
 Asp Leu Met Ile Leu Asn Pro Lys Asp Thr Ala Leu Phe Asp His Leu  
 130 135 140  
 Lys Tyr Asp Ala Leu Asn His Ser Phe Asn Met Leu Leu Tyr His Lys  
 145 150 155 160  
 His Gln Leu Ile Lys Met Tyr Gln Gly Ile Val Pro Ile Glu Met Leu  
 165 170 175  
 Gln Phe Asp Ile Ser Asn Leu Lys Asp  
 180 185

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 <213> Helicobacter pylori

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 Met Pro  
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 atg cgt ttg cac act gcc ttt ttt ggt att aat tca ttg ctt gtt gcc 104  
 Met Arg Leu His Thr Ala Phe Phe Gly Ile Asn Ser Leu Leu Val Ala  
 5 10 15  
 tct ctt ttg ata agc ggt tgc agt ctc ttt aaa aag cgt aac act aac 152  
 Ser Leu Leu Ile Ser Gly Cys Ser Leu Phe Lys Lys Arg Asn Thr Asn

20	25	30	
gcc cag cta atc ccc cct tca gct aat ggc ttg caa gcc ccc att tat			200
Ala Gln Leu Ile Pro Pro Ser Ala Asn Gly Leu Gln Ala Pro Ile Tyr			
35	40	45	50
ccc cca acc aat ttc acc cct aga aag agc att cag cct ctc cca agc			248
Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu Pro Ser			
	55	60	65
cct cgc ctt gag aat aac gat cag ccc gtc att agt tct aac ccc act			296
Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn Pro Thr			
	70	75	80
aac gct atc cct aac acc ccc att ctc acg cct aat aat gtc att gaa			344
Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val Ile Glu			
	85	90	95
ttg aac gca tgg gca tgg gcg tgg ctc cag aat cca cca ttt cac cct			392
Leu Asn Ala Trp Ala Trp Ala Trp Leu Gln Asn Pro Pro Phe His Pro			
	100	105	110
ctc aag ccc tgg ctc tagccaagcg ggcggctatc gttgatggct accgccagtt			447
Leu Lys Pro Trp Leu			
115			
gggtgaaaaa atg			460
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<213> Helicobacter pylori			
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Val Ala Ser Leu Leu Ile Ser Gly Cys Ser Leu Phe Lys Lys Arg Asn			
	20	25	30
Thr Asn Ala Gln Leu Ile Pro Pro Ser Ala Asn Gly Leu Gln Ala Pro			
	35	40	45
Ile Tyr Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu			
	50	55	60
Pro Ser Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn			
65	70	75	80
Pro Thr Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val			
	85	90	95
Ile Glu Leu Asn Ala Trp Ala Trp Ala Trp Leu Gln Asn Pro Pro Phe			
	100	105	110
His Pro Leu Lys Pro Trp Leu			
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<210> 43			
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<212> DNA			

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(1232)

<400> 43

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gaa aca aga ctt tta aaa ttg aga gcg ttg agc tta gca tgt tta atg      104
Glu Thr Arg Leu Leu Lys Leu Arg Ala Leu Ser Leu Ala Cys Leu Met
          5                      10                      15

gga tta ggc gtg agt ggg tgc gcg ttt tta gat aag caa atc tta aac      152
Gly Leu Gly Val Ser Gly Cys Ala Phe Leu Asp Lys Gln Ile Leu Asn
        20                      25                      30

gac cat ttg act aaa gct aaa aat aac cca aaa tac gat tgc caa aaa      200
Asp His Leu Thr Lys Ala Lys Asn Asn Pro Lys Tyr Asp Cys Gln Lys
        35                      40                      45                      50

gaa atg tgg tct ttc cct aaa aaa tac gat ggg ata aat cag tgt tta      248
Glu Met Trp Ser Phe Pro Lys Lys Tyr Asp Gly Ile Asn Gln Cys Leu
          55                      60                      65

aag gct caa gaa gag ctt att gaa cca atc atc act aaa aag atc gat      296
Lys Ala Gln Glu Leu Ile Glu Pro Ile Ile Thr Lys Lys Ile Asp
          70                      75                      80

cag tat caa tgc gat gat ttc act aat gaa ggc tta aaa gat aag tgt      344
Gln Tyr Gln Cys Asp Asp Phe Thr Asn Glu Gly Leu Lys Asp Lys Cys
          85                      90                      95

ttc aaa aga aac gat gcc tac tta aac acc ctt tta acg ccc atc att      392
Phe Lys Arg Asn Asp Ala Tyr Leu Asn Thr Leu Leu Thr Pro Ile Ile
        100                      105                      110

caa aaa caa gag cgt cgt ttt agc tgc tct gat ttc cat aac cca gag      440
Gln Lys Gln Glu Arg Arg Phe Ser Cys Ser Asp Phe His Asn Pro Glu
        115                      120                      125                      130

cta aaa gaa caa tgc atg gat aaa act aac gct tat gaa aag caa aaa      488
Leu Lys Glu Gln Cys Met Asp Lys Thr Asn Ala Tyr Glu Lys Gln Lys
          135                      140                      145

gac cga caa aaa aga cta att aat ctc gtg caa tta gaa gcg ttt gaa      536
Asp Arg Gln Lys Arg Leu Ile Asn Leu Val Gln Leu Glu Ala Phe Glu
          150                      155                      160

aaa gaa tac gcg caa tat aaa cca tac att atc cct tac ttc acc aaa      584
Lys Glu Tyr Ala Gln Tyr Lys Pro Tyr Ile Ile Pro Tyr Phe Thr Lys
          165                      170                      175
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gaa tgc gtt aaa aat gcg ccc cat tta gcc aac aag gaa aga cta tgc	632
Glu Cys Val Lys Asn Ala Pro His Leu Ala Asn Lys Glu Arg Leu Cys	
180 185 190	
caa aaa gaa gtg cat gaa aaa ttt gac gac cct tat tct agc tct aaa	680
Gln Lys Glu Val His Glu Lys Phe Asp Asp Pro Tyr Ser Ser Ser Lys	
195 200 205 210	
gaa ttg agc gtt caa tcg gct att tct ttt tgc att aaa aaa gtt gat	728
Glu Leu Ser Val Gln Ser Ala Ile Ser Phe Cys Ile Lys Lys Val Asp	
215 220 225	
gct aaa tta gaa aaa gcc gct ctt atg aat ggc gtt tat ata agc cct	776
Ala Lys Leu Glu Lys Ala Ala Leu Met Asn Gly Val Tyr Ile Ser Pro	
230 235 240	
tat aaa aaa tcc acc cat tgc caa aga acg cat ttg gaa aat aag agc	824
Tyr Lys Lys Ser Thr His Cys Gln Arg Thr His Leu Glu Asn Lys Ser	
245 250 255	
ttg aaa gaa atc gct tta aat atg aac cct aaa tta gaa aag caa agc	872
Leu Lys Glu Ile Ala Leu Asn Met Asn Pro Lys Leu Glu Lys Gln Ser	
260 265 270	
cct ttt att gat gcg gat aaa atg gct atg caa tct gcg ggg tta ttg	920
Pro Phe Ile Asp Ala Asp Lys Met Ala Met Gln Ser Ala Gly Leu Leu	
275 280 285 290	
aga aag aat aaa ggt gtc ttg att gct ttt gct aca gat att tgc atg	968
Arg Lys Asn Lys Gly Val Leu Ile Ala Phe Ala Thr Asp Ile Cys Met	
295 300 305	
gag cgt aac gaa cat aaa aaa gaa gag ttt atc agc ctt aaa gat agt	1016
Glu Arg Asn Glu His Lys Lys Glu Glu Phe Ile Ser Leu Lys Asp Ser	
310 315 320	
tgc acc caa tcg caa gcc aaa atc tat aac aac aag gag cgc ttt gac	1064
Cys Thr Gln Ser Gln Ala Lys Ile Tyr Asn Asn Lys Glu Arg Phe Asp	
325 330 335	
aaa ttc ata caa gat tac caa aaa gac tta aaa act tgt ctt tta gac	1112
Lys Phe Ile Gln Asp Tyr Gln Lys Asp Leu Lys Thr Cys Leu Leu Asp	
340 345 350	
act tct aac act aaa gaa gaa gtg gag caa aat ttt tca caa tgc caa	1160
Thr Ser Asn Thr Lys Glu Glu Val Glu Gln Asn Phe Ser Gln Cys Gln	
355 360 365 370	
aaa gag caa ttg aga gat gat aac aaa ggc ttg ggt ttc act tta gaa	1208
Lys Glu Gln Leu Arg Asp Asp Asn Lys Gly Leu Gly Phe Thr Leu Glu	
375 380 385	
gaa ttg gtt aaa aaa tac gct aag taaagttatt taattttatg gatgggtttta	1262
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390	

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1285

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<211> 394

<212> PRT

<213> Helicobacter pylori

<400> 44

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			20					25					30		
Leu	Asn	Asp	His	Leu	Thr	Lys	Ala	Lys	Asn	Asn	Pro	Lys	Tyr	Asp	Cys
		35					40					45			
Gln	Lys	Glu	Met	Trp	Ser	Phe	Pro	Lys	Lys	Tyr	Asp	Gly	Ile	Asn	Gln
	50					55					60				
Cys	Leu	Lys	Ala	Gln	Glu	Glu	Leu	Ile	Glu	Pro	Ile	Ile	Thr	Lys	Lys
65					70				75						80
Ile	Asp	Gln	Tyr	Gln	Cys	Asp	Asp	Phe	Thr	Asn	Glu	Gly	Leu	Lys	Asp
				85				90						95	
Lys	Cys	Phe	Lys	Arg	Asn	Asp	Ala	Tyr	Leu	Asn	Thr	Leu	Leu	Thr	Pro
			100				105						110		
Ile	Ile	Gln	Lys	Gln	Glu	Arg	Arg	Phe	Ser	Cys	Ser	Asp	Phe	His	Asn
		115				120						125			
Pro	Glu	Leu	Lys	Glu	Gln	Cys	Met	Asp	Lys	Thr	Asn	Ala	Tyr	Glu	Lys
	130					135					140				
Gln	Lys	Asp	Arg	Gln	Lys	Arg	Leu	Ile	Asn	Leu	Val	Gln	Leu	Glu	Ala
145					150				155						160
Phe	Glu	Lys	Glu	Tyr	Ala	Gln	Tyr	Lys	Pro	Tyr	Ile	Ile	Pro	Tyr	Phe
				165				170						175	
Thr	Lys	Glu	Cys	Val	Lys	Asn	Ala	Pro	His	Leu	Ala	Asn	Lys	Glu	Arg
			180				185						190		
Leu	Cys	Gln	Lys	Glu	Val	His	Glu	Lys	Phe	Asp	Asp	Pro	Tyr	Ser	Ser
		195				200						205			
Ser	Lys	Glu	Leu	Ser	Val	Gln	Ser	Ala	Ile	Ser	Phe	Cys	Ile	Lys	Lys
	210					215					220				
Val	Asp	Ala	Lys	Leu	Glu	Lys	Ala	Ala	Leu	Met	Asn	Gly	Val	Tyr	Ile
225					230				235						240
Ser	Pro	Tyr	Lys	Lys	Ser	Thr	His	Cys	Gln	Arg	Thr	His	Leu	Glu	Asn
				245				250						255	
Lys	Ser	Leu	Lys	Glu	Ile	Ala	Leu	Asn	Met	Asn	Pro	Lys	Leu	Glu	Lys
			260					265					270		
Gln	Ser	Pro	Phe	Ile	Asp	Ala	Asp	Lys	Met	Ala	Met	Gln	Ser	Ala	Gly
	275					280						285			
Leu	Leu	Arg	Lys	Asn	Lys	Gly	Val	Leu	Ile	Ala	Phe	Ala	Thr	Asp	Ile
	290					295					300				
Cys	Met	Glu	Arg	Asn	Glu	His	Lys	Lys	Glu	Glu	Phe	Ile	Ser	Leu	Lys
305					310				315						320
Asp	Ser	Cys	Thr	Gln	Ser	Gln	Ala	Lys	Ile	Tyr	Asn	Asn	Lys	Glu	Arg
				325				330						335	
Phe	Asp	Lys	Phe	Ile	Gln	Asp	Tyr	Gln	Lys	Asp	Leu	Lys	Thr	Cys	Leu
			340				345						350		
Leu	Asp	Thr	Ser	Asn	Thr	Lys	Glu	Glu	Val	Glu	Gln	Asn	Phe	Ser	Gln
			355				360						365		



Cys Gln Lys Glu Gln Leu Arg Asp Asp Asn Lys Gly Leu Gly Phe Thr  
 370 375 380  
 Leu Glu Glu Leu Val Lys Lys Tyr Ala Lys  
 385 390

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (84)...(704)

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 Met Leu Arg Val Leu Ser Val Gly Val Ala  
 1 5 10  
 ttt att tta cta ggg tgt cag ttt ttc aac aaa acg acg ctg cat tta 161  
 Phe Ile Leu Leu Gly Cys Gln Phe Phe Asn Lys Thr Thr Leu His Leu  
 15 20 25  
 aaa tat aaa gat tac ccc aaa aat agc gct tta aaa acc gct ttc act 209  
 Lys Tyr Lys Asp Tyr Pro Lys Asn Ser Ala Leu Lys Thr Ala Phe Thr  
 30 35 40  
 tta acc ccc cct aaa atc ttt ttt aac gcc cgt ttt gtg ccg ccc ttt 257  
 Leu Thr Pro Pro Lys Ile Phe Phe Asn Ala Arg Phe Val Pro Pro Phe  
 45 50 55  
 tac caa aaa gaa ttt aaa aaa gcg atc acc caa caa atc gct tat ttt 305  
 Tyr Gln Lys Glu Phe Lys Lys Ala Ile Thr Gln Gln Ile Ala Tyr Phe  
 60 65 70  
 tta aaa gat aaa agt gct ttt att ctc aat gtt tca ggc aat gtt ttt 353  
 Leu Lys Asp Lys Ser Ala Phe Ile Leu Asn Val Ser Gly Asn Val Phe  
 75 80 85 90  
 ttt tct ttt gaa gag aat cct aaa gat tta aaa gcc att aaa gaa agg 401  
 Phe Ser Phe Glu Glu Asn Pro Lys Asp Leu Lys Ala Ile Lys Glu Arg  
 95 100 105  
 ctt aaa aag acg att gag cct aac gct gac cca aaa gcc gtc atg cgt 449  
 Leu Lys Lys Thr Ile Glu Pro Asn Ala Asp Pro Lys Ala Val Met Arg  
 110 115 120  
 ttt tta aac ctt caa gcg agc ttg att tta gaa tgc gtc ccg caa acc 497  
 Phe Leu Asn Leu Gln Ala Ser Leu Ile Leu Glu Cys Val Pro Gln Thr  
 125 130 135  
 act tgc ccg ttt gac acc ctt tta atc ccc acc gct ttc agc gtg cct 545  
 Thr Cys Pro Phe Asp Thr Leu Leu Ile Pro Thr Ala Phe Ser Val Pro

140	145	150	
ggt tat tac gct aat cgt ttg ggc gat aac ccc tct ctt ttt tcc caa	593		
Val Tyr Tyr Ala Asn Arg Leu Gly Asp Asn Pro Ser Leu Phe Ser Gln			
155	160	165	170
gag gat aaa acc tat cat aac gct ttg atc aaa gcc ctt aat aag gct	641		
Glu Asp Lys Thr Tyr His Asn Ala Leu Ile Lys Ala Leu Asn Lys Ala			
	175	180	185
tac tat tct ctt atg gag ggt tta gaa aag cgt ttg aac gct ata aaa	689		
Tyr Tyr Ser Leu Met Glu Gly Leu Glu Lys Arg Leu Asn Ala Ile Lys			
	190	195	200
aat gca gag tgg ctt taaggcatga aaaagattgc attttttatt tttgtcattt	744		
Asn Ala Glu Trp Leu			
	205		
tgtttttcggt agggatttat ttaatttggc atgttttatt ggaaaaagcc ctagaattga	804		
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	20	25	30
Lys Asn Ser Ala Leu Lys Thr Ala Phe Thr Leu Thr Pro Pro Lys Ile			
	35	40	45
Phe Phe Asn Ala Arg Phe Val Pro Pro Phe Tyr Gln Lys Glu Phe Lys			
	50	55	60
Lys Ala Ile Thr Gln Gln Ile Ala Tyr Phe Leu Lys Asp Lys Ser Ala			
65	70	75	80
Phe Ile Leu Asn Val Ser Gly Asn Val Phe Phe Ser Phe Glu Glu Asn			
	85	90	95
Pro Lys Asp Leu Lys Ala Ile Lys Glu Arg Leu Lys Lys Thr Ile Glu			
	100	105	110
Pro Asn Ala Asp Pro Lys Ala Val Met Arg Phe Leu Asn Leu Gln Ala			
	115	120	125
Ser Leu Ile Leu Glu Cys Val Pro Gln Thr Thr Cys Pro Phe Asp Thr			
	130	135	140
Leu Leu Ile Pro Thr Ala Phe Ser Val Pro Val Tyr Tyr Ala Asn Arg			
145	150	155	160
Leu Gly Asp Asn Pro Ser Leu Phe Ser Gln Glu Asp Lys Thr Tyr His			
	165	170	175
Asn Ala Leu Ile Lys Ala Leu Asn Lys Ala Tyr Tyr Ser Leu Met Glu			
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Gly Leu Glu Lys Arg Leu Asn Ala Ile Lys Asn Ala Glu Trp Leu			
	195	200	205

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Leu	Lys	His	Phe	Lys	Thr	Phe	Leu	Phe	Ile	Thr	Met	Ala	Ile	Ile	Val		
5							10			15							
ata	ggt	acc	ggt	tgc	gcg	aac	aaa	aag	aaa	aaa	aaa	gac	gaa	tac	aac	152	
Ile	Gly	Thr	Gly	Cys	Ala	Asn	Lys	Lys	Lys	Lys	Lys	Asp	Glu	Tyr	Asn		
20							25			30							
aaa	ccg	gcg	atc	ttt	tgg	tat	caa	ggg	att	ttg	aga	gaa	atc	ctt	ttt	200	
Lys	Pro	Ala	Ile	Phe	Trp	Tyr	Gln	Gly	Ile	Leu	Arg	Glu	Ile	Leu	Phe		
35			40				45				50						
gct	aat	tta	gaa	aca	gcg	gac	aat	tac	tat	tct	tct	tta	caa	agc	gaa	248	
Ala	Asn	Leu	Glu	Thr	Ala	Asp	Asn	Tyr	Tyr	Ser	Ser	Leu	Gln	Ser	Glu		
				55			60				65						
cac	atc	aat	tcc	ccc	ctt	gtc	cca	gaa	gcg	atg	cta	gct	tta	ggg	caa	296	
His	Ile	Asn	Ser	Pro	Leu	Val	Pro	Glu	Ala	Met	Leu	Ala	Leu	Gly	Gln		
			70			75				80							
gcg	cac	atg	aaa	aag	aaa	gag	tat	gtt	tta	gcg	tct	ttt	tac	ttt	gat	344	
Ala	His	Met	Lys	Lys	Lys	Glu	Tyr	Val	Leu	Ala	Ser	Phe	Tyr	Phe	Asp		
85							90			95							
gaa	tac	atc	aag	cgc	ttt	ggg	act	aag	gac	aat	gtg	gat	tat	ttg	act	392	
Glu	Tyr	Ile	Lys	Arg	Phe	Gly	Thr	Lys	Asp	Asn	Val	Asp	Tyr	Leu	Thr		
100			105				110										
ttt	tta	aaa	ttg	caa	tcg	cat	tat	tac	gct	ttc	aaa	aac	cat	tct	aaa	440	
Phe	Leu	Lys	Leu	Gln	Ser	His	Tyr	Tyr	Ala	Phe	Lys	Asn	His	Ser	Lys		
115			120				125				130						
gac	cag	gaa	ttt	atc	tct	aat	tct	att	gtg	agt	tta	ggc	gaa	ttt	ata	488	
Asp	Gln	Glu	Phe	Ile	Ser	Asn	Ser	Ile	Val	Ser	Leu	Gly	Glu	Phe	Ile		
				135			140				145						
gaa	aaa	tac	cct	aac	agc	cgt	tac	cgc	ccc	tat	gta	gaa	tac	atg	caa	536	
Glu	Lys	Tyr	Pro	Asn	Ser	Arg	Tyr	Arg	Pro	Tyr	Val	Glu	Tyr	Met	Gln		
			150			155				160							
atc	aaa	ttc	att	tta	ggg	caa	aat	gag	ctc	aat	cgc	gcg	atc	gcg	aat	584	

Ile	Lys	Phe	Ile	Leu	Gly	Gln	Asn	Glu	Leu	Asn	Arg	Ala	Ile	Ala	Asn		
		165					170					175					
gtc	tat	aaa	aaa	cgc	cac	aag	cct	gag	ggc	gtg	aaa	cgc	tat	tta	gaa	632	
Val	Tyr	Lys	Lys	Arg	His	Lys	Pro	Glu	Gly	Val	Lys	Arg	Tyr	Leu	Glu		
		180				185					190						
agg	ata	gat	gag	act	tta	gaa	aaa	gag	act	aaa	ccc	aaa	cca	tcg	cac	680	
Arg	Ile	Asp	Glu	Thr	Leu	Glu	Lys	Glu	Thr	Lys	Pro	Lys	Pro	Ser	His		
		195			200					205				210			
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Met	Pro	Trp	Tyr	Val	Leu	Ile	Phe	Asp	Trp								
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 <211> 220  
 <212> PRT  
 <213> Helicobacter pylori

<400> 48																	
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Ile	Val	Ile	Gly	Thr	Gly	Cys	Ala	Asn	Lys	Lys	Lys	Lys	Lys	Asp	Glu		
			20					25					30				
Tyr	Asn	Lys	Pro	Ala	Ile	Phe	Trp	Tyr	Gln	Gly	Ile	Leu	Arg	Glu	Ile		
		35				40						45					
Leu	Phe	Ala	Asn	Leu	Glu	Thr	Ala	Asp	Asn	Tyr	Tyr	Ser	Ser	Leu	Gln		
	50				55					60							
Ser	Glu	His	Ile	Asn	Ser	Pro	Leu	Val	Pro	Glu	Ala	Met	Leu	Ala	Leu		
	65			70					75						80		
Gly	Gln	Ala	His	Met	Lys	Lys	Lys	Glu	Tyr	Val	Leu	Ala	Ser	Phe	Tyr		
			85					90						95			
Phe	Asp	Glu	Tyr	Ile	Lys	Arg	Phe	Gly	Thr	Lys	Asp	Asn	Val	Asp	Tyr		
		100						105					110				
Leu	Thr	Phe	Leu	Lys	Leu	Gln	Ser	His	Tyr	Tyr	Ala	Phe	Lys	Asn	His		
		115				120						125					
Ser	Lys	Asp	Gln	Glu	Phe	Ile	Ser	Asn	Ser	Ile	Val	Ser	Leu	Gly	Glu		
		130				135					140						
Phe	Ile	Glu	Lys	Tyr	Pro	Asn	Ser	Arg	Tyr	Arg	Pro	Tyr	Val	Glu	Tyr		
	145			150					155					160			
Met	Gln	Ile	Lys	Phe	Ile	Leu	Gly	Gln	Asn	Glu	Leu	Asn	Arg	Ala	Ile		
			165					170						175			
Ala	Asn	Val	Tyr	Lys	Lys	Arg	His	Lys	Pro	Glu	Gly	Val	Lys	Arg	Tyr		
		180						185					190				
Leu	Glu	Arg	Ile	Asp	Glu	Thr	Leu	Glu	Lys	Glu	Thr	Lys	Pro	Lys	Pro		
		195				200						205					
Ser	His	Met	Pro	Trp	Tyr	Val	Leu	Ile	Phe	Asp	Trp						
		210				215					220						

<210> 49  
 <211> 801

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (75)...(749)

<400> 49

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gaaaaaggct ctgctttgat agataaattt gacgctaacc cctataaaac gatttttggga 60
gaaaggaaat aatc atg aga gct acg gcg ata aaa atc ttt tca ctc tca 110
          Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Leu Ser
                1             5             10
```

```
tca gca tta gcc cta ttg ctt cat ggt tgc ttg agc atc aat tta aaa 158
Ser Ala Leu Ala Leu Leu Leu His Gly Cys Leu Ser Ile Asn Leu Lys
          15             20             25
```

```
caa atg cta cca gag atc aga act tac gat ttg aat gcg agt tct ttt 206
Gln Met Leu Pro Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe
          30             35             40
```

```
gaa atc acg caa tgc gct aaa cct ttg act gaa gtg agg ctc att agt 254
Glu Ile Thr Gln Cys Ala Lys Pro Leu Thr Glu Val Arg Leu Ile Ser
          45             50             55             60
```

```
att ttg agc gcg gat tta ttc aac act aaa gag atc gtt ttt aaa gcc 302
Ile Leu Ser Ala Asp Leu Phe Asn Thr Lys Glu Ile Val Phe Lys Ala
          65             70             75
```

```
aaa gac ggg cag atc acg cat ggg aag cac caa aaa tgg ata gac ttg 350
Lys Asp Gly Gln Ile Thr His Gly Lys His Gln Lys Trp Ile Asp Leu
          80             85             90
```

```
cct cgc aac atg cta aaa acc atg ttc atg caa gaa gcg caa aaa gca 398
Pro Arg Asn Met Leu Lys Thr Met Phe Met Gln Glu Ala Gln Lys Ala
          95             100             105
```

```
tgc tta ggc gtg gct ttg cct cct tat ggc gcg ggt gca ccc act tat 446
Cys Leu Gly Val Ala Leu Pro Pro Tyr Gly Ala Gly Ala Pro Thr Tyr
          110             115             120
```

```
gcg gtt cgt ttt acg att tta tcg ttt tct ctt tta gaa aaa gaa aat 494
Ala Val Arg Phe Thr Ile Leu Ser Phe Ser Leu Leu Glu Lys Glu Asn
          125             130             135             140
```

```
tct acc tat agg gcg gaa ttt gca cta ggc tat gac att agc gtg aaa 542
Ser Thr Tyr Arg Ala Glu Phe Ala Leu Gly Tyr Asp Ile Ser Val Lys
          145             150             155
```

```
ggc gat tcg cat tct ggg gtg atc att aag cat gaa aat att tct agc 590
Gly Asp Ser His Ser Gly Val Ile Ile Lys His Glu Asn Ile Ser Ser
          160             165             170
```

```
ttg gaa aat aaa acg acc aaa acg agt aaa aat ggc aat caa gat ttt 638
Leu Glu Asn Lys Thr Thr Lys Thr Ser Lys Asn Gly Asn Gln Asp Phe
```

175	180	185	
caa gaa agc gcg ata caa tct ctc caa cat gta agc gtg caa gcg att			686
Gln Glu Ser Ala Ile Gln Ser Leu Gln His Val Ser Val Gln Ala Ile			
190	195	200	
caa gaa gcg gtt tct ttg att aaa aaa gcc att gaa gcg caa agc gta			734
Gln Glu Ala Val Ser Leu Ile Lys Lys Ala Ile Glu Ala Gln Ser Val			
205	210	215	220
agc ccg tta aaa aaa taaaaaataa ggaggaattg tttgatttta cgattggctg			789
Ser Pro Leu Lys Lys			
225			
gagcaagcgt tt			801

<210> 50  
 <211> 225  
 <212> PRT  
 <213> Helicobacter pylori

<400> 50

Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Leu Ser Ser Ala Leu Ala			
1	5	10	15
Leu Leu Leu His Gly Cys Leu Ser Ile Asn Leu Lys Gln Met Leu Pro			
20	25	30	
Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe Glu Ile Thr Gln			
35	40	45	
Cys Ala Lys Pro Leu Thr Glu Val Arg Leu Ile Ser Ile Leu Ser Ala			
50	55	60	
Asp Leu Phe Asn Thr Lys Glu Ile Val Phe Lys Ala Lys Asp Gly Gln			
65	70	75	80
Ile Thr His Gly Lys His Gln Lys Trp Ile Asp Leu Pro Arg Asn Met			
85	90	95	
Leu Lys Thr Met Phe Met Gln Glu Ala Gln Lys Ala Cys Leu Gly Val			
100	105	110	
Ala Leu Pro Pro Tyr Gly Ala Gly Ala Pro Thr Tyr Ala Val Arg Phe			
115	120	125	
Thr Ile Leu Ser Phe Ser Leu Leu Glu Lys Glu Asn Ser Thr Tyr Arg			
130	135	140	
Ala Glu Phe Ala Leu Gly Tyr Asp Ile Ser Val Lys Gly Asp Ser His			
145	150	155	160
Ser Gly Val Ile Ile Lys His Glu Asn Ile Ser Ser Leu Glu Asn Lys			
165	170	175	
Thr Thr Lys Thr Ser Lys Asn Gly Asn Gln Asp Phe Gln Glu Ser Ala			
180	185	190	
Ile Gln Ser Leu Gln His Val Ser Val Gln Ala Ile Gln Glu Ala Val			
195	200	205	
Ser Leu Ile Lys Lys Ala Ile Glu Ala Gln Ser Val Ser Pro Leu Lys			
210	215	220	
Lys			
225			

<210> 51

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<211> 448
<212> DNA
<213> Helicobacter pylori
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<400>	51															
ttttatgata	agatag	tcaa	attata	catt	gactta	agga	aatttta	attg	atg	aaa					56	
										Met	Lys					
										1						
tct	aaa	atc	act	cat	ttt	atc	gct	atc	tct	ttt	gtt	tta	agc	ctg	ttt	104
Ser	Lys	Ile	Thr	His	Phe	Ile	Ala	Ile	Ser	Phe	Val	Leu	Ser	Leu	Phe	
		5					10					15				
agc	gca	tgc	aaa	gac	gag	cct	aaa	aaa	tcg	tct	caa	tcg	cac	caa	aac	152
Ser	Ala	Cys	Lys	Asp	Glu	Pro	Lys	Lys	Ser	Ser	Gln	Ser	His	Gln	Asn	
	20					25					30					
aac	act	aaa	atc	act	aaa	aac	aat	cca	atc	aat	caa	gcg	aat	aat	gat	200
Asn	Thr	Lys	Ile	Thr	Lys	Asn	Asn	Pro	Ile	Asn	Gln	Ala	Asn	Asn	Asp	
	35				40					45					50	
ata	aga	aaa	att	gag	cat	gaa	gaa	gaa	gat	gaa	aaa	gcc	acc	aaa	gaa	248
Ile	Arg	Lys	Ile	Glu	His	Glu	Glu	Glu	Asp	Glu	Lys	Ala	Thr	Lys	Glu	
			55						60					65		
gtg	aac	gat	ttg	atc	aat	aac	gaa	aat	aaa	att	gat	gaa	atc	aat	aat	296
Val	Asn	Asp	Leu	Ile	Asn	Asn	Glu	Asn	Lys	Ile	Asp	Glu	Ile	Asn	Asn	
			70					75					80			
gaa	gaa	aac	gct	gat	cct	tcg	caa	aaa	aga	acg	aac	aac	gtt	ttg	caa	344
Glu	Glu	Asn	Ala	Asp	Pro	Ser	Gln	Lys	Arg	Thr	Asn	Asn	Val	Leu	Gln	
		85					90					95				
cga	gcc	act	aac	cac	caa	gac	aat	ctc	aat	tcc	cca	ctc	aac	agg	aag	392
Arg	Ala	Thr	Asn	His	Gln	Asp	Asn	Leu	Asn	Ser	Pro	Leu	Asn	Arg	Lys	
	100					105					110					
tat	taaagt	gtga	aactttttt	c	aaaggatt	ta	tttaaaaaa	aag	taacc	ccttt						445
Tyr																
115																
att																448

```
<400> 52
Met Lys Ser Lys Ile Thr His Phe Ile Ala Ile Ser Phe Val Leu Ser
 1             5             10             15
```

Leu	Phe	Ser	Ala	Cys	Lys	Asp	Glu	Pro	Lys	Lys	Ser	Ser	Gln	Ser	His
			20					25					30		
Gln	Asn	Asn	Thr	Lys	Ile	Thr	Lys	Asn	Asn	Pro	Ile	Asn	Gln	Ala	Asn
	35						40					45			
Asn	Asp	Ile	Arg	Lys	Ile	Glu	His	Glu	Glu	Glu	Asp	Glu	Lys	Ala	Thr
	50					55					60				
Lys	Glu	Val	Asn	Asp	Leu	Ile	Asn	Asn	Glu	Asn	Lys	Ile	Asp	Glu	Ile
65					70				75						80
Asn	Asn	Glu	Glu	Asn	Ala	Asp	Pro	Ser	Gln	Lys	Arg	Thr	Asn	Asn	Val
			85						90				95		
Leu	Gln	Arg	Ala	Thr	Asn	His	Gln	Asp	Asn	Leu	Asn	Ser	Pro	Leu	Asn
			100					105					110		
Arg	Lys	Tyr													
		115													

<210> 53  
 <211> 1121  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (121)...(1065)

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 tatccaccag cggttaatatca tccccaccaa caaaaaatta ctcgctacaa gggaatttta 120  
 atg ggt ttg gcg ttg gaa aaa gtt tgt ttt tta ggc gtt att ttt ttg 168  
 Met Gly Leu Ala Leu Glu Lys Val Cys Phe Leu Gly Val Ile Phe Leu  
 1 5 10 15

att agc gct tgc acg gtt aaa aaa gag ggg gta aag aat ttg tct tac 216  
 Ile Ser Ala Cys Thr Val Lys Lys Glu Gly Val Lys Asn Leu Ser Tyr  
 20 25 30

aag cat gaa agc ttg cgc gct tat gaa aac gct aaa gat tat gat ccg 264  
 Lys His Glu Ser Leu Arg Ala Tyr Glu Asn Ala Lys Asp Tyr Asp Pro  
 35 40 45

aca acc aaa aaa gcc gcc tat aaa cgc aat ttt ttt gaa cgc cat ttc 312  
 Thr Thr Lys Lys Ala Ala Tyr Lys Arg Asn Phe Phe Glu Arg His Phe  
 50 55 60

aaa cgc tac tcc gat tcg caa gat agc aac aca aaa gat cag cca cta 360  
 Lys Arg Tyr Ser Asp Ser Gln Asp Ser Asn Thr Lys Asp Gln Pro Leu  
 65 70 75 80

gat aac ggc atg cgc gat tct agc tcg atc caa aga gcc acc atg cgc 408  
 Asp Asn Gly Met Arg Asp Ser Ser Ser Ile Gln Arg Ala Thr Met Arg  
 85 90 95

cct tat caa gtg ggg ggc aag tgg tat tac ccc act aaa gtg gat tta 456  
 Pro Tyr Gln Val Gly Gly Lys Trp Tyr Tyr Pro Thr Lys Val Asp Leu  
 100 105 110



ggc gaa aaa ttt gat ggc gtt gcg agt tgg tat ggc cct aac ttc cat	504
Gly Glu Lys Phe Asp Gly Val Ala Ser Trp Tyr Gly Pro Asn Phe His	
115 120 125	
gcc aaa aaa acc agt aat ggg gaa att tat aac atg tat gcc cac acc	552
Ala Lys Lys Thr Ser Asn Gly Glu Ile Tyr Asn Met Tyr Ala His Thr	
130 135 140	
gcc gcg cac aaa act tta ccc atg aac acc gtg gtg aaa gtc atc aat	600
Ala Ala His Lys Thr Leu Pro Met Asn Thr Val Val Lys Val Ile Asn	
145 150 155 160	
gtt gat aat aac tta agc acc att gtg cgc atc aac gat aga ggg cct	648
Val Asp Asn Asn Leu Ser Thr Ile Val Arg Ile Asn Asp Arg Gly Pro	
165 170 175	
ttt gtg agc gat cgc atc att gat ttg tct aat gcg gcc gct agg gat	696
Phe Val Ser Asp Arg Ile Ile Asp Leu Ser Asn Ala Ala Ala Arg Asp	
180 185 190	
att gac atg gtt aaa aaa ggc aca gcc agc gtg cgt ctc att gtt ttg	744
Ile Asp Met Val Lys Lys Gly Thr Ala Ser Val Arg Leu Ile Val Leu	
195 200 205	
ggc ttt ggt ggg gtt atc tcc acg caa tac gaa caa tcc ttt aac gcc	792
Gly Phe Gly Gly Val Ile Ser Thr Gln Tyr Glu Gln Ser Phe Asn Ala	
210 215 220	
agc tct tca aag atc ttg cac aag gaa ttt aaa gtc ggc gag agc gaa	840
Ser Ser Ser Lys Ile Leu His Lys Glu Phe Lys Val Gly Glu Ser Glu	
225 230 235 240	
aaa agc gtg agc gga ggg aaa ttt tct ttg caa atg ggg gct ttt aga	888
Lys Ser Val Ser Gly Gly Lys Phe Ser Leu Gln Met Gly Ala Phe Arg	
245 250 255	
aac caa ata ggt gct caa act tta gcg gat aaa ttg caa gca gaa aat	936
Asn Gln Ile Gly Ala Gln Thr Leu Ala Asp Lys Leu Gln Ala Glu Asn	
260 265 270	
cca aat tac agc gtc aag gtt gct ttt aaa gac gat ttg tat aaa gtt	984
Pro Asn Tyr Ser Val Lys Val Ala Phe Lys Asp Asp Leu Tyr Lys Val	
275 280 285	
tta gtt caa ggg ttt caa agc gaa gaa gag gct agg gat ttt atg aaa	1032
Leu Val Gln Gly Phe Gln Ser Glu Glu Glu Ala Arg Asp Phe Met Lys	
290 295 300	
aaa tac aac cag aat gcg gtt tta acg aga gaa tgattaagtt attgctttta	1085
Lys Tyr Asn Gln Asn Ala Val Leu Thr Arg Glu	
305 310 315	
gatgtggatg gcacgctcac agacggatcg ttgtat	1121

<210> 54  
 <211> 315  
 <212> PRT  
 <213> Helicobacter pylori

<400> 54  
 Met Gly Leu Ala Leu Glu Lys Val Cys Phe Leu Gly Val Ile Phe Leu  
 1 5 10 15  
 Ile Ser Ala Cys Thr Val Lys Lys Glu Gly Val Lys Asn Leu Ser Tyr  
 20 25 30  
 Lys His Glu Ser Leu Arg Ala Tyr Glu Asn Ala Lys Asp Tyr Asp Pro  
 35 40 45  
 Thr Thr Lys Lys Ala Ala Tyr Lys Arg Asn Phe Phe Glu Arg His Phe  
 50 55 60  
 Lys Arg Tyr Ser Asp Ser Gln Asp Ser Asn Thr Lys Asp Gln Pro Leu  
 65 70 75 80  
 Asp Asn Gly Met Arg Asp Ser Ser Ser Ile Gln Arg Ala Thr Met Arg  
 85 90 95  
 Pro Tyr Gln Val Gly Gly Lys Trp Tyr Tyr Pro Thr Lys Val Asp Leu  
 100 105 110  
 Gly Glu Lys Phe Asp Gly Val Ala Ser Trp Tyr Gly Pro Asn Phe His  
 115 120 125  
 Ala Lys Lys Thr Ser Asn Gly Glu Ile Tyr Asn Met Tyr Ala His Thr  
 130 135 140  
 Ala Ala His Lys Thr Leu Pro Met Asn Thr Val Val Lys Val Ile Asn  
 145 150 155 160  
 Val Asp Asn Asn Leu Ser Thr Ile Val Arg Ile Asn Asp Arg Gly Pro  
 165 170 175  
 Phe Val Ser Asp Arg Ile Ile Asp Leu Ser Asn Ala Ala Ala Arg Asp  
 180 185 190  
 Ile Asp Met Val Lys Lys Gly Thr Ala Ser Val Arg Leu Ile Val Leu  
 195 200 205  
 Gly Phe Gly Gly Val Ile Ser Thr Gln Tyr Glu Gln Ser Phe Asn Ala  
 210 215 220  
 Ser Ser Ser Lys Ile Leu His Lys Glu Phe Lys Val Gly Glu Ser Glu  
 225 230 235 240  
 Lys Ser Val Ser Gly Gly Lys Phe Ser Leu Gln Met Gly Ala Phe Arg  
 245 250 255  
 Asn Gln Ile Gly Ala Gln Thr Leu Ala Asp Lys Leu Gln Ala Glu Asn  
 260 265 270  
 Pro Asn Tyr Ser Val Lys Val Ala Phe Lys Asp Asp Leu Tyr Lys Val  
 275 280 285  
 Leu Val Gln Gly Phe Gln Ser Glu Glu Glu Ala Arg Asp Phe Met Lys  
 290 295 300  
 Lys Tyr Asn Gln Asn Ala Val Leu Thr Arg Glu  
 305 310 315

<210> 55  
 <211> 811  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS

<222> (51)...(761)

<400> 55

tataataagg aaattctaaa cgaaaattaa actgaatgaa aggagtttga atg aaa	56
Met Lys	
1	
aaa atc gtt tta gta gcg ata gcc tta ttg atg agc gct tgc gcg agc	104
Lys Ile Val Leu Val Ala Ile Ala Leu Leu Met Ser Ala Cys Ala Ser	
5 10 15	
tat aag atc acg cct gaa cat gtt act tcc tat aat aat ggg att caa	152
Tyr Lys Ile Thr Pro Glu His Val Thr Ser Tyr Asn Asn Gly Ile Gln	
20 25 30	
gtg atg act tcc acg caa gcc aaa tct aaa gtc cag cta gaa atc gct	200
Val Met Thr Ser Thr Gln Ala Lys Ser Lys Val Gln Leu Glu Ile Ala	
35 40 45 50	
caa agc aag ttg aaa ggc ttg aac gag tcc ccc tta gtg ctg tat gta	248
Gln Ser Lys Leu Lys Gly Leu Asn Glu Ser Pro Leu Val Leu Tyr Val	
55 60 65	
gcg gcg caa gtt ata gag gga agt cct gtg gtg ttt agc cgt aaa gcc	296
Ala Ala Gln Val Ile Glu Gly Ser Pro Val Val Phe Ser Arg Lys Ala	
70 75 80	
att tca gtg tct atc aac caa acg aat tta ccg gtc tta agc ctg aga	344
Ile Ser Val Ser Ile Asn Gln Thr Asn Leu Pro Val Leu Ser Leu Arg	
85 90 95	
cag gtg atg aaa tcc agt ttt gat ttt gag ggt att tta caa agt ttt	392
Gln Val Met Lys Ser Ser Phe Asp Phe Glu Gly Ile Leu Gln Ser Phe	
100 105 110	
aat atc gcc gtg ccg acc acc cct att gat aat gtc aat atg atc acc	440
Asn Ile Ala Val Pro Thr Thr Pro Ile Asp Asn Val Asn Met Ile Thr	
115 120 125 130	
ccg cct atg ttt tat tac ggg caa ggg gga ttt tta gct tat aac ggc	488
Pro Pro Met Phe Tyr Tyr Gly Gln Gly Gly Phe Leu Ala Tyr Asn Gly	
135 140 145	
atg atg tat ggg gga atg ggc atg tat ggg cca ggc ttt ggc atg atg	536
Met Met Tyr Gly Gly Met Gly Met Tyr Gly Pro Gly Phe Gly Met Met	
150 155 160	
atg atg gat gat gta gaa gag caa gaa gtc atg caa gaa agc cgc caa	584
Met Met Asp Asp Val Glu Glu Gln Glu Val Met Gln Glu Ser Arg Gln	
165 170 175	
gct tta aaa atc cta gcg atc aat tac ctt aaa aac aac acc ctt aat	632
Ala Leu Lys Ile Leu Ala Ile Asn Tyr Leu Lys Asn Asn Thr Leu Asn	
180 185 190	

gtt gag agt aag gct aag gga ggg ttt gtg gtg gtg gat acc aaa aac 680  
 Val Glu Ser Lys Ala Lys Gly Gly Phe Val Val Val Asp Thr Lys Asn  
 195 200 205 210

ctt aaa acc ccg ggt gtg gtg gtg gtt aaa gtc ttt tta gaa gat gaa 728  
 Leu Lys Thr Pro Gly Val Val Val Val Lys Val Phe Leu Glu Asp Glu  
 215 220 225

atc cac acc ttt aaa att gat att tct aag atg taatcgcccc ctttaataaa 781  
 Ile His Thr Phe Lys Ile Asp Ile Ser Lys Met  
 230 235

agcctttggg ccattccacct aaagggttttt 811

<210> 56  
 <211> 237  
 <212> PRT  
 <213> Helicobacter pylori

<400> 56  
 Met Lys Lys Ile Val Leu Val Ala Ile Ala Leu Leu Met Ser Ala Cys  
 1 5 10 15  
 Ala Ser Tyr Lys Ile Thr Pro Glu His Val Thr Ser Tyr Asn Asn Gly  
 20 25 30  
 Ile Gln Val Met Thr Ser Thr Gln Ala Lys Ser Lys Val Gln Leu Glu  
 35 40 45  
 Ile Ala Gln Ser Lys Leu Lys Gly Leu Asn Glu Ser Pro Leu Val Leu  
 50 55 60  
 Tyr Val Ala Ala Gln Val Ile Glu Gly Ser Pro Val Val Phe Ser Arg  
 65 70 75 80  
 Lys Ala Ile Ser Val Ser Ile Asn Gln Thr Asn Leu Pro Val Leu Ser  
 85 90 95  
 Leu Arg Gln Val Met Lys Ser Ser Phe Asp Phe Glu Gly Ile Leu Gln  
 100 105 110  
 Ser Phe Asn Ile Ala Val Pro Thr Thr Pro Ile Asp Asn Val Asn Met  
 115 120 125  
 Ile Thr Pro Pro Met Phe Tyr Tyr Gly Gln Gly Gly Phe Leu Ala Tyr  
 130 135 140  
 Asn Gly Met Met Tyr Gly Gly Met Gly Met Tyr Gly Pro Gly Phe Gly  
 145 150 155 160  
 Met Met Met Met Asp Asp Val Glu Glu Gln Glu Val Met Gln Glu Ser  
 165 170 175  
 Arg Gln Ala Leu Lys Ile Leu Ala Ile Asn Tyr Leu Lys Asn Asn Thr  
 180 185 190  
 Leu Asn Val Glu Ser Lys Ala Lys Gly Gly Phe Val Val Val Asp Thr  
 195 200 205  
 Lys Asn Leu Lys Thr Pro Gly Val Val Val Val Lys Val Phe Leu Glu  
 210 215 220  
 Asp Glu Ile His Thr Phe Lys Ile Asp Ile Ser Lys Met  
 225 230 235

<210> 57  
 <211> 1425  
 <212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (97)...(1371)

<400> 57

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taaaaaaaaac tacccttaaa aaaatcaatc taaaattctt aaattaaaaat atagctataa 60
tactactaaaa caatctcaag gtttcaaaat ttagcc atg cgt ctt ctt ctg ttc 114
                                         Met Arg Leu Leu Leu Phe
                                         1           5

aat caa aac gct ttt tta tta gcg tgc atg ttt gtt tca agc gtg tat 162
Asn Gln Asn Ala Phe Leu Leu Ala Cys Met Phe Val Ser Ser Val Tyr
          10           15           20

gtg aac gct gtc tta gac gct tat gca att gaa aac ccc tat att tct 210
Val Asn Ala Val Leu Asp Ala Tyr Ala Ile Glu Asn Pro Tyr Ile Ser
          25           30           35

atc aca ctc aca agc cta tta gcc cct tta agc atg cta gcg ttt tta 258
Ile Thr Leu Thr Ser Leu Leu Ala Pro Leu Ser Met Leu Ala Phe Leu
          40           45           50

aaa acc cct aga aat agt gct ttt gct ttg ggg ttt ttt gtg ggg gcg 306
Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu Gly Phe Phe Val Gly Ala
          55           60           65           70

tta ttg ttt tat tgg tgc gct tta agc ttt cgc tac tcg gat ttc act 354
Leu Leu Phe Tyr Trp Cys Ala Leu Ser Phe Arg Tyr Ser Asp Phe Thr
          75           80           85

tat tta ttg ccc tta atc att gtt tta ata gcg tta gtt tat ggg gtt 402
Tyr Leu Leu Pro Leu Ile Ile Val Leu Ile Ala Leu Val Tyr Gly Val
          90           95           100

tta ttt tat ttg ttg ctc tat ttt gaa aac ccc tat ttc agg ctt ttg 450
Leu Phe Tyr Leu Leu Leu Tyr Phe Glu Asn Pro Tyr Phe Arg Leu Leu
          105           110           115

agt ttt tta ggc tct agt ttt atc cac ccc ttt gga ttt gat tgg tta 498
Ser Phe Leu Gly Ser Ser Phe Ile His Pro Phe Gly Phe Asp Trp Leu
          120           125           130

gtc cca gat agc ttt ttt tct tat agc gtg ttt aga gtg gat aaa tta 546
Val Pro Asp Ser Phe Phe Ser Tyr Ser Val Phe Arg Val Asp Lys Leu
          135           140           145           150

tcg cta ggg ctt gtt ttt ttg gct tgc att ttt ttg agc act aaa cca 594
Ser Leu Gly Leu Val Phe Leu Ala Cys Ile Phe Leu Ser Thr Lys Pro
          155           160           165

ttg aaa aaa tat agg atc ata ggg gtt tta ttg tta ctt ggc gcg ttg 642
Leu Lys Lys Tyr Arg Ile Ile Gly Val Leu Leu Leu Leu Gly Ala Leu
          170           175           180
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gat ttt aat ggt ttc aaa aca agc gat tta aaa aag gtt gga aat att	690
Asp Phe Asn Gly Phe Lys Thr Ser Asp Leu Lys Lys Val Gly Asn Ile	
185 190 195	
gaa tta gtc tct aca aaa acg ccc caa gat ttg aaa ttt gac tca agt	738
Glu Leu Val Ser Thr Lys Thr Pro Gln Asp Leu Lys Phe Asp Ser Ser	
200 205 210	
tac ctt aat gat att gaa aac aac att ctt aaa gaa atc aag ctc gct	786
Tyr Leu Asn Asp Ile Glu Asn Asn Ile Leu Lys Glu Ile Lys Leu Ala	
215 220 225 230	
caa agc aag caa aaa acc ttg att gtt ttt cca gaa acc gcc tac ccc	834
Gln Ser Lys Gln Lys Thr Leu Ile Val Phe Pro Glu Thr Ala Tyr Pro	
235 240 245	
atc gct tta gaa aac tcc ccc ttt aaa gcg aag cta gaa gat tta agc	882
Ile Ala Leu Glu Asn Ser Pro Phe Lys Ala Lys Leu Glu Asp Leu Ser	
250 255 260	
gat aat att gct att tta ata ggg aca tta cgg act caa ggc tat aat	930
Asp Asn Ile Ala Ile Leu Ile Gly Thr Leu Arg Thr Gln Gly Tyr Asn	
265 270 275	
ctt tat aac agc tcg ttt tta ttt tct aaa gaa agc gtt cag atc gct	978
Leu Tyr Asn Ser Ser Phe Leu Phe Ser Lys Glu Ser Val Gln Ile Ala	
280 285 290	
gat aaa gta att tta gcc ccc ttt ggc gag acc atg cct tta ccg gaa	1026
Asp Lys Val Ile Leu Ala Pro Phe Gly Glu Thr Met Pro Leu Pro Glu	
295 300 305 310	
ttt ctt caa aaa ccc ctt gaa aag ctc ttt ttt ggc gag agc act tat	1074
Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe Phe Gly Glu Ser Thr Tyr	
315 320 325	
tta tac cgc aat gct cct cat ttc agc gat ttt aca tta gac gat ttt	1122
Leu Tyr Arg Asn Ala Pro His Phe Ser Asp Phe Thr Leu Asp Asp Phe	
330 335 340	
act ttt cgc ccc ctg att tgc tat gaa ggc act tcc aaa ccc gct tat	1170
Thr Phe Arg Pro Leu Ile Cys Tyr Glu Gly Thr Ser Lys Pro Ala Tyr	
345 350 355	
tca aac agc cct tca aaa att ttt atc gtg atg agc aat aac gca tgg	1218
Ser Asn Ser Pro Ser Lys Ile Phe Ile Val Met Ser Asn Asn Ala Trp	
360 365 370	
ttt agc cca agc att gaa ccc acc tta caa aga acg ctt tta aaa tac	1266
Phe Ser Pro Ser Ile Glu Pro Thr Leu Gln Arg Thr Leu Leu Lys Tyr	
375 380 385 390	
tac gca agg cgt tat gat aag atc atc ttg cac agc gcg aac ttt tca	1314
Tyr Ala Arg Arg Tyr Asp Lys Ile Ile Leu His Ser Ala Asn Phe Ser	

395	400	405	
act tct tac atc tta agc cct agt tta tta ggc gat att ctt ttt agg			1362
Thr Ser Tyr Ile Leu Ser Pro Ser Leu Leu Gly Asp Ile Leu Phe Arg			
410	415	420	
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Lys Arg Ser			
425			
tctttataat ggcg			1425
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20 25 30			
Glu Asn Pro Tyr Ile Ser Ile Thr Leu Thr Ser Leu Leu Ala Pro Leu			
35 40 45			
Ser Met Leu Ala Phe Leu Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu			
50 55 60			
Gly Phe Phe Val Gly Ala Leu Leu Phe Tyr Trp Cys Ala Leu Ser Phe			
65 70 75 80			
Arg Tyr Ser Asp Phe Thr Tyr Leu Leu Pro Leu Ile Ile Val Leu Ile			
85 90 95			
Ala Leu Val Tyr Gly Val Leu Phe Tyr Leu Leu Tyr Phe Glu Asn			
100 105 110			
Pro Tyr Phe Arg Leu Leu Ser Phe Leu Gly Ser Ser Phe Ile His Pro			
115 120 125			
Phe Gly Phe Asp Trp Leu Val Pro Asp Ser Phe Phe Ser Tyr Ser Val			
130 135 140			
Phe Arg Val Asp Lys Leu Ser Leu Gly Leu Val Phe Leu Ala Cys Ile			
145 150 155 160			
Phe Leu Ser Thr Lys Pro Leu Lys Lys Tyr Arg Ile Ile Gly Val Leu			
165 170 175			
Leu Leu Leu Gly Ala Leu Asp Phe Asn Gly Phe Lys Thr Ser Asp Leu			
180 185 190			
Lys Lys Val Gly Asn Ile Glu Leu Val Ser Thr Lys Thr Pro Gln Asp			
195 200 205			
Leu Lys Phe Asp Ser Ser Tyr Leu Asn Asp Ile Glu Asn Asn Ile Leu			
210 215 220			
Lys Glu Ile Lys Leu Ala Gln Ser Lys Gln Lys Thr Leu Ile Val Phe			
225 230 235 240			
Pro Glu Thr Ala Tyr Pro Ile Ala Leu Glu Asn Ser Pro Phe Lys Ala			
245 250 255			
Lys Leu Glu Asp Leu Ser Asp Asn Ile Ala Ile Leu Ile Gly Thr Leu			
260 265 270			
Arg Thr Gln Gly Tyr Asn Leu Tyr Asn Ser Ser Phe Leu Phe Ser Lys			
275 280 285			
Glu Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe Gly Glu			

290		295		300
Thr Met Pro Leu Pro Glu Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe				
305		310		315
Phe Gly Glu Ser Thr Tyr Leu Tyr Arg Asn Ala Pro His Phe Ser Asp				
		325		330
Phe Thr Leu Asp Asp Phe Thr Phe Arg Pro Leu Ile Cys Tyr Glu Gly				
		340		345
Thr Ser Lys Pro Ala Tyr Ser Asn Ser Pro Ser Lys Ile Phe Ile Val				
		355		360
Met Ser Asn Asn Ala Trp Phe Ser Pro Ser Ile Glu Pro Thr Leu Gln				
		370		375
Arg Thr Leu Leu Lys Tyr Tyr Ala Arg Arg Tyr Asp Lys Ile Ile Leu				
385		390		395
His Ser Ala Asn Phe Ser Thr Ser Tyr Ile Leu Ser Pro Ser Leu Leu				
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Gly Asp Ile Leu Phe Arg Lys Arg Ser				
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Ser Leu Ser Tyr Val Ser Lys Lys Phe Leu Ser Val Leu Leu Leu Ile	
5	10
15	
tcg ctg ttt tta agc gct tgc aaa tcc aac aat aaa gac aag tta gac	152
Ser Leu Phe Leu Ser Ala Cys Lys Ser Asn Asn Lys Asp Lys Leu Asp	
20	25
30	
gaa aat ctt tta agc tct ggc tct caa agc tcc aaa gaa tta aac gat	200
Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu Asn Asp	
35	40
45	50
gag cga gac aat ata gac aaa aag agt tac gct ggt tta gaa gat gtt	248
Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu Asp Val	
55	60
65	
ttt tca gac aat aag tcc att agt cct aac gat aaa tac atg ctt tta	296
Phe Ser Asp Asn Lys Ser Ile Ser Pro Asn Asp Lys Tyr Met Leu Leu	
70	75
80	
gtt ttt ggc cgt aat ggt tgc tcc tat tgc gaa agg ttt aaa aaa gat	344
Val Phe Gly Arg Asn Gly Cys Ser Tyr Cys Glu Arg Phe Lys Lys Asp	



85	90	95	
ctc aaa aat gtc aaa gaa ttg cgc gac tac att aaa gag cat ttt agc			392
Leu Lys Asn Val Lys Glu Leu Arg Asp Tyr Ile Lys Glu His Phe Ser			
100	105	110	
gct tac tat gtc aat atc agc tac tcc aaa gag cat gat ttt aaa gtc			440
Ala Tyr Tyr Val Asn Ile Ser Tyr Ser Lys Glu His Asp Phe Lys Val			
115	120	125	130
ggc gat aaa aat aat gaa aaa gaa atc aaa atg tcc aca gaa gaa tta			488
Gly Asp Lys Asn Asn Glu Lys Glu Ile Lys Met Ser Thr Glu Glu Leu			
	135	140	145
gcg caa att tat gcc gtc caa tcc acc cct acg att gtt tta tcc gat			536
Ala Gln Ile Tyr Ala Val Gln Ser Thr Pro Thr Ile Val Leu Ser Asp			
	150	155	160
aaa acc ggc aaa acc atc tat gaa ttg ccc ggc tat atg ccc tct acg			584
Lys Thr Gly Lys Thr Ile Tyr Glu Leu Pro Gly Tyr Met Pro Ser Thr			
	165	170	175
caa ttt tta gcc gtg tta gaa ttt atc ggc gat ggg aag tat caa gac			632
Gln Phe Leu Ala Val Leu Glu Phe Ile Gly Asp Gly Lys Tyr Gln Asp			
	180	185	190
aca aaa gac gat gag gat ctc act aaa aaa tta aag gct tac atc aag			680
Thr Lys Asp Asp Glu Asp Leu Thr Lys Lys Leu Lys Ala Tyr Ile Lys			
195	200	205	210
tat aaa acc aac ctt tct aaa agc aag tct aac taggaaagcc taatgaagaa			733
Tyr Lys Thr Asn Leu Ser Lys Ser Lys Ser Asn			
	215	220	
tctcaaaagc ctgcttttctt ttttgctggc ttc			766
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	20	25	30
Leu Asp Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu			
	35	40	45
Asn Asp Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu			
	50	55	60
Asp Val Phe Ser Asp Asn Lys Ser Ile Ser Pro Asn Asp Lys Tyr Met			
65	70	75	80
Leu Leu Val Phe Gly Arg Asn Gly Cys Ser Tyr Cys Glu Arg Phe Lys			
	85	90	95
Lys Asp Leu Lys Asn Val Lys Glu Leu Arg Asp Tyr Ile Lys Glu His			

		100						105					110				
Phe	Ser	Ala	Tyr	Tyr	Val	Asn	Ile	Ser	Tyr	Ser	Lys	Glu	His	Asp	Phe		
		115						120				125					
Lys	Val	Gly	Asp	Lys	Asn	Asn	Glu	Lys	Glu	Ile	Lys	Met	Ser	Thr	Glu		
		130					135					140					
Glu	Leu	Ala	Gln	Ile	Tyr	Ala	Val	Gln	Ser	Thr	Pro	Thr	Ile	Val	Leu		
145					150				155					160			
Ser	Asp	Lys	Thr	Gly	Lys	Thr	Ile	Tyr	Glu	Leu	Pro	Gly	Tyr	Met	Pro		
			165						170					175			
Ser	Thr	Gln	Phe	Leu	Ala	Val	Leu	Glu	Phe	Ile	Gly	Asp	Gly	Lys	Tyr		
		180						185					190				
Gln	Asp	Thr	Lys	Asp	Asp	Glu	Asp	Leu	Thr	Lys	Lys	Leu	Lys	Ala	Tyr		
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Ile	Lys	Tyr	Lys	Thr	Asn	Leu	Ser	Lys	Ser	Lys	Ser	Asn					
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Leu	Leu	Phe	Leu	Leu	Leu	Ser	Ala	Ala	Phe	Met	Leu	Leu	Ala	Glu	Glu	
		5					10					15				

aaa	ata	tct	tta	aac	gat	gac	gcc	ccc	att	aaa	cta	gtg	cat	tgg	caa	154
Lys	Ile	Ser	Leu	Asn	Asp	Asp	Ala	Pro	Ile	Lys	Leu	Val	His	Trp	Gln	
		20				25					30					

aat	gca	tta	aaa	gaa	gtc	caa	cct	gat	tca	aac	gct	cca	gca	aca	cca	202
Asn	Ala	Leu	Lys	Glu	Val	Gln	Pro	Asp	Ser	Asn	Ala	Pro	Ala	Thr	Pro	
		35				40				45					50	

cct	ata	aaa	gcc	gtg	caa	acc	acg	ctc	act	ttt	gaa	acg	cct	ttt	aac	250
Pro	Ile	Lys	Ala	Val	Gln	Thr	Thr	Leu	Thr	Phe	Glu	Thr	Pro	Phe	Asn	
				55				60						65		

aaa	acg	cct	aaa	atc	atg	gaa	gtt	gaa	ggg	caa	aag	gtg	atc	gtc	tta	298
Lys	Thr	Pro	Lys	Ile	Met	Glu	Val	Glu	Gly	Gln	Lys	Val	Ile	Val	Leu	
			70					75					80			

aaa	aac	gct	aaa	ctg	gat	tct	aaa	aaa	acc	atg	gat	ttt	aaa	gaa	gcc	346
Lys	Asn	Ala	Lys	Leu	Asp	Ser	Lys	Lys	Thr	Met	Asp	Phe	Lys	Glu	Ala	
		85					90					95				

tct ttg aat gct tta gaa atg ttt tcc tac caa aat gac atc tac ctc	394
Ser Leu Asn Ala Leu Glu Met Phe Ser Tyr Gln Asn Asp Ile Tyr Leu	
100 105 110	
ttg tct aaa aaa gct aaa gtg gaa tta gaa atc caa gct tca aac agc	442
Leu Ser Lys Lys Ala Lys Val Glu Leu Glu Ile Gln Ala Ser Asn Ser	
115 120 125 130	
aag gat aaa aaa cgg ctc cgc ttt ctc ttt tta ccc aaa ggt ttt cat	490
Lys Asp Lys Lys Arg Leu Arg Phe Leu Phe Leu Pro Lys Gly Phe His	
135 140 145	
tta gcc cca ccg cct aac ctg aaa gaa aaa tct cag caa act aac ctt	538
Leu Ala Pro Pro Pro Asn Leu Lys Glu Lys Ser Gln Gln Thr Asn Leu	
150 155 160	
gca caa aaa gac acc aac gag caa ccc caa agc cct tta aac act cta	586
Ala Gln Lys Asp Thr Asn Glu Gln Pro Gln Ser Pro Leu Asn Thr Leu	
165 170 175	
gag tta aaa ccc cca cta aat tta agc cat gct tat aag gcg cta gcg	634
Glu Leu Lys Pro Pro Leu Asn Leu Ser His Ala Tyr Lys Ala Leu Ala	
180 185 190	
gtt att gct gcc tta ctc tta ata ttg tat gtc atc aaa aaa aaa att	682
Val Ile Ala Ala Leu Leu Leu Ile Leu Tyr Val Ile Lys Lys Lys Ile	
195 200 205 210	
gtt ccc aca caa ggg tct ttt tct gca aaa gat ttt aag tta gaa att	730
Val Pro Thr Gln Gly Ser Phe Ser Ala Lys Asp Phe Lys Leu Glu Ile	
215 220 225	
agc gtt ttg ggt cgt gtt gat gcg aac cat aaa atc att tca ata gaa	778
Ser Val Leu Gly Arg Val Asp Ala Asn His Lys Ile Ile Ser Ile Glu	
230 235 240	
acc aat aag gag cgt tac ttg gtc tta cta agc gat aaa tac ggc ctg	826
Thr Asn Lys Glu Arg Tyr Leu Val Leu Leu Ser Asp Lys Tyr Gly Leu	
245 250 255	
ctt tta gac aaa ata agc cca aaa aca tct aaa gaa gaa ctg att aaa	874
Leu Leu Asp Lys Ile Ser Pro Lys Thr Ser Lys Glu Glu Leu Ile Lys	
260 265 270	
gaa gct gaa aat aat ata aag aat tca aaa tta gga aat tta tat gcc	922
Glu Ala Glu Asn Asn Ile Lys Asn Ser Lys Leu Gly Asn Leu Tyr Ala	
275 280 285 290	
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Gly Lys Phe	
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 20 25 30  
 Trp Gln Asn Ala Leu Lys Glu Val Gln Pro Asp Ser Asn Ala Pro Ala  
 35 40 45  
 Thr Pro Pro Ile Lys Ala Val Gln Thr Thr Leu Thr Phe Glu Thr Pro  
 50 55 60  
 Phe Asn Lys Thr Pro Lys Ile Met Glu Val Glu Gly Gln Lys Val Ile  
 65 70 75 80  
 Val Leu Lys Asn Ala Lys Leu Asp Ser Lys Lys Thr Met Asp Phe Lys  
 85 90 95  
 Glu Ala Ser Leu Asn Ala Leu Glu Met Phe Ser Tyr Gln Asn Asp Ile  
 100 105 110  
 Tyr Leu Leu Ser Lys Lys Ala Lys Val Glu Leu Glu Ile Gln Ala Ser  
 115 120 125  
 Asn Ser Lys Asp Lys Lys Arg Leu Arg Phe Leu Phe Leu Pro Lys Gly  
 130 135 140  
 Phe His Leu Ala Pro Pro Pro Asn Leu Lys Glu Lys Ser Gln Gln Thr  
 145 150 155 160  
 Asn Leu Ala Gln Lys Asp Thr Asn Glu Gln Pro Gln Ser Pro Leu Asn  
 165 170 175  
 Thr Leu Glu Leu Lys Pro Pro Leu Asn Leu Ser His Ala Tyr Lys Ala  
 180 185 190  
 Leu Ala Val Ile Ala Ala Leu Leu Ile Leu Tyr Val Ile Lys Lys  
 195 200 205  
 Lys Ile Val Pro Thr Gln Gly Ser Phe Ser Ala Lys Asp Phe Lys Leu  
 210 215 220  
 Glu Ile Ser Val Leu Gly Arg Val Asp Ala Asn His Lys Ile Ile Ser  
 225 230 235 240  
 Ile Glu Thr Asn Lys Glu Arg Tyr Leu Val Leu Leu Ser Asp Lys Tyr  
 245 250 255  
 Gly Leu Leu Leu Asp Lys Ile Ser Pro Lys Thr Ser Lys Glu Glu Leu  
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 275 280 285  
 Tyr Ala Gly Lys Phe  
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 <212> DNA  
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<400> 63

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atc gct tca aga cta atc gtt gta atc cta tat gct ttt atc ttt att 159
Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe Ile Phe Ile
  15             20             25             30

gtt ctc tct ttt tat atg ctc aat atc atc act att ctt aat ttt aaa 207
Val Leu Ser Phe Tyr Met Leu Asn Ile Ile Thr Ile Leu Asn Phe Lys
              35             40             45

gcg ctt att ttg ggg ttt gtt agt gtt ttt tca agc gca ttg ttt tgt 255
Ala Leu Ile Leu Gly Phe Val Ser Val Phe Ser Ser Ala Leu Phe Cys
              50             55             60

ttt tgc ttg gca att ttt gta gct aga att ttt caa aac gaa caa agc 303
Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn Glu Gln Ser
              65             70             75

atc tta gga ttt tgt aat atc atc aat ctc tat gcg cta atg tct tgt 351
Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu Met Ser Cys
              80             85             90

aat gtt ttt gtt cct tta gaa tac cta cct agt att ggt caa tta ttt 399
Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Ser Ile Gly Gln Leu Phe
  95             100             105             110

atc aaa aca tct att ttt tac tac ctt aat caa ctt cta atc aaa gct 447
Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu Ile Lys Ala
              115             120             125

ttt caa ggg att gat act ata ctg gtt tta gca act tca aca ttt ttc 495
Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser Thr Phe Phe
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att att ggt ggc att att tta ttt tta cta agc gct aat cgc atg tta 543
Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn Arg Met Leu
              145             150             155

cta aca cca aaa gaa cgc atg cgt taaaggctta gtcccaccat tgatttattt 597
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  160             165

aatggctcaa aaaaggggta agc 620

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<212> PRT
<213> Helicobacter pylori

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Ser Glu Arg Tyr Lys Asp Glu Ile Lys Glu Leu Ile Pro Glu Val Asp	
85 90 95	
att ttt acc ggc gtg ggg gat tat gac aag atc gat ata atg att gct	394
Ile Phe Thr Gly Val Gly Asp Tyr Asp Lys Ile Asp Ile Met Ile Ala	
100 105 110 115	
aaa aaa caa aac cag ttc agc gag caa gtg ttt tta agc gag cat tac	442
Lys Lys Gln Asn Gln Phe Ser Glu Gln Val Phe Leu Ser Glu His Tyr	
120 125 130	
aac gca cgc atc atc acg gga tgc agc gtg cat gcg tat gtg aaa att	490
Asn Ala Arg Ile Ile Thr Gly Ser Ser Val His Ala Tyr Val Lys Ile	
135 140 145	
tct gag ggt tgc aat caa aaa tgt tct ttt tgc gct atc cct agc ttt	538
Ser Glu Gly Cys Asn Gln Lys Cys Ser Phe Cys Ala Ile Pro Ser Phe	
150 155 160	
aag ggg aaa ttg caa agc agg gaa ttg gac tcc att tta aaa gaa gtg	586
Lys Gly Lys Leu Gln Ser Arg Glu Leu Asp Ser Ile Leu Lys Glu Val	
165 170 175	
gaa aat ctc gcg ctt aaa ggc tat acg gat atg act ttt atc gct caa	634
Glu Asn Leu Ala Leu Lys Gly Tyr Thr Asp Met Thr Phe Ile Ala Gln	
180 185 190 195	
gac tct agc tcc ttt tta tac gat aag ggg caa aaa gac ggc ttg atc	682
Asp Ser Ser Ser Phe Leu Tyr Asp Lys Gly Gln Lys Asp Gly Leu Ile	
200 205 210	
cag ctc att aga gcg att gat aaa cag caa gcc tta aag agc gcg cgt	730
Gln Leu Ile Arg Ala Ile Asp Lys Gln Gln Ala Leu Lys Ser Ala Arg	
215 220 225	
att tta tat ctc tac ccc tct agc acc acg cta gag ctt att ggc gcg	778
Ile Leu Tyr Leu Tyr Pro Ser Ser Thr Thr Leu Glu Leu Ile Gly Ala	
230 235 240	
att gaa agt tgc ccc att ttt caa aat tat ttt gac atg ccc atc cag	826
Ile Glu Ser Ser Pro Ile Phe Gln Asn Tyr Phe Asp Met Pro Ile Gln	
245 250 255	
cac atc agc gac tcc atg ctc aaa aag atg cgg cgc aac tct agc caa	874
His Ile Ser Asp Ser Met Leu Lys Lys Met Arg Arg Asn Ser Ser Gln	
260 265 270 275	
gcg cac cat tta aag ctt tta gat gcc atg aag cag gtt aaa gaa agc	922
Ala His His Leu Lys Leu Leu Asp Ala Met Lys Gln Val Lys Glu Ser	
280 285 290	
ttt atc aga agc acg atc att gta ggg cat ccg gaa gaa aat gag agc	970
Phe Ile Arg Ser Thr Ile Ile Val Gly His Pro Glu Glu Asn Glu Ser	

295	300	305	
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Glu Phe Glu Glu Leu Ser Ala Phe Leu Asp Glu Phe Gln Phe Asp Arg			
310	315	320	
ttg aat att ttt gct ttc agc gct gaa gaa aac acg cat gcc tat tct			1066
Leu Asn Ile Phe Ala Phe Ser Ala Glu Glu Asn Thr His Ala Tyr Ser			
325	330	335	
tta gaa aaa gtg cct aaa aaa acc atc aac gct cgc atc aaa gcc ttg			1114
Leu Glu Lys Val Pro Lys Lys Thr Ile Asn Ala Arg Ile Lys Ala Leu			
340	345	350	355
aat aaa atc gct tta aag cac caa aac cat tcc ttt aag gct ttg ttg			1162
Asn Lys Ile Ala Leu Lys His Gln Asn His Ser Phe Lys Ala Leu Leu			
360	365	370	
aat aag ccc att aag gcg tta gtg gaa aat aaa gag ggc gag tat ttt			1210
Asn Lys Pro Ile Lys Ala Leu Val Glu Asn Lys Glu Gly Glu Tyr Phe			
375	380	385	
tac aaa gca agg gat ctc aga tgg gcg cct gaa gtg gat ggg gaa atc			1258
Tyr Lys Ala Arg Asp Leu Arg Trp Ala Pro Glu Val Asp Gly Glu Ile			
390	395	400	
ttg atc aat gat agc gaa cta acc acc ccc tta aaa ccc ggg cat tat			1306
Leu Ile Asn Asp Ser Glu Leu Thr Thr Pro Leu Lys Pro Gly His Tyr			
405	410	415	
acg att gca cct agc gaa ttt aaa gat aat atc cta ctc gct aag gtt			1354
Thr Ile Ala Pro Ser Glu Phe Lys Asp Asn Ile Leu Leu Ala Lys Val			
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 Tyr Thr Leu Thr Asn Asp Ala Lys Ser Ala Asp Val Ile Leu Ile Asn  
 35 40 45  
 Thr Cys Gly Phe Ile Glu Ser Ala Lys Gln Glu Ser Ile Gln Thr Ile  
 50 55 60  
 Leu Asn Ala Ala Lys Asp Lys Lys Glu Gly Ala Ile Leu Ile Ala Ser  
 65 70 75 80



Gly	Cys	Leu	Ser	Glu	Arg	Tyr	Lys	Asp	Glu	Ile	Lys	Glu	Leu	Ile	Pro	
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Glu	Val	Asp	Ile	Phe	Thr	Gly	Val	Gly	Asp	Tyr	Asp	Lys	Ile	Asp	Ile	
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Glu	His	Tyr	Asn	Ala	Arg	Ile	Ile	Thr	Gly	Ser	Ser	Val	His	Ala	Tyr	
	130					135					140					
Val	Lys	Ile	Ser	Glu	Gly	Cys	Asn	Gln	Lys	Cys	Ser	Phe	Cys	Ala	Ile	
145					150					155					160	
Pro	Ser	Phe	Lys	Gly	Lys	Leu	Gln	Ser	Arg	Glu	Leu	Asp	Ser	Ile	Leu	
			165					170						175		
Lys	Glu	Val	Glu	Asn	Leu	Ala	Leu	Lys	Gly	Tyr	Thr	Asp	Met	Thr	Phe	
		180						185					190			
Ile	Ala	Gln	Asp	Ser	Ser	Ser	Phe	Leu	Tyr	Asp	Lys	Gly	Gln	Lys	Asp	
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Gly	Leu	Ile	Gln	Leu	Ile	Arg	Ala	Ile	Asp	Lys	Gln	Gln	Ala	Leu	Lys	
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Ser	Ala	Arg	Ile	Leu	Tyr	Leu	Tyr	Pro	Ser	Ser	Thr	Thr	Leu	Glu	Leu	
225					230					235					240	
Ile	Gly	Ala	Ile	Glu	Ser	Ser	Pro	Ile	Phe	Gln	Asn	Tyr	Phe	Asp	Met	
			245					250						255		
Pro	Ile	Gln	His	Ile	Ser	Asp	Ser	Met	Leu	Lys	Lys	Met	Arg	Arg	Asn	
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Ser	Ser	Gln	Ala	His	His	Leu	Lys	Leu	Leu	Asp	Ala	Met	Lys	Gln	Val	
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Lys	Glu	Ser	Phe	Ile	Arg	Ser	Thr	Ile	Ile	Val	Gly	His	Pro	Glu	Glu	
	290					295				300						
Asn	Glu	Ser	Glu	Phe	Glu	Glu	Leu	Ser	Ala	Phe	Leu	Asp	Glu	Phe	Gln	
305				310						315					320	
Phe	Asp	Arg	Leu	Asn	Ile	Phe	Ala	Phe	Ser	Ala	Glu	Glu	Asn	Thr	His	
			325					330						335		
Ala	Tyr	Ser	Leu	Glu	Lys	Val	Pro	Lys	Lys	Thr	Ile	Asn	Ala	Arg	Ile	
		340						345					350			
Lys	Ala	Leu	Asn	Lys	Ile	Ala	Leu	Lys	His	Gln	Asn	His	Ser	Phe	Lys	
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	370					375					380					
Glu	Tyr	Phe	Tyr	Lys	Ala	Arg	Asp	Leu	Arg	Trp	Ala	Pro	Glu	Val	Asp	
385				390						395					400	
Gly	Glu	Ile	Leu	Ile	Asn	Asp	Ser	Glu	Leu	Thr	Thr	Pro	Leu	Lys	Pro	
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Gly	His	Tyr	Thr	Ile	Ala	Pro	Ser	Glu	Phe	Lys	Asp	Asn	Ile	Leu	Leu	
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tgttttcact ttaatttttg cccttttctt tctcacttcg tttaaaaaac ctttaactca 180
agtcttggtg attgtttta atg gtt ttt ttg ttt ttt agg tgt tat ttc caa 232
      Met Val Phe Leu Phe Phe Arg Cys Tyr Phe Gln
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gcg tct ttg aaa gaa act ttc gca att aat cat tta aaa aca atg tct 280
Ala Ser Leu Lys Glu Thr Phe Ala Ile Asn His Leu Lys Thr Met Ser
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Phe Lys Trp Leu Thr Leu Ala Phe Leu Gly Val Phe Leu Ser Ile Phe
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cct aac atg ttt aac atg cat gat agc caa act ttc cgc tac aat tta 376
Pro Asn Met Phe Asn Met His Asp Ser Gln Thr Phe Arg Tyr Asn Leu
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ttc gct cta aac atg tcc tta act tat gct tgc ggg gcg tta tgc ttg 424
Phe Ala Leu Asn Met Ser Leu Thr Tyr Ala Cys Gly Ala Leu Cys Leu
              60             65             70             75

ctt ttt gcc agt tgc tta aga atc aaa ttg aat caa aaa atc ctt ttt 472
Leu Phe Ala Ser Cys Leu Arg Ile Lys Leu Asn Gln Lys Ile Leu Phe
              80             85             90

tac agc atg gct gtt gca aat ttc atc aac ggc ttg ctc tca ttg gtg 520
Tyr Ser Met Ala Val Ala Asn Phe Ile Asn Gly Leu Leu Ser Leu Val
              95             100             105

caa aaa att tat ttt aac atg ccc aga gcg caa ggg ttt agc acg gtt 568
Gln Lys Ile Tyr Phe Asn Met Pro Arg Ala Gln Gly Phe Ser Thr Val
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aag gag tat gtg gtt tta gtg agc gtg tcc att tta ggc tgt tat att 616
Lys Glu Tyr Val Val Leu Val Ser Val Ser Ile Leu Gly Cys Tyr Ile
              125             130             135

tat gcg ctt tat tcg cac aat caa aaa gaa aaa ctt ttt ttc acg ctt 664
Tyr Ala Leu Tyr Ser His Asn Gln Lys Glu Lys Leu Phe Phe Thr Leu
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tct gtt ttt gtg ggg ttt tta gtc gtt att tta agc gcc aca agg agc 712
Ser Val Phe Val Gly Phe Leu Val Val Ile Leu Ser Ala Thr Arg Ser
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gcg aca atc gct ttt gtt att act ttt tta atc ctt tct tgc ttt att 760
Ala Thr Ile Ala Phe Val Ile Thr Phe Leu Ile Leu Ser Cys Phe Ile
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tta tac gcc aaa aaa tcg ctc aaa cca ttg ggt tat atg gtg gtc gtg 808
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aag	ggg	gca	ata	gag	caa	tct	aga	ggt	caa	aat	caa	agc	ttt	gaa	gaa	904	
Lys	Gly	Ala	Ile	Glu	Gln	Ser	Arg	Val	Gln	Asn	Gln	Ser	Phe	Glu	Glu		
	220				225					230					235		
gat	ctg	aaa	cgc	tac	gct	aaa	aag	gac	gct	gat	agc	agt	atc	gga	tgg	952	
Asp	Leu	Lys	Arg	Tyr	Ala	Lys	Lys	Asp	Ala	Asp	Ser	Ser	Ile	Gly	Trp		
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cgt	ttg	gag	cgt	tgg	aaa	gaa	gcc	cta	acg	ggt	ttg	cgt	tta	agg	ccc	1000	
Arg	Leu	Glu	Arg	Trp	Lys	Glu	Ala	Leu	Thr	Val	Leu	Arg	Leu	Arg	Pro		
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Phe	Phe	Gly	Met	Ala	Ala	Ser	Glu	Lys	Cys	Gln	Arg	Leu	Glu	Glu	Ile		
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tta	tcc	tta	tca	aag	tct	tat	agg	gcc	aaa	gat	ttg	att	ctc	tgt	tat	1096	
Leu	Ser	Leu	Ser	Lys	Ser	Tyr	Arg	Ala	Lys	Asp	Leu	Ile	Leu	Cys	Tyr		
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gaa	aga	tac	gac	aat	caa	atc	att	cac	att	tta	gcc	act	agg	ggg	atc	1144	
Glu	Arg	Tyr	Asp	Asn	Gln	Ile	Ile	His	Ile	Leu	Ala	Thr	Arg	Gly	Ile		
	300				305					310					315		
ata	ggc	ttt	ttg	atc	tgg	ctc	ttt	ttt	tta	tta	ggt	att	gta	aag	att	1192	
Ile	Gly	Phe	Leu	Ile	Trp	Leu	Phe	Phe	Leu	Leu	Val	Ile	Val	Lys	Ile		
				320					325					330			
ttt	tgg	agc	ggg	ata	aag	caa	aac	tct	tta	ata	tcg	ttt	ttt	ata	cta	1240	
Phe	Trp	Ser	Gly	Ile	Lys	Gln	Asn	Ser	Leu	Ile	Ser	Phe	Phe	Ile	Leu		
			335					340					345				
atg	aca	ctc	gcc	ttt	tac	ctc	att	ttt	ggc	att	ggg	ttt	gac	ccc	ttt	1288	
Met	Thr	Leu	Ala	Phe	Tyr	Leu	Ile	Phe	Gly	Ile	Gly	Phe	Asp	Pro	Phe		
		350				355						360					
gat	ttc	ttc	att	acg	gga	agt	ttt	ttt	gta	gga	atg	atc	atg	atg	gct	1336	
Asp	Phe	Phe	Ile	Thr	Gly	Ser	Phe	Phe	Val	Gly	Met	Ile	Met	Met	Ala		
		365				370					375						
ggt	ttt	tta	aaa	aaa	gat	aaa	agt	gct	ttt	tagcatcaag	gggtttgaca					1386	
Val	Phe	Leu	Lys	Lys	Asp	Lys	Ser	Ala	Phe								
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<212> PRT

<213> Helicobacter pylori

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Leu	Ala	Phe	Leu	Gly	Val	Phe	Leu	Ser	Ile	Phe	Pro	Asn	Met	Phe	Asn
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Met	His	Asp	Ser	Gln	Thr	Phe	Arg	Tyr	Asn	Leu	Phe	Ala	Leu	Asn	Met
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Ser	Leu	Thr	Tyr	Ala	Cys	Gly	Ala	Leu	Cys	Leu	Phe	Ala	Ser	Cys	
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Leu	Arg	Ile	Lys	Leu	Asn	Gln	Lys	Ile	Leu	Phe	Tyr	Ser	Met	Ala	Val
				85					90					95	
Ala	Asn	Phe	Ile	Asn	Gly	Leu	Leu	Ser	Leu	Val	Gln	Lys	Ile	Tyr	Phe
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Asn	Met	Pro	Arg	Ala	Gln	Gly	Phe	Ser	Thr	Val	Lys	Glu	Tyr	Val	Val
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Leu	Val	Ser	Val	Ser	Ile	Leu	Gly	Cys	Tyr	Ile	Tyr	Ala	Leu	Tyr	Ser
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Phe	Leu	Val	Val	Ile	Leu	Ser	Ala	Thr	Arg	Ser	Ala	Thr	Ile	Ala	Phe
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Val	Ile	Thr	Phe	Leu	Ile	Leu	Ser	Cys	Phe	Ile	Leu	Tyr	Ala	Lys	Lys
			180					185					190		
Ser	Leu	Lys	Pro	Leu	Gly	Tyr	Met	Val	Val	Val	Ser	Leu	Ile	Leu	Ser
		195					200					205			
Ala	Leu	Tyr	Val	Gly	Ser	Asn	Ala	Leu	Glu	Lys	Lys	Gly	Ala	Ile	Glu
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Gln	Ser	Arg	Val	Gln	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Leu	Lys	Arg	Tyr
225					230					235					240
Ala	Lys	Lys	Asp	Ala	Asp	Ser	Ser	Ile	Gly	Trp	Arg	Leu	Glu	Arg	Trp
			245						250					255	
Lys	Glu	Ala	Leu	Thr	Val	Leu	Arg	Leu	Arg	Pro	Phe	Phe	Gly	Met	Ala
			260					265					270		
Ala	Ser	Glu	Lys	Cys	Gln	Arg	Leu	Glu	Glu	Ile	Leu	Ser	Leu	Ser	Lys
		275					280					285			
Ser	Tyr	Arg	Ala	Lys	Asp	Leu	Ile	Leu	Cys	Tyr	Glu	Arg	Tyr	Asp	Asn
	290					295					300				
Gln	Ile	Ile	His	Ile	Leu	Ala	Thr	Arg	Gly	Ile	Ile	Gly	Phe	Leu	Ile
305					310					315					320
Trp	Leu	Phe	Phe	Leu	Leu	Val	Ile	Val	Lys	Ile	Phe	Trp	Ser	Gly	Ile
				325					330					335	
Lys	Gln	Asn	Ser	Leu	Ile	Ser	Phe	Phe	Ile	Leu	Met	Thr	Leu	Ala	Phe
			340					345					350		
Tyr	Leu	Ile	Phe	Gly	Ile	Gly	Phe	Asp	Pro	Phe	Asp	Phe	Phe	Ile	Thr
		355					360					365			
Gly	Ser	Phe	Phe	Val	Gly	Met	Ile	Met	Met	Ala	Val	Phe	Leu	Lys	Lys
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Asp	Lys	Ser	Ala	Phe											
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 Met Leu Ile Ser Ile Ala Phe Leu  
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 Leu Val Leu Tyr Leu Leu Asn Tyr Ser Ser Phe Arg Met Leu Lys Ser  
 10 15 20

ttt tta acc tta aag aaa atc tct caa tac gct tat tta tgg ttt ttt 208  
 Phe Leu Thr Leu Lys Lys Ile Ser Gln Tyr Ala Tyr Leu Trp Phe Phe  
 25 30 35 40

atc ctt ttg agc ata ggc gag gcg gct ttt gtt ttt tat aga aat att 256  
 Ile Leu Leu Ser Ile Gly Glu Ala Ala Phe Val Phe Tyr Arg Asn Ile  
 45 50 55

atg cct agc cat ttg ttt gtt ttg act tca gcg tgt tcg ttt gtg tct 304  
 Met Pro Ser His Leu Phe Val Leu Thr Ser Ala Cys Ser Phe Val Ser  
 60 65 70

ttt att att ttt atc ctt tct tta agt ttt tac ggg ttt tcc tat tcc 352  
 Phe Ile Ile Phe Ile Leu Ser Leu Ser Phe Tyr Gly Phe Ser Tyr Ser  
 75 80 85

ata gaa aaa ata gat ttt ttg cat tca agg cgt aaa agt tta aaa aac 400  
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 90 95 100

ttt tta aaa ttg ggg ttt tat ctg gcg tta tta ggg tat ttt tgg cgt 448  
 Phe Leu Lys Leu Gly Phe Tyr Leu Ala Leu Leu Gly Tyr Phe Trp Arg  
 105 110 115 120

ggg ttt tat gaa ggg ttg gcc cgc cct aaa atc aaa gaa acc cct att 496  
 Gly Phe Tyr Glu Gly Leu Ala Arg Pro Lys Ile Lys Glu Thr Pro Ile  
 125 130 135

tat ttg gat aag ctg gat aaa gaa tta aag att att tta ctc aca gac 544  
 Tyr Leu Asp Lys Leu Asp Lys Glu Leu Lys Ile Ile Leu Leu Thr Asp  
 140 145 150

atg cat gtg ggg agt ttg ttg caa aaa gat ttt gtt gat tac att gta 592  
 Met His Val Gly Ser Leu Leu Gln Lys Asp Phe Val Asp Tyr Ile Val  
 155 160 165

gaa gaa gtc aat caa aaa gaa gtg gat atg gtg ctg att ggg ggg gat	640
Glu Glu Val Asn Gln Lys Glu Val Asp Met Val Leu Ile Gly Gly Asp	
170 175 180	
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Leu Val Asp Glu Ser Ile Glu Lys Val Lys Ser Phe Leu Leu Pro Leu	
185 190 195 200	
aac aac ctt aaa agc acg cat ggc act ttt tat gtg cca gga aat cat	736
Asn Asn Leu Lys Ser Thr His Gly Thr Phe Tyr Val Pro Gly Asn His	
205 210 215	
gag tat tat cat ggc ata gag ccg att tta tcg ttt ctt gac acg ctt	784
Glu Tyr Tyr His Gly Ile Glu Pro Ile Leu Ser Phe Leu Asp Thr Leu	
220 225 230	
aat ttg acg att tta ggg aat gag tgc gtg cat tta ggg ggg atc aat	832
Asn Leu Thr Ile Leu Gly Asn Glu Cys Val His Leu Gly Gly Ile Asn	
235 240 245	
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250 255 260	
cct gat att gac aaa gct tta aaa aag cgc aat gag agt aag ccc acg	928
Pro Asp Ile Asp Lys Ala Leu Lys Lys Arg Asn Glu Ser Lys Pro Thr	
265 270 275 280	
atc ctt ttg gcc cac caa cct aaa caa att aga agc ctc aaa gaa agc	976
Ile Leu Leu Ala His Gln Pro Lys Gln Ile Arg Ser Leu Lys Glu Ser	
285 290 295	
cac tct gta gat tta gtc ctt tca ggg cat acc cat gca ggg caa atc	1024
His Ser Val Asp Leu Val Leu Ser Gly His Thr His Ala Gly Gln Ile	
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Phe Pro Phe Ser Leu Leu Val Lys Leu Ala Gln Thr Tyr Leu His Gly	
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Leu Tyr Lys His Ser Pro Thr Thr Gln Ile Tyr Val Ser Ser Gly Ala	
330 335 340	
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Gly Tyr Trp Gly Ile Pro Leu Arg Phe Leu Ala Pro Ser Glu Ile Ala	
345 350 355 360	
tac ctt agg ctt tta cct aaa aat caa gct tagttaaaca aaatcttaaa	1218
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 35 40 45  
 Ala Phe Val Phe Tyr Arg Asn Ile Met Pro Ser His Leu Phe Val Leu  
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 Thr Ser Ala Cys Ser Phe Val Ser Phe Ile Ile Phe Ile Leu Ser Leu  
 65 70 75 80  
 Ser Phe Tyr Gly Phe Ser Tyr Ser Ile Glu Lys Ile Asp Phe Leu His  
 85 90 95  
 Ser Arg Arg Lys Ser Leu Lys Asn Phe Leu Lys Leu Gly Phe Tyr Leu  
 100 105 110  
 Ala Leu Leu Gly Tyr Phe Trp Arg Gly Phe Tyr Glu Gly Leu Ala Arg  
 115 120 125  
 Pro Lys Ile Lys Glu Thr Pro Ile Tyr Leu Asp Lys Leu Asp Lys Glu  
 130 135 140  
 Leu Lys Ile Ile Leu Leu Thr Asp Met His Val Gly Ser Leu Leu Gln  
 145 150 155 160  
 Lys Asp Phe Val Asp Tyr Ile Val Glu Glu Val Asn Gln Lys Glu Val  
 165 170 175  
 Asp Met Val Leu Ile Gly Gly Asp Leu Val Asp Glu Ser Ile Glu Lys  
 180 185 190  
 Val Lys Ser Phe Leu Leu Pro Leu Asn Asn Leu Lys Ser Thr His Gly  
 195 200 205  
 Thr Phe Tyr Val Pro Gly Asn His Glu Tyr Tyr His Gly Ile Glu Pro  
 210 215 220  
 Ile Leu Ser Phe Leu Asp Thr Leu Asn Leu Thr Ile Leu Gly Asn Glu  
 225 230 235 240  
 Cys Val His Leu Gly Gly Ile Asn Leu Cys Gly Val Tyr Asp Tyr Phe  
 245 250 255  
 Ala Arg Lys Arg Gln Asn Phe Ala Pro Asp Ile Asp Lys Ala Leu Lys  
 260 265 270  
 Lys Arg Asn Glu Ser Lys Pro Thr Ile Leu Leu Ala His Gln Pro Lys  
 275 280 285  
 Gln Ile Arg Ser Leu Lys Glu Ser His Ser Val Asp Leu Val Leu Ser  
 290 295 300  
 Gly His Thr His Ala Gly Gln Ile Phe Pro Phe Ser Leu Leu Val Lys  
 305 310 315 320  
 Leu Ala Gln Thr Tyr Leu His Gly Leu Tyr Lys His Ser Pro Thr Thr  
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 Gln Ala  
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 Met Ile Phe Val  
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aat aaa tat ctc tat ggg att aaa agc gtt gtg cct ttg gcg gtt ggt 162  
 Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro Leu Ala Val Gly  
 5 10 15 20

ttt agc aaa tac cct tta aaa aag ttt tta tgg ctt aat gtt ttt tcc 210  
 Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu Asn Val Phe Ser  
 25 30 35

agt ttt ttg tgg gcg ctc atc gtg ggg agc gtt tct ttt caa gcg agc 258  
 Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser Phe Gln Ala Ser  
 40 45 50

gat tgg gtg aaa acg ctg tat gaa agg ctt tct cat tac act tcg ttt 306  
 Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His Tyr Thr Ser Phe  
 55 60 65

ttt atc ata agt ttt gtt ctt ata gcg ctt tta ata tgg ttt tta ttg 354  
 Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile Trp Phe Leu Leu  
 70 75 80

aaa cga tat tcg cgc aaa atg ggt ttt taagcaagat gtttaattaa 401  
 Lys Arg Tyr Ser Arg Lys Met Gly Phe  
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atgcgctaga ctacgccac aagcattcgc 431

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 <212> PRT  
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 Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser  
 35 40 45  
 Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His  
 50 55 60



Tyr Thr Ser Phe Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile  
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Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly Phe  
85 90

<210> 73  
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aattttcaa atg tta agg aaa aac att tta gct tac tat ggg gcg aat ttt 111  
Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe  
1 5 10

ctc tta atc atc gct caa agc tta ccc cat gcg att tta acc ccc ttg 159  
Leu Leu Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu  
15 20 25 30

ttg ctt tct aaa ggg ctt agt ttg agt gaa atc ttg ctc gtg caa acc 207  
Leu Leu Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr  
35 40 45

ttt ttt agc ttt tgc gtg cta gtg gct gaa tac cca agc ggc gtt tta 255  
Phe Phe Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu  
50 55 60

gcg gat ttg atg agc cga aaa aat tta ttc ctg gtt tct aat gcc ttt 303  
Ala Asp Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe  
65 70 75

tta atc gct agt ttt tcg ttt gtg ctg ttt ttt gat agc ttt att ttc 351  
Leu Ile Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe  
80 85 90

atg ctt tta gcg tgg ggg ttg tat ggt ttg tat agc gca tgc tct agc 399  
Met Leu Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser  
95 100 105 110

ggc acg att gaa gct tca ctc atc aca gac att aag gaa aac aaa aaa 447  
Gly Thr Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys  
115 120 125

gat tta tcc aag ttt tta gcc aaa aac aat caa att act tat tta ggc 495  
Asp Leu Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly  
130 135 140

atg att ata ggg agt tct ttg gga tcg ttt ttg tat ctc aaa gtc cat 543  
Met Ile Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His

145	150	155	
gcg atg ctg tat att gtg ggg att ttt tta atc atg ctc tgt gtg cta			591
Ala Met Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu			
160	165	170	
acg atc att ttt tat ttt aaa gag aaa gaa ggg gat ttt aaa agc caa			639
Thr Ile Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln			
175	180	185	190
aaa agc ctg aaa ctc ctt aaa gag caa gtc aaa ggc agt ctt aaa gag			687
Lys Ser Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu			
	195	200	205
ctt aaa gat aac ccc aaa ctt aaa att ctg tta gtg ggg cat ttg att			735
Leu Lys Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile			
	210	215	220
acg ccc gtc ttt ttt atg agc cat ttt caa atg tgg caa gcg tat ttt			783
Thr Pro Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe			
	225	230	235
tta aaa caa ggc gtt aaa gag caa tac ctt ttt gtg ttt tat atc gct			831
Leu Lys Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala			
	240	245	250
ttt caa gtg att tct att ctc att cat ttt tta aaa gcc tct agt tat			879
Phe Gln Val Ile Ser Ile Leu Ile His Phe Leu Lys Ala Ser Ser Tyr			
255	260	265	270
agc caa aaa atc gcc ttg agt tcg ctt gtg gtg ttg tta ggc gtt agc			927
Ser Gln Lys Ile Ala Leu Ser Ser Leu Val Val Leu Leu Gly Val Ser			
	275	280	285
ccc tta ttg ctt agc aat atc cct tat tgt ttc ata ggg gtg tat gcg			975
Pro Leu Leu Leu Ser Asn Ile Pro Tyr Cys Phe Ile Gly Val Tyr Ala			
	290	295	300
ctc atg gtg gcg ttt ttc act tac atg agc tat tgc tta aac tat caa			1023
Leu Met Val Ala Phe Phe Thr Tyr Met Ser Tyr Cys Leu Asn Tyr Gln			
	305	310	315
ttc tcc aaa ttc gtt tct aaa aac aac att tcc tcg ctc tca tcg ctt			1071
Phe Ser Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu Ser Ser Leu			
	320	325	330
tta tca agc tgt gtg cgc gtg gtc tct gtg cta atc tta tcg ctc agc			1119
Leu Ser Ser Cys Val Arg Val Val Ser Val Leu Ile Leu Ser Leu Ser			
335	340	345	350
agt ctg gaa ctg cgt tac ttc tca ccc cta act atc ata acc atg cat			1167
Ser Leu Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile Thr Met His			
	355	360	365
ttt gcc ttg acg ctt atc atc ctc ttt ttc ttt ttg tat aag gct aag			1215

Phe Ala Leu Thr Leu Ile Ile Leu Phe Phe Phe Leu Tyr Lys Ala Lys  
 370 375 380

ccg ttt gat gag tgagcggctt taagagtgca accttttagc gatttctata 1267  
 Pro Phe Asp Glu  
 385

gcaacatcat agcc 1281

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 20 25 30  
 Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe  
 35 40 45  
 Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp  
 50 55 60  
 Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe Leu Ile  
 65 70 75 80  
 Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe Met Leu  
 85 90 95  
 Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr  
 100 105 110  
 Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu  
 115 120 125  
 Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile  
 130 135 140  
 Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met  
 145 150 155 160  
 Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu Thr Ile  
 165 170 175  
 Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Ser  
 180 185 190  
 Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys  
 195 200 205  
 Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro  
 210 215 220  
 Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys  
 225 230 235 240  
 Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln  
 245 250 255  
 Val Ile Ser Ile Leu Ile His Phe Leu Lys Ala Ser Ser Tyr Ser Gln  
 260 265 270  
 Lys Ile Ala Leu Ser Ser Leu Val Val Leu Leu Gly Val Ser Pro Leu  
 275 280 285  
 Leu Leu Ser Asn Ile Pro Tyr Cys Phe Ile Gly Val Tyr Ala Leu Met  
 290 295 300  
 Val Ala Phe Phe Thr Tyr Met Ser Tyr Cys Leu Asn Tyr Gln Phe Ser  
 305 310 315 320

Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu Ser Ser Leu Leu Ser  
                                   325                                  330                                  335  
 Ser Cys Val Arg Val Val Ser Val Leu Ile Leu Ser Leu Ser Ser Leu  
                                   340                                  345                                  350  
 Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile Thr Met His Phe Ala  
                                   355                                  360                                  365  
 Leu Thr Leu Ile Ile Leu Phe Phe Phe Leu Tyr Lys Ala Lys Pro Phe  
                                   370                                  375                                  380  
 Asp Glu  
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<220>  
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                   Met Ile Lys Gln Ser Leu Asn Gly Glu Asp Met Gln  
                                   1                                  5                                  10

aaa agt tta gtt tct ttg gct tgg gtt ttt gta gct att tta ggg gcg 160  
 Lys Ser Leu Val Ser Leu Ala Trp Val Phe Val Ala Ile Leu Gly Ala  
                   15                                  20                                  25

atc tgt tta ggg gtg tta gcc tta cac aag ggt gag agc att aac acg 208  
 Ile Cys Leu Gly Val Leu Ala Leu His Lys Gly Glu Ser Ile Asn Thr  
                   30                                  35                                  40

cta tgg ctt gta gta gcg agc gct tgt att tat agc ata ggc tat cgt 256  
 Leu Trp Leu Val Val Ala Ser Ala Cys Ile Tyr Ser Ile Gly Tyr Arg  
                   45                                  50                                  55                                  60

ttt tat agc cat ttt atc gct tat aag gtg tta aag cta gat gat agc 304  
 Phe Tyr Ser His Phe Ile Ala Tyr Lys Val Leu Lys Leu Asp Asp Ser  
                                   65                                  70                                  75

aga gcc acg ccc gca tgc gta agg aat gat ggc aag gat ttt gtg cca 352  
 Arg Ala Thr Pro Ala Cys Val Arg Asn Asp Gly Lys Asp Phe Val Pro  
                                   80                                  85                                  90

acc gat aaa gcg atc act ttt ggg cac cat ttc gcc gct att gct ggg 400  
 Thr Asp Lys Ala Ile Thr Phe Gly His His Phe Ala Ala Ile Ala Gly  
                   95                                  100                                  105

gct ggc cct tta gta ggc ccg ata cta gcc gct caa atg ggt tac ttg 448  
 Ala Gly Pro Leu Val Gly Pro Ile Leu Ala Ala Gln Met Gly Tyr Leu  
                   110                                  115                                  120

ccc tct atc tta tgg att ttg ata ggc tgc gtt tta ggg ggt tgc gtg	496
Pro Ser Ile Leu Trp Ile Leu Ile Gly Ser Val Leu Gly Gly Cys Val	
125 130 135 140	
cat gat ttt gtg gtg ctt ttt gct tct att agg cgc gat ggc aag tct	544
His Asp Phe Val Val Leu Phe Ala Ser Ile Arg Arg Asp Gly Lys Ser	
145 150 155	
tta ggc gaa atg atc aaa ctt gaa atg ggc caa ttt gta ggc atg atc	592
Leu Gly Glu Met Ile Lys Leu Glu Met Gly Gln Phe Val Gly Met Ile	
160 165 170	
gca agt ctg ggc att tta ggg atc atg ctc att atc att gcg att tta	640
Ala Ser Leu Gly Ile Leu Gly Ile Met Leu Ile Ile Ile Ala Ile Leu	
175 180 185	
gcg atg gtg gtg gtg aag gct tta gcg cat tgc cct tgg ggc ttt ttt	688
Ala Met Val Val Val Lys Ala Leu Ala His Ser Pro Trp Gly Phe Phe	
190 195 200	
acg atc gca atg act att ccc att gcg att ctt atg ggg ctt tac atg	736
Thr Ile Ala Met Thr Ile Pro Ile Ala Ile Leu Met Gly Leu Tyr Met	
205 210 215 220	
cgg ttt ttc agg cca cac aag att tta gag gtt tct gtt att ggc ttt	784
Arg Phe Phe Arg Pro His Lys Ile Leu Glu Val Ser Val Ile Gly Phe	
225 230 235	
atc cta ttg att ata gcg att tat gcg ggt aaa tac gtt tct tta gat	832
Ile Leu Leu Ile Ile Ala Ile Tyr Ala Gly Lys Tyr Val Ser Leu Asp	
240 245 250	
cct aaa tta gcg tca ata ttc act ttt gag gcc agt tct tta gcg tgg	880
Pro Lys Leu Ala Ser Ile Phe Thr Phe Glu Ala Ser Ser Leu Ala Trp	
255 260 265	
atg atc atg ggc tat ggg ttt gtg gct tct att tta ccg gta tgg ttt	928
Met Ile Met Gly Tyr Gly Phe Val Ala Ser Ile Leu Pro Val Trp Phe	
270 275 280	
tta ctc gct cca cga gat tat cta agc act ttt tta aaa att ggc gtt	976
Leu Leu Ala Pro Arg Asp Tyr Leu Ser Thr Phe Leu Lys Ile Gly Val	
285 290 295 300	
ata ggg gtg ttg gtt gtg gcc att att ttt gtc gct ccg cct tta caa	1024
Ile Gly Val Leu Val Val Ala Ile Ile Phe Val Ala Pro Pro Leu Gln	
305 310 315	
atc cct aaa atc acg ccc ttt gta gat ggc agt ggg cct gtg ttt gca	1072
Ile Pro Lys Ile Thr Pro Phe Val Asp Gly Ser Gly Pro Val Phe Ala	
320 325 330	
gga agc gtg ttc cct ttc ttg ttt atc acg gtg gct tgc ggg acg att	1120
Gly Ser Val Phe Pro Phe Leu Phe Ile Thr Val Ala Cys Gly Thr Ile	
335 340 345	

agc gga ttc cat gct tta att tct tca ggc acg acc cct aaa atg ctc	1168
Ser Gly Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Met Leu	
350 355 360	
gct aaa gaa agc gac gca agg cta gtg ggc tat ggc tct atg gtg atg	1216
Ala Lys Glu Ser Asp Ala Arg Leu Val Gly Tyr Gly Ser Met Val Met	
365 370 375 380	
gag agc gtt gtg gct ctt atg gcg ttg gtg tgc gca ggg atc ttg cac	1264
Glu Ser Val Val Ala Leu Met Ala Leu Val Cys Ala Gly Ile Leu His	
385 390 395	
cca ggg ctt tat ttc gct atc aat tgc cca gaa gtg agc atc ggt aaa	1312
Pro Gly Leu Tyr Phe Ala Ile Asn Ser Pro Glu Val Ser Ile Gly Lys	
400 405 410	
gat ata gct gat gcg gct tca gtg att agc tca tgg ggg ttt aat atc	1360
Asp Ile Ala Asp Ala Ala Ser Val Ile Ser Ser Trp Gly Phe Asn Ile	
415 420 425	
agc gct gaa gaa att cgt gag atg act aaa aac atc ggc gaa agc tcc	1408
Ser Ala Glu Glu Ile Arg Glu Met Thr Lys Asn Ile Gly Glu Ser Ser	
430 435 440	
att ttg agc cgc acc ggt ggg gcg ccc act ttt gcg atc ggt tta gcg	1456
Ile Leu Ser Arg Thr Gly Gly Ala Pro Thr Phe Ala Ile Gly Leu Ala	
445 450 455 460	
atg att gtg tat cac att tta ggg gat cca agc gtg atg gcg ttt tgg	1504
Met Ile Val Tyr His Ile Leu Gly Asp Pro Ser Val Met Ala Phe Trp	
465 470 475	
tat cat ttt gcg att ttg ttt gaa gct ttg ttc att tta acc gct gtg	1552
Tyr His Phe Ala Ile Leu Phe Glu Ala Leu Phe Ile Leu Thr Ala Val	
480 485 490	
gat gct ggc aca cga acc gct cgt ttc atg att caa gat ttg ctc ggt	1600
Asp Ala Gly Thr Arg Thr Ala Arg Phe Met Ile Gln Asp Leu Leu Gly	
495 500 505	
aat gtt tat aag cct ttg ggc gat ctt agc tct tat aag gct ggg att	1648
Asn Val Tyr Lys Pro Leu Gly Asp Leu Ser Ser Tyr Lys Ala Gly Ile	
510 515 520	
ttt gcc act ctt ttg tgc gtg gca ggg tgg ggg tat ttc ttg tat caa	1696
Phe Ala Thr Leu Leu Cys Val Ala Gly Trp Gly Tyr Phe Leu Tyr Gln	
525 530 535 540	
ggc acg att gat cct aaa ggg ggg att tat acg cta tgg cct tta ttt	1744
Gly Thr Ile Asp Pro Lys Gly Gly Ile Tyr Thr Leu Trp Pro Leu Phe	
545 550 555	
ggc gtg agc aat cag atg tta gcg ggc atg gcg ttg ttg ttg gtc acg	1792
Gly Val Ser Asn Gln Met Leu Ala Gly Met Ala Leu Leu Leu Val Thr	

560	565	570	
gtg gtg ttg ttt aaa atg ggg cgt ttt aag ggg gcg atg ata agc gcc			1840
Val Val Leu Phe Lys Met Gly Arg Phe Lys Gly Ala Met Ile Ser Ala			
575	580	585	
tta ccg gca gtt ttg att tta tcc atc act ttt tat agc ggt att tta			1888
Leu Pro Ala Val Leu Ile Leu Ser Ile Thr Phe Tyr Ser Gly Ile Leu			
590	595	600	
aag gtg gtg cca aag agc gat aac agc gtg ctg aat aat gtt tcc cat			1936
Lys Val Val Pro Lys Ser Asp Asn Ser Val Leu Asn Asn Val Ser His			
605	610	615	620
gtg gcg caa atg caa atc atc aaa gaa aaa atg gct acc act acc gat			1984
Val Ala Gln Met Gln Ile Ile Lys Glu Lys Met Ala Thr Thr Thr Asp			
	625	630	635
gaa aaa gcg ctc aaa acg ctc caa aaa tcc ttt ttt aac cac gct att			2032
Glu Lys Ala Leu Lys Thr Leu Gln Lys Ser Phe Phe Asn His Ala Ile			
	640	645	650
gat gcg att ttg tgc gtg ttt ttc atg ctt gtg gcg cta ttg gtt tta			2080
Asp Ala Ile Leu Cys Val Phe Phe Met Leu Val Ala Leu Leu Val Leu			
	655	660	665
atc gtg agc gtt agg att tgc tca aac gct tat ttt aaa aac aaa att			2128
Ile Val Ser Val Arg Ile Cys Ser Asn Ala Tyr Phe Lys Asn Lys Ile			
	670	675	680
tac cca ccg ctg gct gaa acg ccc tac atc aaa gcc tct tgaataaaaa			2177
Tyr Pro Pro Leu Ala Glu Thr Pro Tyr Ile Lys Ala Ser			
685	690	695	
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<211> 697			
<212> PRT			
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20 25 30			
Val Leu Ala Leu His Lys Gly Glu Ser Ile Asn Thr Leu Trp Leu Val			
35 40 45			
Val Ala Ser Ala Cys Ile Tyr Ser Ile Gly Tyr Arg Phe Tyr Ser His			
50 55 60			
Phe Ile Ala Tyr Lys Val Leu Lys Leu Asp Asp Ser Arg Ala Thr Pro			
65 70 75 80			
Ala Cys Val Arg Asn Asp Gly Lys Asp Phe Val Pro Thr Asp Lys Ala			
85 90 95			
Ile Thr Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro Leu			

			100					105				110					
Val	Gly	Pro	Ile	Leu	Ala	Ala	Gln	Met	Gly	Tyr	Leu	Pro	Ser	Ile	Leu		
		115					120					125					
Trp	Ile	Leu	Ile	Gly	Ser	Val	Leu	Gly	Gly	Cys	Val	His	Asp	Phe	Val		
		130					135					140					
Val	Leu	Phe	Ala	Ser	Ile	Arg	Arg	Asp	Gly	Lys	Ser	Leu	Gly	Glu	Met		
145					150					155					160		
Ile	Lys	Leu	Glu	Met	Gly	Gln	Phe	Val	Gly	Met	Ile	Ala	Ser	Leu	Gly		
			165						170						175		
Ile	Leu	Gly	Ile	Met	Leu	Ile	Ile	Ile	Ala	Ile	Leu	Ala	Met	Val	Val		
		180							185						190		
Val	Lys	Ala	Leu	Ala	His	Ser	Pro	Trp	Gly	Phe	Phe	Thr	Ile	Ala	Met		
		195					200					205					
Thr	Ile	Pro	Ile	Ala	Ile	Leu	Met	Gly	Leu	Tyr	Met	Arg	Phe	Phe	Arg		
		210					215					220					
Pro	His	Lys	Ile	Leu	Glu	Val	Ser	Val	Ile	Gly	Phe	Ile	Leu	Leu	Ile		
225					230					235					240		
Ile	Ala	Ile	Tyr	Ala	Gly	Lys	Tyr	Val	Ser	Leu	Asp	Pro	Lys	Leu	Ala		
			245						250						255		
Ser	Ile	Phe	Thr	Phe	Glu	Ala	Ser	Ser	Leu	Ala	Trp	Met	Ile	Met	Gly		
			260					265							270		
Tyr	Gly	Phe	Val	Ala	Ser	Ile	Leu	Pro	Val	Trp	Phe	Leu	Leu	Ala	Pro		
		275					280								285		
Arg	Asp	Tyr	Leu	Ser	Thr	Phe	Leu	Lys	Ile	Gly	Val	Ile	Gly	Val	Leu		
		290					295								300		
Val	Val	Ala	Ile	Ile	Phe	Val	Ala	Pro	Pro	Leu	Gln	Ile	Pro	Lys	Ile		
305					310					315					320		
Thr	Pro	Phe	Val	Asp	Gly	Ser	Gly	Pro	Val	Phe	Ala	Gly	Ser	Val	Phe		
			325						330						335		
Pro	Phe	Leu	Phe	Ile	Thr	Val	Ala	Cys	Gly	Thr	Ile	Ser	Gly	Phe	His		
			340					345							350		
Ala	Leu	Ile	Ser	Ser	Gly	Thr	Thr	Pro	Lys	Met	Leu	Ala	Lys	Glu	Ser		
		355					360								365		
Asp	Ala	Arg	Leu	Val	Gly	Tyr	Gly	Ser	Met	Val	Met	Glu	Ser	Val	Val		
		370					375								380		
Ala	Leu	Met	Ala	Leu	Val	Cys	Ala	Gly	Ile	Leu	His	Pro	Gly	Leu	Tyr		
385					390					395					400		
Phe	Ala	Ile	Asn	Ser	Pro	Glu	Val	Ser	Ile	Gly	Lys	Asp	Ile	Ala	Asp		
			405						410						415		
Ala	Ala	Ser	Val	Ile	Ser	Ser	Trp	Gly	Phe	Asn	Ile	Ser	Ala	Glu	Glu		
			420					425							430		
Ile	Arg	Glu	Met	Thr	Lys	Asn	Ile	Gly	Glu	Ser	Ser	Ile	Leu	Ser	Arg		
		435					440								445		
Thr	Gly	Gly	Ala	Pro	Thr	Phe	Ala	Ile	Gly	Leu	Ala	Met	Ile	Val	Tyr		
		450					455					460					
His	Ile	Leu	Gly	Asp	Pro	Ser	Val	Met	Ala	Phe	Trp	Tyr	His	Phe	Ala		
465					470					475					480		
Ile	Leu	Phe	Glu	Ala	Leu	Phe	Ile	Leu	Thr	Ala	Val	Asp	Ala	Gly	Thr		
			485						490						495		
Arg	Thr	Ala	Arg	Phe	Met	Ile	Gln	Asp	Leu	Leu	Gly	Asn	Val	Tyr	Lys		
			500					505							510		
Pro	Leu	Gly	Asp	Leu	Ser	Ser	Tyr	Lys	Ala	Gly	Ile	Phe	Ala	Thr	Leu		
		515					520					525					
Leu	Cys	Val	Ala	Gly	Trp	Gly	Tyr	Phe	Leu	Tyr	Gln	Gly	Thr	Ile	Asp		
		530					535					540					



Pro	Lys	Gly	Gly	Ile	Tyr	Thr	Leu	Trp	Pro	Leu	Phe	Gly	Val	Ser	Asn	
545					550				555						560	
Gln	Met	Leu	Ala	Gly	Met	Ala	Leu	Leu	Leu	Val	Thr	Val	Val	Leu	Phe	
				565					570					575		
Lys	Met	Gly	Arg	Phe	Lys	Gly	Ala	Met	Ile	Ser	Ala	Leu	Pro	Ala	Val	
			580					585					590			
Leu	Ile	Leu	Ser	Ile	Thr	Phe	Tyr	Ser	Gly	Ile	Leu	Lys	Val	Val	Pro	
		595					600					605				
Lys	Ser	Asp	Asn	Ser	Val	Leu	Asn	Asn	Val	Ser	His	Val	Ala	Gln	Met	
	610					615					620					
Gln	Ile	Ile	Lys	Glu	Lys	Met	Ala	Thr	Thr	Thr	Asp	Glu	Lys	Ala	Leu	
625				630						635					640	
Lys	Thr	Leu	Gln	Lys	Ser	Phe	Phe	Asn	His	Ala	Ile	Asp	Ala	Ile	Leu	
			645						650					655		
Cys	Val	Phe	Phe	Met	Leu	Val	Ala	Leu	Leu	Val	Leu	Ile	Val	Ser	Val	
			660					665					670			
Arg	Ile	Cys	Ser	Asn	Ala	Tyr	Phe	Lys	Asn	Lys	Ile	Tyr	Pro	Pro	Leu	
		675					680					685				
Ala	Glu	Thr	Pro	Tyr	Ile	Lys	Ala	Ser								
	690					695										

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<220>  
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 atg caa aaa act tct aac act ctg gcg ctg ggg agt ttg aca gcg cta 168  
 Met Gln Lys Thr Ser Asn Thr Leu Ala Leu Gly Ser Leu Thr Ala Leu  
 1 5 10 15  
 ttc ttt cta atg ggt ttt atc acg gtt tta aac gat att tta atc cca 216  
 Phe Phe Leu Met Gly Phe Ile Thr Val Leu Asn Asp Ile Leu Ile Pro  
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 His Leu Lys Pro Ile Phe Asp Leu Thr Tyr Phe Glu Ala Ser Leu Ile  
 35 40 45  
 caa ttt tgc ttt ttt ggg gcg tat ttc atc atg gga gga gtt ttt ggg 312  
 Gln Phe Cys Phe Phe Gly Ala Tyr Phe Ile Met Gly Gly Val Phe Gly  
 50 55 60  
 aat gtg atc agt aaa atc ggc tac cct ttt ggc gtg gtg ctt ggt ttt 360

Asn	Val	Ile	Ser	Lys	Ile	Gly	Tyr	Pro	Phe	Gly	Val	Val	Leu	Gly	Phe									
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gtg	atc	aca	gcg	acg	ggg	tgc	gcg	ttg	ttt	tat	ccg	gcg	gcg	cat	ttt	408								
Val	Ile	Thr	Ala	Thr	Gly	Cys	Ala	Leu	Phe	Tyr	Pro	Ala	Ala	His	Phe									
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gga	tcc	tat	ggg	ttt	ttt	tta	gga	gcg	ttg	ttt	att	tta	gcg	agc	ggg	456								
Gly	Ser	Tyr	Gly	Phe	Phe	Leu	Gly	Ala	Leu	Phe	Ile	Leu	Ala	Ser	Gly									
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Ile	Val	Cys	Leu	Gln	Thr	Ala	Gly	Asn	Pro	Phe	Val	Thr	Leu	Leu	Ser									
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Lys	Gly	Lys	Glu	Ala	Arg	Asn	Leu	Val	Leu	Val	Gln	Ala	Phe	Asn	Ser									
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ctt	ggc	aca	act	tta	ggg	cct	att	ttt	ggg	agc	ttg	ttg	att	ttt	agc	600								
Leu	Gly	Thr	Thr	Leu	Gly	Pro	Ile	Phe	Gly	Ser	Leu	Leu	Ile	Phe	Ser									
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Thr	Thr	Lys	Met	Gly	Asp	Asn	Ala	Ser	Leu	Ile	Asp	Lys	Leu	Ala	Asp									
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gct	aaa	agc	gtt	caa	atg	cct	tat	ttg	ggc	ttg	gcg	gtg	ttt	tcg	ctt	696								
Ala	Lys	Ser	Val	Gln	Met	Pro	Tyr	Leu	Gly	Leu	Ala	Val	Phe	Ser	Leu									
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ctt	tta	gcg	ctc	atc	atg	tat	ctt	ttg	aaa	ttg	cct	gat	gtg	gaa	aaa	744								
Leu	Leu	Ala	Leu	Ile	Met	Tyr	Leu	Leu	Lys	Leu	Pro	Asp	Val	Glu	Lys									
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gaa	atg	ccc	aaa	gag	acg	act	caa	aaa	agc	ttg	ttt	tcg	cac	aaa	cac	792								
Glu	Met	Pro	Lys	Glu	Thr	Thr	Gln	Lys	Ser	Leu	Phe	Ser	His	Lys	His									
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Phe	Val	Phe	Gly	Ala	Trp	Gly	Ser	Phe	Phe	Met	Trp	Gly	Glu	Xaa	Trp									
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cga	ttg	gct	cat	tct	tgg	tgc	taagcttttga aaagctttttg aatttagact									891								
Arg	Leu	Ala	His	Ser	Trp	Cys																		
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 His Leu Lys Pro Ile Phe Asp Leu Thr Tyr Phe Glu Ala Ser Leu Ile  
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 Asn Val Ile Ser Lys Ile Gly Tyr Pro Phe Gly Val Val Leu Gly Phe  
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 Val Ile Thr Ala Thr Gly Cys Ala Leu Phe Tyr Pro Ala Ala His Phe  
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 Gly Ser Tyr Gly Phe Phe Leu Gly Ala Leu Phe Ile Leu Ala Ser Gly  
 100 105 110  
 Ile Val Cys Leu Gln Thr Ala Gly Asn Pro Phe Val Thr Leu Leu Ser  
 115 120 125  
 Lys Gly Lys Glu Ala Arg Asn Leu Val Leu Val Gln Ala Phe Asn Ser  
 130 135 140  
 Leu Gly Thr Thr Leu Gly Pro Ile Phe Gly Ser Leu Leu Ile Phe Ser  
 145 150 155 160  
 Thr Thr Lys Met Gly Asp Asn Ala Ser Leu Ile Asp Lys Leu Ala Asp  
 165 170 175  
 Ala Lys Ser Val Gln Met Pro Tyr Leu Gly Leu Ala Val Phe Ser Leu  
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 Glu Met Pro Lys Glu Thr Thr Gln Lys Ser Leu Phe Ser His Lys His  
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 Phe Val Phe Gly Ala Trp Gly Ser Phe Phe Met Trp Gly Glu Xaa Trp  
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 Arg Leu Ala His Ser Trp Cys  
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 Lys Ile Pro Leu Lys Asn Arg Leu Arg Ala Asp Phe Thr Lys Thr Pro

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aca gat tta gaa gtc cct aat tta tta tta tta caa cga gac agc tat			153
Thr Asp Leu Glu Val Pro Asn Leu Leu Leu Leu Gln Arg Asp Ser Tyr			
20	25	30	35
gat tct ttc ttg tat tct aaa gag ggt aaa gag agc ggg att gaa aag			201
Asp Ser Phe Leu Tyr Ser Lys Glu Gly Lys Glu Ser Gly Ile Glu Lys			
	40	45	50
gtt ttt aaa tcc att ttc cct atc caa gat gag cat aac cgc atc act			249
Val Phe Lys Ser Ile Phe Pro Ile Gln Asp Glu His Asn Arg Ile Thr			
	55	60	65
tta gaa tac gcg ggt tgc gaa ttt ggc aag tct aaa tac acc gtt aga			297
Leu Glu Tyr Ala Gly Cys Glu Phe Gly Lys Ser Lys Tyr Thr Val Arg			
	70	75	80
gaa gcg atg gag agg ggc att acc tac tct atc cct ctc aaa att aag			345
Glu Ala Met Glu Arg Gly Ile Thr Tyr Ser Ile Pro Leu Lys Ile Lys			
	85	90	95
gtg cgc ttg atc ttg tgg gaa aaa gat acc aag agt ggc gaa aag aac			393
Val Arg Leu Ile Leu Trp Glu Lys Asp Thr Lys Ser Gly Glu Lys Asn			
100	105	110	115
ggc att aag gat att aaa gaa caa agc att ttc att cgt gag atc cct			441
Gly Ile Lys Asp Ile Lys Glu Gln Ser Ile Phe Ile Arg Glu Ile Pro			
	120	125	130
ttg atg aca gaa cgc act tca ttt att att aat ggg gtg gag cgc gtg			489
Leu Met Thr Glu Arg Thr Ser Phe Ile Ile Asn Gly Val Glu Arg Val			
	135	140	145
gtg gtc aat caa ctc cac aga agc ccc ggt gtg att ttc aaa gaa gaa			537
Val Val Asn Gln Leu His Arg Ser Pro Gly Val Ile Phe Lys Glu Glu			
	150	155	160
gag tct agc act tct tta aac aag ctc att tac aca ggg caa atc att			585
Glu Ser Ser Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly Gln Ile Ile			
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cct gat agg ggt tgc tgg ttg tat ttt gaa tac gat tct aaa gat gtt			633
Pro Asp Arg Gly Ser Trp Leu Tyr Phe Glu Tyr Asp Ser Lys Asp Val			
180	185	190	195
tta tac gct cgt atc aat aaa cgc cgt aaa gtg cct gtt acc att tta			681
Leu Tyr Ala Arg Ile Asn Lys Arg Arg Lys Val Pro Val Thr Ile Leu			
	200	205	210
ttc agg gcg atg gat tat caa aaa caa gac atc atc aaa atg ttc tac			729
Phe Arg Ala Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys Met Phe Tyr			
	215	220	225
ccg ctt gtt aaa gtg cgt tat gaa aac gat aaa tat ttg atc ccg ttt			777

Pro	Leu	Val	Lys	Val	Arg	Tyr	Glu	Asn	Asp	Lys	Tyr	Leu	Ile	Pro	Phe		
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gct	tca	tta	gac	gcc	aat	caa	aga	atg	gaa	ttt	gac	ttg	aaa	gat	cct	825	
Ala	Ser	Leu	Asp	Ala	Asn	Gln	Arg	Met	Glu	Phe	Asp	Leu	Lys	Asp	Pro		
		245				250					255						
caa	ggc	aag	gtt	att	ctt	tta	gcg	ggg	aaa	aag	ctc	act	tca	aga	aag	873	
Gln	Gly	Lys	Val	Ile	Leu	Leu	Ala	Gly	Lys	Lys	Leu	Thr	Ser	Arg	Lys		
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att	aaa	gag	ctt	aaa	gaa	aac	cat	tta	gaa	tgg	gtg	gaa	tac	cct	atg	921	
Ile	Lys	Glu	Leu	Lys	Glu	Asn	His	Leu	Glu	Trp	Val	Glu	Tyr	Pro	Met		
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gat	att	tta	ctc	aat	cgc	cat	tta	gct	gag	cct	gtt	atg	gta	ggg	aaa	969	
Asp	Ile	Leu	Leu	Asn	Arg	His	Leu	Ala	Glu	Pro	Val	Met	Val	Gly	Lys		
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gaa	gtc	tta	ttg	gac	atg	ctc	act	cag	cta	gat	aaa	aac	aaa	tta	gaa	1017	
Glu	Val	Leu	Leu	Asp	Met	Leu	Thr	Gln	Leu	Asp	Lys	Asn	Lys	Leu	Glu		
		310					315					320					
aaa	atc	cac	gat	tta	ggc	gtg	caa	gaa	ttt	gtg	atc	atc	aac	gat	ctg	1065	
Lys	Ile	His	Asp	Leu	Gly	Val	Gln	Glu	Phe	Val	Ile	Ile	Asn	Asp	Leu		
		325				330					335						
gcg	tta	ggg	cat	gac	gct	tcc	att	atc	caa	tct	ttt	tca	gcc	gat	tct	1113	
Ala	Leu	Gly	His	Asp	Ala	Ser	Ile	Ile	Gln	Ser	Phe	Ser	Ala	Asp	Ser		
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gag	tct	ttg	aaa	tta	ctc	aag	caa	acc	gaa	aaa	att	gat	gat	gaa	aac	1161	
Glu	Ser	Leu	Lys	Leu	Leu	Lys	Gln	Thr	Glu	Lys	Ile	Asp	Asp	Glu	Asn		
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gct	cta	gcg	gcg	att	cgt	atc	cat	aag	gtt	atg	aaa	cca	ggc	gat	ccc	1209	
Ala	Leu	Ala	Ala	Ile	Arg	Ile	His	Lys	Val	Met	Lys	Pro	Gly	Asp	Pro		
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gtt	acg	act	gaa	gtg	gct	aag	cag	ttt	gtc	aaa	aaa	ctt	ttc	ttt	gat	1257	
Val	Thr	Thr	Glu	Val	Ala	Lys	Gln	Phe	Val	Lys	Lys	Leu	Phe	Phe	Asp		
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cca	gaa	cgc	tat	gat	ttg	acc	atg	gtg	ggc	cgc	atg	aaa	atg	aat	cac	1305	
Pro	Glu	Arg	Tyr	Asp	Leu	Thr	Met	Val	Gly	Arg	Met	Lys	Met	Asn	His		
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aag	tta	ggc	ttg	cat	gtg	cct	gat	tac	att	acg	act	tta	acg	cat	gaa	1353	
Lys	Leu	Gly	Leu	His	Val	Pro	Asp	Tyr	Ile	Thr	Thr	Leu	Thr	His	Glu		
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Asp	Ile	Ile	Thr	Thr	Val	Lys	Tyr	Leu	Met	Lys	Ile	Lys	Asn	Asn	Gln		
				440					445					450			

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Gly Lys Ile Asp Asp Arg Asp His Leu Gly Asn Arg Arg Ile Arg Ala	
455 460 465	
gta ggg gaa ttg ttg gcc aat gaa ttg cat tca ggt tta gtg aaa atg	1497
Val Gly Glu Leu Leu Ala Asn Glu Leu His Ser Gly Leu Val Lys Met	
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caa aag acc att aaa gac aag ctc act acc atg agc ggg gct ttt gat	1545
Gln Lys Thr Ile Lys Asp Lys Leu Thr Thr Met Ser Gly Ala Phe Asp	
485 490 495	
tcg ctc atg ccc cat gac ttg gtc aat tct aaa atg atc aca agc acc	1593
Ser Leu Met Pro His Asp Leu Val Asn Ser Lys Met Ile Thr Ser Thr	
500 505 510 515	
atc atg gaa ttt ttc atg ggc ggt cag ctc tcg caa ttt atg gat caa	1641
Ile Met Glu Phe Phe Met Gly Gly Gln Leu Ser Gln Phe Met Asp Gln	
520 525 530	
acg aat ccc ttg agt gag gtt acg cac aag cgc cgc ctt tca gcg ctc	1689
Thr Asn Pro Leu Ser Glu Val Thr His Lys Arg Arg Leu Ser Ala Leu	
535 540 545	
ggc gaa ggg ggg ttg gtg aaa gac aga gtg ggg ttt gaa gcc agg gat	1737
Gly Glu Gly Gly Leu Val Lys Asp Arg Val Gly Phe Glu Ala Arg Asp	
550 555 560	
gtg cac ccc acg cat tat ggc cga att tgt ccc att gag acc cca gaa	1785
Val His Pro Thr His Tyr Gly Arg Ile Cys Pro Ile Glu Thr Pro Glu	
565 570 575	
ggc caa aat atc ggt ctg atc aac acc ctt tcc act ttc aca aga gtg	1833
Gly Gln Asn Ile Gly Leu Ile Asn Thr Leu Ser Thr Phe Thr Arg Val	
580 585 590 595	
aat gat tta ggc ttt att gaa gcc cct tat aaa aag gtt gtg gat ggc	1881
Asn Asp Leu Gly Phe Ile Glu Ala Pro Tyr Lys Lys Val Val Asp Gly	
600 605 610	
aag gtc gtg ggt gag acg att tat ttg acc gct att caa gaa gac agc	1929
Lys Val Val Gly Glu Thr Ile Tyr Leu Thr Ala Ile Gln Glu Asp Ser	
615 620 625	
cac atc atc gct ccc gca agc acc ccc att gat gaa gag ggg aat att	1977
His Ile Ile Ala Pro Ala Ser Thr Pro Ile Asp Glu Glu Gly Asn Ile	
630 635 640	
ttg ggc gat ttg att gaa acg cgc gtg gaa ggc gag atc gtt tta aac	2025
Leu Gly Asp Leu Ile Glu Thr Arg Val Glu Gly Glu Ile Val Leu Asn	
645 650 655	
gaa aaa agc aaa gta acc tta atg gat tta agc tct agc atg cta gtg	2073
Glu Lys Ser Lys Val Thr Leu Met Asp Leu Ser Ser Ser Met Leu Val	
660 665 670 675	

ggg gta gcc gca tgc ctc att cct ttc tta gag cat gat gac gcc aac	2121
Gly Val Ala Ala Ser Leu Ile Pro Phe Leu Glu His Asp Asp Ala Asn	
680 685 690	
cggt gcc tta atg ggg act aac atg cag cgc caa gcg gtg ccc tta tta	2169
Arg Ala Leu Met Gly Thr Asn Met Gln Arg Gln Ala Val Pro Leu Leu	
695 700 705	
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Arg Ser Asp Ala Pro Ile Val Gly Thr Gly Ile Glu Lys Ile Ile Ala	
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Arg Asp Ser Trp Gly Ala Ile Lys Ala Asn Arg Ala Gly Val Val Glu	
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aaa att gat tct aaa aat att tat att tta ggc gaa agc aaa gaa gaa	2313
Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser Lys Glu Glu	
740 745 750 755	
gcc tat att gat gcg tat tct ttg caa aaa aac ttg cgc acc aac caa	2361
Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg Thr Asn Gln	
760 765 770	
aac acc agt ttc aat caa gtc cct atc gtt aaa gtg ggc gat aaa gtg	2409
Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly Asp Lys Val	
775 780 785	
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Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp Arg Gly Glu	
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Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro Trp Asn Gly	
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Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile Thr Lys Asp	
820 825 830 835	
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Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile Pro Asp Val	
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Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile Val Lys Val	
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Lys Gly Glu Ile Lys Ser Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile			
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Phe Gly Asp Lys Ala Gly His Val Val Asn Lys Ser Leu Tyr Cys Pro			
	920	925	930
ccc agt ttg gaa ggc acg gtg att gat gtg aaa gtc ttc act aaa aaa			2889
Pro Ser Leu Glu Gly Thr Val Ile Asp Val Lys Val Phe Thr Lys Lys			
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ggc tat gag aaa gac gcg cga gtt ttg agc gcg tat gaa gaa gaa aaa			2937
Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu Glu Glu Lys			
	950	955	960
gcc aag ctt gat atg gag cat ttt gat cgc ttg acc atg ctc aat aga			2985
Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met Leu Asn Arg			
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Glu Ile Pro Leu Met Thr Glu Arg Thr Ser Phe Ile Ile Asn Gly Val			
130 135 140			
Glu Arg Val Val Val Asn Gln Leu His Arg Ser Pro Gly Val Ile Phe			
145 150 155 160			
Lys Glu Glu Glu Ser Ser Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly			





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Glu	Asp	Ser	His	Ile	Ile	Ala	Pro	Ala	Ser	Thr	Pro	Ile	Asp	Glu	Glu
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Gly	Asn	Ile	Leu	Gly	Asp	Leu	Ile	Glu	Thr	Arg	Val	Glu	Gly	Glu	Ile
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Val	Leu	Asn	Glu	Lys	Ser	Lys	Val	Thr	Leu	Met	Asp	Leu	Ser	Ser	Ser
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Asp	Ala	Asn	Arg	Ala	Leu	Met	Gly	Thr	Asn	Met	Gln	Arg	Gln	Ala	Val
690						695					700				
Pro	Leu	Leu	Arg	Ser	Asp	Ala	Pro	Ile	Val	Gly	Thr	Gly	Ile	Glu	Lys
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Ile	Ile	Ala	Arg	Asp	Ser	Trp	Gly	Ala	Ile	Lys	Ala	Asn	Arg	Ala	Gly
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Thr	Asn	Gln	Asn	Thr	Ser	Phe	Asn	Gln	Val	Pro	Ile	Val	Lys	Val	Gly
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Asp	Lys	Val	Gly	Ala	Gly	Gln	Ile	Ile	Ala	Asp	Gly	Pro	Ser	Met	Asp
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Asp	Ala	Arg	Glu	Leu	Lys	His	Gly	Val	Glu	Glu	Phe	Thr	Ala	Asp	Ile
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Pro	Asp	Val	Lys	Glu	Glu	Ala	Leu	Ala	His	Leu	Asp	Glu	Ser	Gly	Ile
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Val	Lys	Val	Gly	Thr	Tyr	Val	Ser	Ala	Gly	Met	Ile	Leu	Val	Gly	Lys
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		930				935					940				
Thr	Lys	Lys	Gly	Tyr	Glu	Lys	Asp	Ala	Arg	Val	Leu	Ser	Ala	Tyr	Glu
945					950					955					960
Glu	Glu	Lys	Ala	Lys	Leu	Asp	Met	Glu	His	Phe	Asp	Arg	Leu	Thr	Met
				965					970					975	
Leu	Asn	Arg	Glu	Glu	Leu	Leu	Arg	Val	Thr	Arg	Ser	Phe	Leu	Lys	Arg
			980					985					990		
Phe															

<210> 81  
 <211> 581  
 <212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (49)...(525)

<400> 81

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agggttaaagt ttaagacaaa ccaaagagtt tgtcttggtt gtttttga atg cac tct 57
                                     Met His Ser
                                     1

cca aat tta gaa aaa gaa gaa acc gaa atc ata gaa aca ctc ctt atg 105
Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr Leu Leu Met
      5              10              15

cgt gaa aaa atg cgt tta tgc ccc ttg tat tgg cgc atc tta gcg ttt 153
Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile Leu Ala Phe
    20              25              30              35

tta acc gat ggt ttg tta gtg gcg ttt tta ttg agc gat ctt tta gac 201
Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp Leu Leu Asp
              40              45              50

gca tgc gat ttc ttg cat tct tta tat tgg cta gct aac cct att tat 249
Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn Pro Ile Tyr
              55              60              65

cac agc gca ttt gtt gcg atg ggt ttt atc atc ttg tat ggc gtt tat 297
His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr Gly Val Tyr
              70              75              80

gaa atc ttt ttt gtg tgt ttg tgc aag atg agc ttg gct aaa ctg gtt 345
Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala Lys Leu Val
    85              90              95

ttt agg att aag att att gat att tat ttg gca gat tgc ccc agt agg 393
Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys Pro Ser Arg
100              105              110              115

gct att tta ttg aag cgt tta ggg tta aag atc gtg gtt ttt cta tgc 441
Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val Phe Leu Cys
              120              125              130

ccc ttt tta tgg ttt gtt gcg ttt aaa aac ccc tat cat agg gcg tgg 489
Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His Arg Ala Trp
              135              140              145

cat gaa gaa aaa agc aaa agt ctt ttg gta ttg ttt taatcatgat 535
His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe
    150              155

ttattggttg tatttggcgg tctttttttt gttgagcgca ttagac 581
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<210> 82

<211> 159

<212> PRT

<213> Helicobacter pylori

<400> 82

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Met His Ser Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr
 1          5          10          15
Leu Leu Met Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile
          20          25          30
Leu Ala Phe Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp
          35          40          45
Leu Leu Asp Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn
          50          55          60
Pro Ile Tyr His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr
65          70          75          80
Gly Val Tyr Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala
          85          90          95
Lys Leu Val Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys
          100          105          110
Pro Ser Arg Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val
          115          120          125
Phe Leu Cys Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His
          130          135          140
Arg Ala Trp His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe
145          150          155
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<210> 83

<211> 901

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (67)...(852)

<400> 83

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gaatttaagc ggcagagggg ataaggattt aagcaccggt tataacgctt taaaaggagg 60
tttaaa atg agg tat caa aac atg ttt gaa acc tta aaa aaa cac gaa 108
      Met Arg Tyr Gln Asn Met Phe Glu Thr Leu Lys Lys His Glu
          1          5          10

aaa atg gcg ttt atc ccg ttt gta acc ttg ggc gat cct aat tat gaa 156
Lys Met Ala Phe Ile Pro Phe Val Thr Leu Gly Asp Pro Asn Tyr Glu
15          20          25          30

ttg agt ttt gaa atc att aaa acc cta att att agc ggg gtg agc gct 204
Leu Ser Phe Glu Ile Ile Lys Thr Leu Ile Ile Ser Gly Val Ser Ala
          35          40          45

tta gaa ttg ggt ctt gct ttt tct gat cct gtg gcg gat ggc att acc 252
Leu Glu Leu Gly Leu Ala Phe Ser Asp Pro Val Ala Asp Gly Ile Thr
          50          55          60

ata caa gcg agc cat tta agg gcg tta aaa cac gct agc atg gct aaa 300
Ile Gln Ala Ser His Leu Arg Ala Leu Lys His Ala Ser Met Ala Lys
```

65	70	75	
aat ttc cag ctt tta aaa aag att aga gat tac aac cac aat att ccc			348
Asn Phe Gln Leu Leu Lys Lys Ile Arg Asp Tyr Asn His Asn Ile Pro			
80	85	90	
ata ggg ctt tta gcg tat gcg aat tta att ttt tct tat ggc gtt gat			396
Ile Gly Leu Leu Ala Tyr Ala Asn Leu Ile Phe Ser Tyr Gly Val Asp			
95	100	105	110
ggc ttt tac gct caa gct aaa gaa tgc ggt ata gat agc gtt tta ata			444
Gly Phe Tyr Ala Gln Ala Lys Glu Cys Gly Ile Asp Ser Val Leu Ile			
	115	120	125
gcg gac atg ccc cta ata gaa aaa gaa tta gtc atc aaa tcc gct caa			492
Ala Asp Met Pro Leu Ile Glu Lys Glu Leu Val Ile Lys Ser Ala Gln			
	130	135	140
aaa cac caa atc aag caa atc ttt atc gcc agc ccc aat gcg agc agt			540
Lys His Gln Ile Lys Gln Ile Phe Ile Ala Ser Pro Asn Ala Ser Ser			
	145	150	155
aaa gat tta gaa caa gtc gct acg cat tcg caa ggc tat atc tac gct			588
Lys Asp Leu Glu Gln Val Ala Thr His Ser Gln Gly Tyr Ile Tyr Ala			
160	165	170	
tta gcc agg agt ggg gtt aca ggg gcg agc cgt att tta gag aat gat			636
Leu Ala Arg Ser Gly Val Thr Gly Ala Ser Arg Ile Leu Glu Asn Asp			
175	180	185	190
tcg agt gct att att aaa acc tta aaa gct ttt agc cct acc cca gcc			684
Ser Ser Ala Ile Ile Lys Thr Leu Lys Ala Phe Ser Pro Thr Pro Ala			
	195	200	205
tta ctg ggc ttt ggc att tcc aaa aaa gaa cac atc aca aac gct aaa			732
Leu Leu Gly Phe Gly Ile Ser Lys Lys Glu His Ile Thr Asn Ala Lys			
	210	215	220
ggc atg ggt gct gat ggc gtg att tgc gga tca gcg tta gtc aaa atc			780
Gly Met Gly Ala Asp Gly Val Ile Cys Gly Ser Ala Leu Val Lys Ile			
225	230	235	
ata gaa gaa aat tta aac aat gaa aac gcc atg ctg gaa aaa att aaa			828
Ile Glu Glu Asn Leu Asn Asn Glu Asn Ala Met Leu Glu Lys Ile Lys			
240	245	250	
ggg ttt ata gga gga atg att ttt taaggctttt aggcttttggt gcgttaaaaa			882
Gly Phe Ile Gly Gly Met Ile Phe			
255	260		
ttaaagatca cagattaac			901
<210> 84			
<211> 262			
<212> PRT			

<213> Helicobacter pylori

<400> 84

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Met Arg Tyr Gln Asn Met Phe Glu Thr Leu Lys Lys His Glu Lys Met
 1          5          10          15
Ala Phe Ile Pro Phe Val Thr Leu Gly Asp Pro Asn Tyr Glu Leu Ser
          20          25          30
Phe Glu Ile Ile Lys Thr Leu Ile Ile Ser Gly Val Ser Ala Leu Glu
          35          40          45
Leu Gly Leu Ala Phe Ser Asp Pro Val Ala Asp Gly Ile Thr Ile Gln
          50          55          60
Ala Ser His Leu Arg Ala Leu Lys His Ala Ser Met Ala Lys Asn Phe
65          70          75          80
Gln Leu Leu Lys Lys Ile Arg Asp Tyr Asn His Asn Ile Pro Ile Gly
          85          90          95
Leu Leu Ala Tyr Ala Asn Leu Ile Phe Ser Tyr Gly Val Asp Gly Phe
          100          105          110
Tyr Ala Gln Ala Lys Glu Cys Gly Ile Asp Ser Val Leu Ile Ala Asp
          115          120          125
Met Pro Leu Ile Glu Lys Glu Leu Val Ile Lys Ser Ala Gln Lys His
          130          135          140
Gln Ile Lys Gln Ile Phe Ile Ala Ser Pro Asn Ala Ser Ser Lys Asp
145          150          155          160
Leu Glu Gln Val Ala Thr His Ser Gln Gly Tyr Ile Tyr Ala Leu Ala
          165          170          175
Arg Ser Gly Val Thr Gly Ala Ser Arg Ile Leu Glu Asn Asp Ser Ser
          180          185          190
Ala Ile Ile Lys Thr Leu Lys Ala Phe Ser Pro Thr Pro Ala Leu Leu
          195          200          205
Gly Phe Gly Ile Ser Lys Lys Glu His Ile Thr Asn Ala Lys Gly Met
          210          215          220
Gly Ala Asp Gly Val Ile Cys Gly Ser Ala Leu Val Lys Ile Ile Glu
225          230          235          240
Glu Asn Leu Asn Asn Glu Asn Ala Met Leu Glu Lys Ile Lys Gly Phe
          245          250          255
Ile Gly Gly Met Ile Phe
          260
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<210> 85

<211> 1081

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (49)...(954)

<221> misc\_feature

<222> 919

<223> n = A,T,C or G

<400> 85

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aagtaatgcc cctgttgat cagcttgatt taagaggaat aagttatt atg aat aaa 57
                               Met Asn Lys
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gct att gct agt aag ata ctc atc act ttg ggt ttt tta ttt ctc tac	105
Ala Ile Ala Ser Lys Ile Leu Ile Thr Leu Gly Phe Leu Phe Leu Tyr	
5 10 15	
aga gtc tta gct tat atc ccc att cct ggc gta gat tta gca gcg atc	153
Arg Val Leu Ala Tyr Ile Pro Ile Pro Gly Val Asp Leu Ala Ala Ile	
20 25 30 35	
aag gct ttt ttt gac agc aat tcc aac aac gct ttg ggg ttg ttt aat	201
Lys Ala Phe Phe Asp Ser Asn Ser Asn Ala Leu Gly Leu Phe Asn	
40 45 50	
atg ttt agc ggg aat gcg gtt tct cgc ttg agc atc atc tcg ttg ggt	249
Met Phe Ser Gly Asn Ala Val Ser Arg Leu Ser Ile Ile Ser Leu Gly	
55 60 65	
atc atg ccc tat atc act tct tca att atc atg gag ctt ttg agc gcg	297
Ile Met Pro Tyr Ile Thr Ser Ser Ile Ile Met Glu Leu Leu Ser Ala	
70 75 80	
act ttc cct aac ctg gct aaa atg aaa aaa gag cgg gat ggc atg caa	345
Thr Phe Pro Asn Leu Ala Lys Met Lys Lys Glu Arg Asp Gly Met Gln	
85 90 95	
aaa tac atg caa atc gtg cgt tat ttg acc att tta atc acc cta atc	393
Lys Tyr Met Gln Ile Val Arg Tyr Leu Thr Ile Leu Ile Thr Leu Ile	
100 105 110 115	
caa gcg gtg agc gtt tca gta ggc tta agg agc att agt gga gga gcc	441
Gln Ala Val Ser Val Ser Val Gly Leu Arg Ser Ile Ser Gly Gly Ala	
120 125 130	
aat ggg gcg atc atg att gat atg caa gtt ttt atg atc gtt tca gcg	489
Asn Gly Ala Ile Met Ile Asp Met Gln Val Phe Met Ile Val Ser Ala	
135 140 145	
ttt tct atg ctt aca gga acg atg cta ctc atg tgg ata ggg gag caa	537
Phe Ser Met Leu Thr Gly Thr Met Leu Leu Met Trp Ile Gly Glu Gln	
150 155 160	
atc acg caa agg ggc gtg ggg aat ggg atc agt ctc att att ttt gcc	585
Ile Thr Gln Arg Gly Val Gly Asn Gly Ile Ser Leu Ile Ile Phe Ala	
165 170 175	
ggg att gtt tca ggg atc cca tca gct att tca ggc aca ttc aat ttg	633
Gly Ile Val Ser Gly Ile Pro Ser Ala Ile Ser Gly Thr Phe Asn Leu	
180 185 190 195	
gtc aat acg ggc gtt att aat atc tta atg ctc att ggt att gtg ctg	681
Val Asn Thr Gly Val Ile Asn Ile Leu Met Leu Ile Gly Ile Val Leu	
200 205 210	
att gtt tta gcg act att ttt gcg att atc tat gtg gaa tta gct gag	729

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Ile Val Leu Ala Thr Ile Phe Ala Ile Ile Tyr Val Glu Leu Ala Glu
      215                      220                      225

cgc agg atc cct att tct tat gcg cgt aaa gtg gtg atg caa aac caa 777
Arg Arg Ile Pro Ile Ser Tyr Ala Arg Lys Val Val Met Gln Asn Gln
      230                      235                      240

aac aag cgc atc atg aat tac att cct att aag ttg aat tta agt ggg 825
Asn Lys Arg Ile Met Asn Tyr Ile Pro Ile Lys Leu Asn Leu Ser Gly
      245                      250                      255

gtg atc ccc cct att ttc gct tca gct ttg ctc gtg ttc cct tct acg 873
Val Ile Pro Pro Ile Phe Ala Ser Ala Leu Leu Val Phe Pro Ser Thr
      260                      265                      270                      275

att ttg cag caa gcc aca agc aac aaa acc ttg caa gcg gtt gcg nat 921
Ile Leu Gln Gln Ala Thr Ser Asn Lys Thr Leu Gln Ala Val Ala Xaa
      280                      285                      290

ttt tta agc ccg caa ggt atg cgt ata ata ttt tgatgttctt gctcatcatc 974
Phe Leu Ser Pro Gln Gly Met Arg Ile Ile Phe
      295                      300

ttttttgctt actttttattc ttctattgtg ttcaattcta aggatattgc ggataatttg 1034
aggcgtaatg gcgggtatat tccagggtc aggcctggag agggggac 1081

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<210> 86
<211> 302
<212> PRT
<213> Helicobacter pylori

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<220>
<221> VARIANT
<222> 291
<223> Xaa = Any Amino Acid

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<400> 86
Met Asn Lys Ala Ile Ala Ser Lys Ile Leu Ile Thr Leu Gly Phe Leu
 1          5          10          15
Phe Leu Tyr Arg Val Leu Ala Tyr Ile Pro Ile Pro Gly Val Asp Leu
      20          25          30
Ala Ala Ile Lys Ala Phe Phe Asp Ser Asn Ser Asn Asn Ala Leu Gly
      35          40          45
Leu Phe Asn Met Phe Ser Gly Asn Ala Val Ser Arg Leu Ser Ile Ile
      50          55          60
Ser Leu Gly Ile Met Pro Tyr Ile Thr Ser Ser Ile Ile Met Glu Leu
      65          70          75          80
Leu Ser Ala Thr Phe Pro Asn Leu Ala Lys Met Lys Lys Glu Arg Asp
      85          90          95
Gly Met Gln Lys Tyr Met Gln Ile Val Arg Tyr Leu Thr Ile Leu Ile
      100         105         110
Thr Leu Ile Gln Ala Val Ser Val Ser Val Gly Leu Arg Ser Ile Ser
      115         120         125
Gly Gly Ala Asn Gly Ala Ile Met Ile Asp Met Gln Val Phe Met Ile
      130         135         140

```



Val	Ser	Ala	Phe	Ser	Met	Leu	Thr	Gly	Thr	Met	Leu	Leu	Met	Trp	Ile
145					150					155					160
Gly	Glu	Gln	Ile	Thr	Gln	Arg	Gly	Val	Gly	Asn	Gly	Ile	Ser	Leu	Ile
				165					170					175	
Ile	Phe	Ala	Gly	Ile	Val	Ser	Gly	Ile	Pro	Ser	Ala	Ile	Ser	Gly	Thr
			180					185					190		
Phe	Asn	Leu	Val	Asn	Thr	Gly	Val	Ile	Asn	Ile	Leu	Met	Leu	Ile	Gly
		195				200					205				
Ile	Val	Leu	Ile	Val	Leu	Ala	Thr	Ile	Phe	Ala	Ile	Ile	Tyr	Val	Glu
	210				215					220					
Leu	Ala	Glu	Arg	Arg	Ile	Pro	Ile	Ser	Tyr	Ala	Arg	Lys	Val	Val	Met
225					230				235						240
Gln	Asn	Gln	Asn	Lys	Arg	Ile	Met	Asn	Tyr	Ile	Pro	Ile	Lys	Leu	Asn
			245					250					255		
Leu	Ser	Gly	Val	Ile	Pro	Pro	Ile	Phe	Ala	Ser	Ala	Leu	Leu	Val	Phe
			260					265					270		
Pro	Ser	Thr	Ile	Leu	Gln	Gln	Ala	Thr	Ser	Asn	Lys	Thr	Leu	Gln	Ala
		275				280					285				
Val	Ala	Xaa	Phe	Leu	Ser	Pro	Gln	Gly	Met	Arg	Ile	Ile	Phe		
	290					295					300				

<210> 87  
 <211> 423  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (109)...(363)

<400> 87  
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 gatttcaata aaattttgca tcaatgttcc tttttgtttt gcgcatgc atg cgt ttt 117  
 Met Arg Phe  
 1

tta ttc tct aag act tta ttg atg atg agt tgt tgc aac acc gaa agg 165  
 Leu Phe Ser Lys Thr Leu Leu Met Met Ser Cys Cys Asn Thr Glu Arg  
 5 10 15

atg ttg ttc gtg gtc caa tac aag act aac cct gcc ggg aaa gtg att 213  
 Met Leu Phe Val Val Gln Tyr Lys Thr Asn Pro Ala Gly Lys Val Ile  
 20 25 30 35

aaa aag att gtg aat aat agg ggt aag agt tta aaa atc ttt gct tgc 261  
 Lys Lys Ile Val Asn Asn Arg Gly Lys Ser Leu Lys Ile Phe Ala Cys  
 40 45 50

atg gga tcg gtc atg gtg ttt ggc gta acg ctt tgg tgc caa tac ata 309  
 Met Gly Ser Val Met Val Phe Gly Val Thr Leu Trp Cys Gln Tyr Ile  
 55 60 65

gac gct ccc ata aga agc ggt aaa ata aaa tac gga tcc atg atg gat 357  
 Asp Ala Pro Ile Arg Ser Gly Lys Ile Lys Tyr Gly Ser Met Met Asp

70	75	80	
aaa tca tgaatccata agatccactc tgagcttttc aattccacag cggtataaag			413
Lys Ser			
85			
cactctataa			423
<210> 88			
<211> 85			
<212> PRT			
<213> Helicobacter pylori			
<400> 88			
Met Arg Phe Leu Phe Ser Lys Thr Leu Leu Met Met Ser Cys Cys Asn			
1 5 10 15			
Thr Glu Arg Met Leu Phe Val Val Gln Tyr Lys Thr Asn Pro Ala Gly			
20 25 30			
Lys Val Ile Lys Lys Ile Val Asn Asn Arg Gly Lys Ser Leu Lys Ile			
35 40 45			
Phe Ala Cys Met Gly Ser Val Met Val Phe Gly Val Thr Leu Trp Cys			
50 55 60			
Gln Tyr Ile Asp Ala Pro Ile Arg Ser Gly Lys Ile Lys Tyr Gly Ser			
65 70 75 80			
Met Met Asp Lys Ser			
85			
<210> 89			
<211> 740			
<212> DNA			
<213> Helicobacter pylori			
<220>			
<221> CDS			
<222> (59)...(688)			
<400> 89			
tttaaaatta gaaacagatg tatctgtttt aaattttgaa tagggagttt ctatcatt			58
atg tta ttg aaa aca aaa tta aaa att ata agc tcg gtg att ttg agc			106
Met Leu Leu Lys Thr Lys Leu Lys Ile Ile Ser Ser Val Ile Leu Ser			
1 5 10 15			
gct tta ttg tgg gtg ggt tgc tca agc gaa atg gca act tat caa aac			154
Ala Leu Leu Trp Val Gly Cys Ser Ser Glu Met Ala Thr Tyr Gln Asn			
20 25 30			
gtg aat gat gcc act aaa aat acg act gca agc att aat agc acg gat			202
Val Asn Asp Ala Thr Lys Asn Thr Thr Ala Ser Ile Asn Ser Thr Asp			
35 40 45			
tta ttg cta acc gct aac gcg atg tta gat tcc atg ttt agc gac cct			250
Leu Leu Leu Thr Ala Asn Ala Met Leu Asp Ser Met Phe Ser Asp Pro			
50 55 60			

aat ttt gag caa ctc aag ggc aag cat ttg att gaa gtt tca gat gtg	298
Asn Phe Glu Gln Leu Lys Gly Lys His Leu Ile Glu Val Ser Asp Val	
65 70 75 80	
att aac gac acc acg cag ccc aat ttg gac atg aat ctt ttg acg act	346
Ile Asn Asp Thr Thr Gln Pro Asn Leu Asp Met Asn Leu Leu Thr Thr	
85 90 95	
gaa atc gcg cgg cag ttg cgg ttg cga tct aat ggg agg ttc aat atc	394
Glu Ile Ala Arg Gln Leu Arg Leu Arg Ser Asn Gly Arg Phe Asn Ile	
100 105 110	
aca agg gcg agc gga ggg agt ggc att gca gcc gat agc aga atg gtg	442
Thr Arg Ala Ser Gly Gly Ser Gly Ile Ala Ala Asp Ser Arg Met Val	
115 120 125	
aaa cag cgc gaa aaa gaa cga gag agc gaa gag tat aat caa gac acc	490
Lys Gln Arg Glu Lys Glu Arg Glu Ser Glu Glu Tyr Asn Gln Asp Thr	
130 135 140	
act gta gaa aaa ggc act tta aaa gcc gct gat tta tct tta agt ggt	538
Thr Val Glu Lys Gly Thr Leu Lys Ala Ala Asp Leu Ser Leu Ser Gly	
145 150 155 160	
aaa gta tct agt atc gca gcc tct att agt agt tct agg cag cgc ttg	586
Lys Val Ser Ser Ile Ala Ala Ser Ile Ser Ser Ser Arg Gln Arg Leu	
165 170 175	
gac tat gac ttc acc cta agc ctt acc aac agg aaa acg ggt gaa gag	634
Asp Tyr Asp Phe Thr Leu Ser Leu Thr Asn Arg Lys Thr Gly Glu Glu	
180 185 190	
gta tgg agc gat gtt aag cct att gtg aag aac gct agc aat aag cgt	682
Val Trp Ser Asp Val Lys Pro Ile Val Lys Asn Ala Ser Asn Lys Arg	
195 200 205	
atg ttt taaatttata tttgaaagga tgaacaatga aaaatcaagt taaaaaaatt	738
Met Phe	
210	
tt	740
<210> 90	
<211> 210	
<212> PRT	
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<400> 90	
Met Leu Leu Lys Thr Lys Leu Lys Ile Ile Ser Ser Val Ile Leu Ser	
1 5 10 15	
Ala Leu Leu Trp Val Gly Cys Ser Ser Glu Met Ala Thr Tyr Gln Asn	
20 25 30	
Val Asn Asp Ala Thr Lys Asn Thr Thr Ala Ser Ile Asn Ser Thr Asp	
35 40 45	
Leu Leu Leu Thr Ala Asn Ala Met Leu Asp Ser Met Phe Ser Asp Pro	

50	55	60																	
Asn	Phe	Glu	Gln	Leu	Lys	Gly	Lys	His	Leu	Ile	Glu	Val	Ser	Asp	Val				
65					70					75					80				
Ile	Asn	Asp	Thr	Thr	Gln	Pro	Asn	Leu	Asp	Met	Asn	Leu	Leu	Thr	Thr				
				85					90					95					
Glu	Ile	Ala	Arg	Gln	Leu	Arg	Leu	Arg	Ser	Asn	Gly	Arg	Phe	Asn	Ile				
			100					105					110						
Thr	Arg	Ala	Ser	Gly	Gly	Ser	Gly	Ile	Ala	Ala	Asp	Ser	Arg	Met	Val				
	115						120					125							
Lys	Gln	Arg	Glu	Lys	Glu	Arg	Glu	Ser	Glu	Glu	Tyr	Asn	Gln	Asp	Thr				
	130					135					140								
Thr	Val	Glu	Lys	Gly	Thr	Leu	Lys	Ala	Ala	Asp	Leu	Ser	Leu	Ser	Gly				
145					150					155					160				
Lys	Val	Ser	Ser	Ile	Ala	Ala	Ser	Ile	Ser	Ser	Ser	Arg	Gln	Arg	Leu				
			165					170					175						
Asp	Tyr	Asp	Phe	Thr	Leu	Ser	Leu	Thr	Asn	Arg	Lys	Thr	Gly	Glu	Glu				
	180						185					190							
Val	Trp	Ser	Asp	Val	Lys	Pro	Ile	Val	Lys	Asn	Ala	Ser	Asn	Lys	Arg				
	195					200						205							
Met	Phe																		
	210																		

<210> 91  
 <211> 1269  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (84)...(1214)

<400> 91  
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 atctgagaga gaattatatt tta atg aag aca gag aaa caa aaa ttt tta gag 113  
 Met Lys Thr Glu Lys Gln Lys Phe Leu Glu  
 1 5 10

atg cgt aaa gat ggg gcg aac tct gtg ctg att tta aga ggg gat tgg 161  
 Met Arg Lys Asp Gly Ala Asn Ser Val Leu Ile Leu Arg Gly Asp Trp  
 15 20 25

gat ttt aaa acg agc gtg ttt cgt tta gat gag ttg aaa aaa aat tta 209  
 Asp Phe Lys Thr Ser Val Phe Arg Leu Asp Glu Leu Lys Lys Asn Leu  
 30 35 40

tta gat cat caa ggg cct tta aaa atg gat ttt tca ggg tgc caa aaa 257  
 Leu Asp His Gln Gly Pro Leu Lys Met Asp Phe Ser Gly Cys Gln Lys  
 45 50 55

gtg gat ttt gtt ttt ggc atg ttt tta ttt gat tta gtt aag gag cgt 305  
 Val Asp Phe Val Phe Gly Met Phe Leu Phe Asp Leu Val Lys Glu Arg  
 60 65 70

tct tta aac att gaa ttg tgt aac gtg agt gag aat aac gca tgc gct 353

Ser	Leu	Asn	Ile	Glu	Leu	Cys	Asn	Val	Ser	Glu	Asn	Asn	Ala	Cys	Ala	
75					80					85					90	
ttg	aaa	gtg	gtt	aaa	gac	tgg	ctt	gaa	aaa	gaa	gag	gat	tta	gag	tct	401
Leu	Lys	Val	Val	Lys	Asp	Trp	Leu	Glu	Lys	Glu	Glu	Asp	Leu	Glu	Ser	
				95					100					105		
aaa	aaa	gcg	ggc	aaa	cac	tac	gaa	ctt	ttg	atc	act	aaa	ttg	ggg	aag	449
Lys	Lys	Ala	Gly	Lys	His	Tyr	Glu	Leu	Leu	Ile	Thr	Lys	Leu	Gly	Lys	
			110					115					120			
agt	atc	gta	gag	act	tat	aat	acc	ttt	tta	aac	gca	ttc	aat	ttt	tgc	497
Ser	Ile	Val	Glu	Thr	Tyr	Asn	Thr	Phe	Leu	Asn	Ala	Phe	Asn	Phe	Cys	
		125					130					135				
ggc	atg	att	tta	ttc	tac	ttc	att	aaa	agc	gtt	ttc	aac	ccc	aaa	cgc	545
Gly	Met	Ile	Leu	Phe	Tyr	Phe	Ile	Lys	Ser	Val	Phe	Asn	Pro	Lys	Arg	
	140					145					150					
ttt	tgt	atc	act	cct	ttg	ctc	tat	cat	atc	aat	gaa	tcc	ggg	ttt	aag	593
Phe	Cys	Ile	Thr	Pro	Leu	Leu	Tyr	His	Ile	Asn	Glu	Ser	Gly	Phe	Lys	
155					160					165					170	
gtt	ttg	cca	gtg	agt	att	tta	acg	gtg	ttt	atc	gtg	ggg	ttt	gcc	gtt	641
Val	Leu	Pro	Val	Ser	Ile	Leu	Thr	Val	Phe	Ile	Val	Gly	Phe	Ala	Val	
				175					180					185		
gct	tta	caa	ggg	gct	tta	caa	tta	caa	gac	atg	ggc	gcg	cct	tta	atg	689
Ala	Leu	Gln	Gly	Ala	Leu	Gln	Leu	Gln	Asp	Met	Gly	Ala	Pro	Leu	Met	
			190					195					200			
tcg	gtg	gaa	atg	acg	gct	aaa	ctc	gct	tta	aga	gaa	atc	ggc	cct	ttt	737
Ser	Val	Glu	Met	Thr	Ala	Lys	Leu	Ala	Leu	Arg	Glu	Ile	Gly	Pro	Phe	
		205					210					215				
att	tta	acc	ctt	gtg	gtg	gcc	ggg	agg	agc	gcg	agc	agt	ttt	acc	gcg	785
Ile	Leu	Thr	Leu	Val	Val	Ala	Gly	Arg	Ser	Ala	Ser	Ser	Phe	Thr	Ala	
	220					225					230					
caa	att	ggg	gtg	atg	aag	atc	act	gag	gaa	tta	gac	gcg	atg	aaa	acc	833
Gln	Ile	Gly	Val	Met	Lys	Ile	Thr	Glu	Glu	Leu	Asp	Ala	Met	Lys	Thr	
235					240					245				250		
atg	ggc	ttt	aac	cct	ttt	gaa	ttt	tta	gtg	ttg	cct	agg	gtg	tta	gcc	881
Met	Gly	Phe	Asn	Pro	Phe	Glu	Phe	Leu	Val	Leu	Pro	Arg	Val	Leu	Ala	
				255					260					265		
tta	gtg	att	gtt	ttg	cct	tta	ttg	gtg	ttt	att	gcc	gat	gcg	ttc	gcc	929
Leu	Val	Ile	Val	Leu	Pro	Leu	Leu	Val	Phe	Ile	Ala	Asp	Ala	Phe	Ala	
			270					275					280			
att	ctt	ggg	ggc	atg	ttt	gcg	att	aaa	tac	caa	ttg	gat	tta	ggc	ttc	977
Ile	Leu	Gly	Gly	Met	Phe	Ala	Ile	Lys	Tyr	Gln	Leu	Asp	Leu	Gly	Phe	
		285					290					295				

ccg agc tat att gac aga ttc cat gac aca gtg ggt tgg aac cat ttt	1025
Pro Ser Tyr Ile Asp Arg Phe His Asp Thr Val Gly Trp Asn His Phe	
300 305 310	

ttg gta ggg att gtc aaa gcc cct ttt tgg ggg ttt gcg att gcg atg	1073
Leu Val Gly Ile Val Lys Ala Pro Phe Trp Gly Phe Ala Ile Ala Met	
315 320 325 330	

gta ggg tgc atg cgc ggg ttt gaa gtc aag ggg gat act gag agc att	1121
Val Gly Cys Met Arg Gly Phe Glu Val Lys Gly Asp Thr Glu Ser Ile	
335 340 345	

ggg cgc ttg acc act att agc gtc gtg aac gct ttg ttt tgg atc att	1169
Gly Arg Leu Thr Thr Ile Ser Val Val Asn Ala Leu Phe Trp Ile Ile	
350 355 360	

ttc tta gac gct att ttt tct atc atc ttt tct aag ttg aac ata	1214
Phe Leu Asp Ala Ile Phe Ser Ile Ile Phe Ser Lys Leu Asn Ile	
365 370 375	

taatgaacgc tactaacaat caagtcttaa ttgaagtgaaggatctccat agcgc	1269
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 <213> Helicobacter pylori

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Phe Arg Leu Asp Glu Leu Lys Lys Asn Leu Leu Asp His Gln Gly Pro	
35 40 45	
Leu Lys Met Asp Phe Ser Gly Cys Gln Lys Val Asp Phe Val Phe Gly	
50 55 60	
Met Phe Leu Phe Asp Leu Val Lys Glu Arg Ser Leu Asn Ile Glu Leu	
65 70 75 80	
Cys Asn Val Ser Glu Asn Asn Ala Cys Ala Leu Lys Val Val Lys Asp	
85 90 95	
Trp Leu Glu Lys Glu Glu Asp Leu Glu Ser Lys Lys Ala Gly Lys His	
100 105 110	
Tyr Glu Leu Leu Ile Thr Lys Leu Gly Lys Ser Ile Val Glu Thr Tyr	
115 120 125	
Asn Thr Phe Leu Asn Ala Phe Asn Phe Cys Gly Met Ile Leu Phe Tyr	
130 135 140	
Phe Ile Lys Ser Val Phe Asn Pro Lys Arg Phe Cys Ile Thr Pro Leu	
145 150 155 160	
Leu Tyr His Ile Asn Glu Ser Gly Phe Lys Val Leu Pro Val Ser Ile	
165 170 175	
Leu Thr Val Phe Ile Val Gly Phe Ala Val Ala Leu Gln Gly Ala Leu	
180 185 190	
Gln Leu Gln Asp Met Gly Ala Pro Leu Met Ser Val Glu Met Thr Ala	
195 200 205	
Lys Leu Ala Leu Arg Glu Ile Gly Pro Phe Ile Leu Thr Leu Val Val	

210	215	220
Ala Gly Arg Ser Ala Ser Ser Phe Thr Ala Gln Ile Gly Val Met Lys		
225	230	235
Ile Thr Glu Glu Leu Asp Ala Met Lys Thr Met Gly Phe Asn Pro Phe		
	245	250
Glu Phe Leu Val Leu Pro Arg Val Leu Ala Leu Val Ile Val Leu Pro		
	260	265
Leu Leu Val Phe Ile Ala Asp Ala Phe Ala Ile Leu Gly Gly Met Phe		
	275	280
Ala Ile Lys Tyr Gln Leu Asp Leu Gly Phe Pro Ser Tyr Ile Asp Arg		
	290	295
Phe His Asp Thr Val Gly Trp Asn His Phe Leu Val Gly Ile Val Lys		
305	310	315
Ala Pro Phe Trp Gly Phe Ala Ile Ala Met Val Gly Cys Met Arg Gly		
	325	330
Phe Glu Val Lys Gly Asp Thr Glu Ser Ile Gly Arg Leu Thr Thr Ile		
	340	345
Ser Val Val Asn Ala Leu Phe Trp Ile Ile Phe Leu Asp Ala Ile Phe		
	355	360
Ser Ile Ile Phe Ser Lys Leu Asn Ile		
370	375	

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<220>  
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 atg gga ttt ttg aat ggg tat ttt tta tgg gtt aag gct ttc cat gtg 107  
 Met Gly Phe Leu Asn Gly Tyr Phe Leu Trp Val Lys Ala Phe His Val  
 1 5 10 15  
  
 ata gcg gtc att tcg tgg atg gca gcg ttg ttt tat ttg ccg cgc ctt 155  
 Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu  
 20 25 30  
  
 ttt gtc tat cat gca gaa aac gcg cat aaa aaa gag ttt gta gga gtg 203  
 Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val  
 35 40 45  
  
 gtt caa atc caa gaa aaa aag ctt tat tcc ttt atc gct tca ccg gct 251  
 Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala  
 50 55 60  
  
 atg ggt ttt acg ctt att aca ggg att tta atg ctg ttg ata gag cct 299  
 Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Glu Pro  
 65 70 75 80  
  
 acg ctc ttt aaa agt ggg ggt tgg ttg cat gct aaa ttg gct tta gtg 347

Thr Leu Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val  
                                     85                                    90                                    95  
  
 gtt tta ctt tta gcc tat cat ttt tat tgc aaa aaa tgc atg cgc gag 395  
 Val Leu Leu Leu Ala Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu  
                                     100                                    105                                    110  
  
 ctg gaa aaa gac ccc aca agg aga aac gca agg ttt tat cgc gtg ttt 443  
 Leu Glu Lys Asp Pro Thr Arg Arg Asn Ala Arg Phe Tyr Arg Val Phe  
                                     115                                    120                                    125  
  
 aat gag gcg cca acg att tta atg atc ctc att gtg att tta gtg gtt 491  
 Asn Glu Ala Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val  
                                     130                                    135                                    140  
  
 gtc aag cct ttt taaagacaag ccatgaaaaa agaaaagtca tgaaaaaaga 543  
 Val Lys Pro Phe  
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 aaagcatctc aagc 557  
  
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   1                                    5                                    10                                    15  
 Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu  
                                     20                                    25                                    30  
 Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val  
                                     35                                    40                                    45  
 Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala  
                                     50                                    55                                    60  
 Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Glu Pro  
  65                                    70                                    75                                    80  
 Thr Leu Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val  
                                     85                                    90                                    95  
 Val Leu Leu Leu Ala Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu  
                                     100                                    105                                    110  
 Leu Glu Lys Asp Pro Thr Arg Arg Asn Ala Arg Phe Tyr Arg Val Phe  
                                     115                                    120                                    125  
 Asn Glu Ala Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val  
                                     130                                    135                                    140  
 Val Lys Pro Phe  
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<221> CDS

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<400> 95

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Met Lys Leu

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ttt aac gct cgt tta atc gtt ttt att ggc gcg ctt ctt tta ggg gta 106  
Phe Asn Ala Arg Leu Ile Val Phe Ile Gly Ala Leu Leu Leu Gly Val  
5 10 15

ggg ttt tct gtg cct tct tta cta gaa act aaa ggc cct aaa atc act 154  
Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro Lys Ile Thr  
20 25 30 35

tta ggt ttg gat tta agg ggg ggg ttg aac atg ctt tta ggg gta caa 202  
Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu Gly Val Gln  
40 45 50

acc gat gag gct tta aaa aac aag tat tta agc ttg gcg tcc gct tta 250  
Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala Ser Ala Leu  
55 60 65

gaa tac aac gct aaa aag caa aat atc ttg ctt aaa gat att aaa tcc 298  
Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp Ile Lys Ser  
70 75 80

aat tta gaa ggg atc agt ttt gag ctt tta gat gaa gat gaa gcg aaa 346  
Asn Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp Glu Ala Lys  
85 90 95

aaa tta gac gcg ctt tta ttg gaa ttg caa ggc cat agc cag ttt gaa 394  
Lys Leu Asp Ala Leu Leu Leu Glu Leu Gln Gly His Ser Gln Phe Glu  
100 105 110 115

atc aaa aag gaa gcg ggg ttt tat agc gtg aat ctc acc cct tta gag 442  
Ile Lys Lys Glu Ala Gly Phe Tyr Ser Val Asn Leu Thr Pro Leu Glu  
120 125 130

caa gaa gaa ttg cgt aaa aac acg att ttg caa gtg ata ggg atc att 490  
Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile Gly Ile Ile  
135 140 145

cgt aac cgc ttg gat caa ttt ggt ttg gca gag cct gta gtc att cag 538  
Arg Asn Arg Leu Asp Gln Phe Gly Leu Ala Glu Pro Val Val Ile Gln  
150 155 160

caa ggt aaa gaa gaa att ttc gtg caa ttg cct ggc att aag act tta 586  
Gln Gly Lys Glu Glu Ile Ser Val Gln Leu Pro Gly Ile Lys Thr Leu  
165 170 175

gaa gaa gaa cgg cgc gct aaa gac ttg att tca aga tcc gct cat ttg 634  
Glu Glu Glu Arg Arg Ala Lys Asp Leu Ile Ser Arg Ser Ala His Leu  
180 185 190 195

cag atg atg gcg gtg gat gaa gaa cac aat aaa gat gcg atg aaa atg	682
Gln Met Met Ala Val Asp Glu Glu His Asn Lys Asp Ala Met Lys Met	
200 205 210	
acg gat tta gag gct caa aaa tta ggc agc gtg ttg ttg tct gat gtg	730
Thr Asp Leu Glu Ala Gln Lys Leu Gly Ser Val Leu Leu Ser Asp Val	
215 220 225	
gaa atg ggg ggt aaa atc ttg ctc aaa gcg atc ccc att tta gat ggc	778
Glu Met Gly Gly Lys Ile Leu Leu Lys Ala Ile Pro Ile Leu Asp Gly	
230 235 240	
gaa atg ctt aca gat gcg aaa gtg gtg tat gac caa aac aac cag ccg	826
Glu Met Leu Thr Asp Ala Lys Val Val Tyr Asp Gln Asn Asn Gln Pro	
245 250 255	
gtg gtg agc ttc acg ctg gat gcg caa ggg gct aag att ttt ggg gat	874
Val Val Ser Phe Thr Leu Asp Ala Gln Gly Ala Lys Ile Phe Gly Asp	
260 265 270 275	
ttc tca ggt gcg aat gtg ggc aaa cgc atg gcg att gtt tta gac aat	922
Phe Ser Gly Ala Asn Val Gly Lys Arg Met Ala Ile Val Leu Asp Asn	
280 285 290	
aag gtc tat tca gcc ccg gtg att agg gag cgt atc ggt ggg ggg agc	970
Lys Val Tyr Ser Ala Pro Val Ile Arg Glu Arg Ile Gly Gly Gly Ser	
295 300 305	
ggg cag att agc ggg aat ttt agc gtg gct caa gcg agc gat tta gcg	1018
Gly Gln Ile Ser Gly Asn Phe Ser Val Ala Gln Ala Ser Asp Leu Ala	
310 315 320	
atc gct tta agg agt ggg gcg atg agc gct ccc att cag gtt tta gaa	1066
Ile Ala Leu Arg Ser Gly Ala Met Ser Ala Pro Ile Gln Val Leu Glu	
325 330 335	
aaa aga att ata ggc cca agt tta ggg aaa gac agc gtt aaa act tcc	1114
Lys Arg Ile Ile Gly Pro Ser Leu Gly Lys Asp Ser Val Lys Thr Ser	
340 345 350 355	
att atc gct cta gtt ggg ggc ttt att tta gtg atg ggc ttt atg gtg	1162
Ile Ile Ala Leu Val Gly Gly Phe Ile Leu Val Met Gly Phe Met Val	
360 365 370	
ctt tat tac tct atg gcg ggg gtg atc gct tgt ttg gcg tta gtg gtc	1210
Leu Tyr Tyr Ser Met Ala Gly Val Ile Ala Cys Leu Ala Leu Val Val	
375 380 385	
aat ctt ttt ttg att gtg gcg gtc atg gcg att ttt gga gcg acg ctg	1258
Asn Leu Phe Leu Ile Val Ala Val Met Ala Ile Phe Gly Ala Thr Leu	
390 395 400	
act tta ccg gga atg gcg ggg att gtt tta acc gtg ggg att gcc gtg	1306
Thr Leu Pro Gly Met Ala Gly Ile Val Leu Thr Val Gly Ile Ala Val	

405	410	415	
gat gct aat atc atc atc aac gag cgc att aga gaa gtc tta aga gag			1354
Asp Ala Asn Ile Ile Ile Asn Glu Arg Ile Arg Glu Val Leu Arg Glu			
420	425	430	435
aat gag ggc atc gct aaa gcg atc cat tta ggc tat atc aat gcg agc			1402
Asn Glu Gly Ile Ala Lys Ala Ile His Leu Gly Tyr Ile Asn Ala Ser			
	440	445	450
cgg gcg att ttt gat tct aat atc act tct ttg atc gct tca gtg tta			1450
Arg Ala Ile Phe Asp Ser Asn Ile Thr Ser Leu Ile Ala Ser Val Leu			
	455	460	465
tta tac gct tat ggc aca gga gcg att aaa ggc ttt gcc cta act aca			1498
Leu Tyr Ala Tyr Gly Thr Gly Ala Ile Lys Gly Phe Ala Leu Thr Thr			
	470	475	480
ggc att ggg att tta gcc tct att atc acc gct att gtt ggc acg caa			1546
Gly Ile Gly Ile Leu Ala Ser Ile Ile Thr Ala Ile Val Gly Thr Gln			
	485	490	495
ggg att tat caa gcc ctt tta cct aaa ctc act caa aca aaa agc ctt			1594
Gly Ile Tyr Gln Ala Leu Leu Pro Lys Leu Thr Gln Thr Lys Ser Leu			
500	505	510	515
tac ttt tgg ttt ggc gtg aat aaa aga gct taggaggttt tatggaatta			1644
Tyr Phe Trp Phe Gly Val Asn Lys Arg Ala			
	520	525	
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Leu Gly Val Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro			
	20	25	30
Lys Ile Thr Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu			
	35	40	45
Gly Val Gln Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala			
	50	55	60
Ser Ala Leu Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp			
65	70	75	80
Ile Lys Ser Asn Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp			
	85	90	95
Glu Ala Lys Lys Leu Asp Ala Leu Leu Leu Glu Leu Gln Gly His Ser			
	100	105	110
Gln Phe Glu Ile Lys Lys Glu Ala Gly Phe Tyr Ser Val Asn Leu Thr			
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Pro Leu Glu Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile			



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<221> CDS

<222> (64)...(654)

<400> 97

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aag atg aag cgc tca agc ttt acc tct aat agc gtt tta aac ttt ttt 108
  Met Lys Arg Ser Ser Phe Thr Ser Asn Ser Val Leu Asn Phe Phe
    1             5             10             15

gta gtt ttg tct ttc att acg ata gga tta gtg ttt ttc ttt ttg cgt 156
Val Val Leu Ser Phe Ile Thr Ile Gly Leu Val Phe Phe Phe Leu Arg
          20             25             30

tcc caa ccc act agc gta gtt tct aaa gaa aat atc cct aaa att gaa 204
Ser Gln Pro Thr Ser Val Val Ser Lys Glu Asn Ile Pro Lys Ile Glu
          35             40             45

tta gaa aat ttt aaa gcg ttt caa atc aac gat aaa atc ctt gat ctg 252
Leu Glu Asn Phe Lys Ala Phe Gln Ile Asn Asp Lys Ile Leu Asp Leu
          50             55             60

tcc ata gag ggc aaa aaa gcc cta caa tac gat gat cat gaa atc ttt 300
Ser Ile Glu Gly Lys Lys Ala Leu Gln Tyr Asp Asp His Glu Ile Phe
          65             70             75

ttt gat tcc aaa atc aag cgc tat gat gaa gac acc att gaa agc gtt 348
Phe Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile Glu Ser Val
          80             85             90             95

gag tct cct aag gcc aaa cgg cag cag gat ttg tat ttc ttc cct aat 396
Glu Ser Pro Lys Ala Lys Arg Gln Gln Asp Leu Tyr Phe Phe Pro Asn
          100             105             110

ggg gtt act tat aaa aga agc gat gat tcc agt ttt tgg agt gaa aca 444
Gly Val Thr Tyr Lys Arg Ser Asp Asp Ser Ser Phe Trp Ser Glu Thr
          115             120             125

ggg att tat aac cat aag gag caa aat ttt aaa ggc aag ggc cgt ttc 492
Gly Ile Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe
          130             135             140

att ctc act tca aag gac agc aag att gaa ggg ctt gac att tct tat 540
Ile Leu Thr Ser Lys Asp Ser Lys Ile Glu Gly Leu Asp Ile Ser Tyr
          145             150             155

tcg cat gca tta gct att att gaa gct caa agc att caa gcg cat tta 588
Ser His Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala His Leu
          160             165             170             175

ttc tta gat gaa atc aaa caa agc caa aaa gaa aag aaa aaa ttc ccc 636
Phe Leu Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro
          180             185             190

act ttc aaa gga ggt ttt taatgcgttg gtggtgtttt ttggtgtgtt 684
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195

gttttggtat tttaagcgtg at

706

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<212> PRT  
<213> Helicobacter pylori

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20 25 30  
Gln Pro Thr Ser Val Val Ser Lys Glu Asn Ile Pro Lys Ile Glu Leu  
35 40 45  
Glu Asn Phe Lys Ala Phe Gln Ile Asn Asp Lys Ile Leu Asp Leu Ser  
50 55 60  
Ile Glu Gly Lys Lys Ala Leu Gln Tyr Asp Asp His Glu Ile Phe Phe  
65 70 75 80  
Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile Glu Ser Val Glu  
85 90 95  
Ser Pro Lys Ala Lys Arg Gln Gln Asp Leu Tyr Phe Phe Pro Asn Gly  
100 105 110  
Val Thr Tyr Lys Arg Ser Asp Asp Ser Ser Phe Trp Ser Glu Thr Gly  
115 120 125  
Ile Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe Ile  
130 135 140  
Leu Thr Ser Lys Asp Ser Lys Ile Glu Gly Leu Asp Ile Ser Tyr Ser  
145 150 155 160  
His Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala His Leu Phe  
165 170 175  
Leu Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro Thr  
180 185 190  
Phe Lys Gly Gly Phe  
195

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<212> DNA  
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<221> CDS  
<222> (130)...(957)

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ggaaaagtc atg aaa act tct aaa aca aaa acc cct aaa tcc gtt tta atc 171  
Met Lys Thr Ser Lys Thr Lys Thr Pro Lys Ser Val Leu Ile  
1 5 10

gct ggg cca tgc gtc att gag agc tta gaa aat cta aga agt atc gcc	219
Ala Gly Pro Cys Val Ile Glu Ser Leu Glu Asn Leu Arg Ser Ile Ala	
15 20 25 30	
act aaa ttg caa ccc cta gcc aac aac gag cgg ttg gat ttt tat ttt	267
Thr Lys Leu Gln Pro Leu Ala Asn Asn Glu Arg Leu Asp Phe Tyr Phe	
35 40 45	
aaa gcg agt ttt gat aag gcg aac cgc acg agt tta gag agt tac aga	315
Lys Ala Ser Phe Asp Lys Ala Asn Arg Thr Ser Leu Glu Ser Tyr Arg	
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Gly Pro Gly Leu Glu Lys Gly Leu Glu Met Leu Gln Thr Ile Lys Glu	
65 70 75	
gaa ttt ggt tat aaa atc tta acc gat gtg cat gag agt tat caa gca	411
Glu Phe Gly Tyr Lys Ile Leu Thr Asp Val His Glu Ser Tyr Gln Ala	
80 85 90	
agc gtg gca gcc aaa gtg gcg gat att tta caa atc ccg gcg ttt ttg	459
Ser Val Ala Ala Lys Val Ala Asp Ile Leu Gln Ile Pro Ala Phe Leu	
95 100 105 110	
tgc cgc caa acg gat ctg att gta gaa gtg agc cag act aac gct att	507
Cys Arg Gln Thr Asp Leu Ile Val Glu Val Ser Gln Thr Asn Ala Ile	
115 120 125	
gtc aat atc aaa aaa ggg caa ttc atg aac cca aaa gac atg caa tat	555
Val Asn Ile Lys Lys Gly Gln Phe Met Asn Pro Lys Asp Met Gln Tyr	
130 135 140	
tct gtt cta aag gcc ctt aaa acg aga gat aaa agc att caa agc ccc	603
Ser Val Leu Lys Ala Leu Lys Thr Arg Asp Lys Ser Ile Gln Ser Pro	
145 150 155	
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Thr Tyr Glu Thr Ala Leu Lys Asn Gly Val Trp Leu Cys Glu Arg Gly	
160 165 170	
agc agc ttt ggg tat ggg aat tta gtg gtg gat atg cgc tct tta aaa	699
Ser Ser Phe Gly Tyr Gly Asn Leu Val Val Asp Met Arg Ser Leu Lys	
175 180 185 190	
atc atg cga gaa ttt gcc cct gtg att ttt gac gct acc cat agc gtg	747
Ile Met Arg Glu Phe Ala Pro Val Ile Phe Asp Ala Thr His Ser Val	
195 200 205	
caa atg cca ggg gga gcg aac ggg aaa agt tca gga gac agc tct ttt	795
Gln Met Pro Gly Gly Ala Asn Gly Lys Ser Ser Gly Asp Ser Ser Phe	
210 215 220	
gcc cct att tta gcg aga gct gcg gcg gcg gtg ggg att gat ggg ttg	843
Ala Pro Ile Leu Ala Arg Ala Ala Ala Val Gly Ile Asp Gly Leu	
225 230 235	

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Phe Ala Glu Thr His Val Asp Pro Lys Asn Ala Leu Ser Asp Gly Ala
240 245 250

aac atg cta aaa cct gac gag cta gaa caa tta gta acc gac atg tta 939
Asn Met Leu Lys Pro Asp Glu Leu Glu Gln Leu Val Thr Asp Met Leu
255 260 265 270

aaa atc caa aat tta ttt taaaggaatt tcatgcaaat catagaaggg 987
Lys Ile Gln Asn Leu Phe
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35 40 45
Ser Phe Asp Lys Ala Asn Arg Thr Ser Leu Glu Ser Tyr Arg Gly Pro
50 55 60
Gly Leu Glu Lys Gly Leu Glu Met Leu Gln Thr Ile Lys Glu Glu Phe
65 70 75 80
Gly Tyr Lys Ile Leu Thr Asp Val His Glu Ser Tyr Gln Ala Ser Val
85 90 95
Ala Ala Lys Val Ala Asp Ile Leu Gln Ile Pro Ala Phe Leu Cys Arg
100 105 110
Gln Thr Asp Leu Ile Val Glu Val Ser Gln Thr Asn Ala Ile Val Asn
115 120 125
Ile Lys Lys Gly Gln Phe Met Asn Pro Lys Asp Met Gln Tyr Ser Val
130 135 140
Leu Lys Ala Leu Lys Thr Arg Asp Lys Ser Ile Gln Ser Pro Thr Tyr
145 150 155 160
Glu Thr Ala Leu Lys Asn Gly Val Trp Leu Cys Glu Arg Gly Ser Ser
165 170 175
Phe Gly Tyr Gly Asn Leu Val Val Asp Met Arg Ser Leu Lys Ile Met
180 185 190
Arg Glu Phe Ala Pro Val Ile Phe Asp Ala Thr His Ser Val Gln Met
195 200 205
Pro Gly Gly Ala Asn Gly Lys Ser Ser Gly Asp Ser Ser Phe Ala Pro
210 215 220
Ile Leu Ala Arg Ala Ala Ala Val Gly Ile Asp Gly Leu Phe Ala
225 230 235 240
Glu Thr His Val Asp Pro Lys Asn Ala Leu Ser Asp Gly Ala Asn Met
245 250 255
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Gln Asn Leu Phe  
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Met Lys Gly Arg Val Ala Gln Leu Val Glu His Tyr Leu Asp Met Val  
1 5 10 15  
gtg gcc gct ggt tca agt cca gtc gtg gcc acc att atc act cca att 154  
Val Ala Ala Gly Ser Ser Pro Val Val Ala Thr Ile Ile Thr Pro Ile  
20 25 30  
tta att ctc att ttt ttg cga gtt ttt gat ctt tat aaa ttc 196  
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	Met	Ala	Gln	Glu	Lys	Ala	Val	Pro	
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Arg Asp Pro Lys Lys Leu Asn Ala Phe Asp Leu Arg Trp Met Val Ser									
10 15 20									
tta ttt ggc acg gcg gtg ggg gct ggg att tta ttt ttg cct att aga									210
Leu Phe Gly Thr Ala Val Gly Ala Gly Ile Leu Phe Leu Pro Ile Arg									
25 30 35 40									
gcc ggt ggg cat ggg gta tgg gct att gtg gta atg agc gcg atc att									258
Ala Gly Gly His Gly Val Trp Ala Ile Val Val Met Ser Ala Ile Ile									
45 50 55									
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Phe Pro Leu Thr Tyr Leu Gly His Arg Ala Leu Ala Tyr Phe Ile Gly									
60 65 70									
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Ser Lys Asp Lys Glu Asp Ile Thr Met Val Val Arg Ser His Phe Gly									
75 80 85									
gct caa tgg ggt ttt ctt atc act ttg ctt tat ttc tta gcg att tat									402
Ala Gln Trp Gly Phe Leu Ile Thr Leu Leu Tyr Phe Leu Ala Ile Tyr									
90 95 100									
cct att tgc ttg gtt tat ggg gtg ggt atc act aac gtg ttt gat cat									450
Pro Ile Cys Leu Val Tyr Gly Val Gly Ile Thr Asn Val Phe Asp His									
105 110 115 120									
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Phe Phe Thr Asn Gln Leu His Leu Ala Pro Phe His Arg Gly Leu Leu									
125 130 135									
gct gta gcg tta gtt tct tta atg atg ttg gtg atg gtt ttt aac gct									546
Ala Val Ala Leu Val Ser Leu Met Met Leu Val Met Val Phe Asn Ala									
140 145 150									
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Thr Ile Val Thr Arg Ile Cys Asn Ala Leu Val Tyr Pro Leu Cys Leu									
155 160 165									
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Ile Leu Leu Leu Phe Ser Leu Tyr Leu Ile Pro Tyr Trp Gln Gly Ala									
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Asn Leu Phe Val Val Pro Ser Phe Lys Glu Phe Val Leu Ala Ile Trp									
185 190 195 200									
cta acc tta ccg gtg ctt gtg ttt gca ttc gac cat agc ccc atc att									738
Leu Thr Leu Pro Val Leu Val Phe Ala Phe Asp His Ser Pro Ile Ile									
205 210 215									

tca acc ttc act caa aat gtg gga aaa gaa tac ggc gtt ttc aaa gaa	786
Ser Thr Phe Thr Gln Asn Val Gly Lys Glu Tyr Gly Val Phe Lys Glu	
220 225 230	
tac aaa ctc aat caa att gaa tta ggg aca tcg ctg atg ctt tta ggg	834
Tyr Lys Leu Asn Gln Ile Glu Leu Gly Thr Ser Leu Met Leu Leu Gly	
235 240 245	
ttt gtg atg ttt ttt gtg ttt tcg tgc gtc atg tgc ttg aat gct gat	882
Phe Val Met Phe Phe Val Phe Ser Cys Val Met Cys Leu Asn Ala Asp	
250 255 260	
gat ttt gtg aaa gca agg gaa caa aat atc ccc att tta agc tat ttg	930
Asp Phe Val Lys Ala Arg Glu Gln Asn Ile Pro Ile Leu Ser Tyr Leu	
265 270 275 280	
gct aac act tta aac aac cct tta atc aat tat gcg ggg cct gtg gtg	978
Ala Asn Thr Leu Asn Asn Pro Leu Ile Asn Tyr Ala Gly Pro Val Val	
285 290 295	
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Ala Phe Leu Ala Ile Phe Ser Ser Phe Phe Gly His Tyr Tyr Gly Ala	
300 305 310	
aag gag ggt tta gaa ggc att att att caa agc tta aaa ttg aaa aaa	1074
Lys Glu Gly Leu Glu Gly Ile Ile Ile Gln Ser Leu Lys Leu Lys Lys	
315 320 325	
gct tct aaa ccc ttg agc gtt agc gta acg att ttt tta tgg ctg act	1122
Ala Ser Lys Pro Leu Ser Val Ser Val Thr Ile Phe Leu Trp Leu Thr	
330 335 340	
atc acg ctt gtg gct tat att aac ccc aat atc ttg gat ttt att gaa	1170
Ile Thr Leu Val Ala Tyr Ile Asn Pro Asn Ile Leu Asp Phe Ile Glu	
345 350 355 360	
aat tta ggc ggc ccc att atc gcg ctc att ctg ttt gtg atg ccc atg	1218
Asn Leu Gly Gly Pro Ile Ile Ala Leu Ile Leu Phe Val Met Pro Met	
365 370 375	
ata gct ttt tat agt gtt tct agt ttg aag cgt ttt aga aat ttc aaa	1266
Ile Ala Phe Tyr Ser Val Ser Ser Leu Lys Arg Phe Arg Asn Phe Lys	
380 385 390	
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Val Asp Ile Phe Val Phe Val Phe Gly Ser Leu Thr Ala Leu Ser Val	
395 400 405	
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 <213> Helicobacter pylori

<400> 104

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		20						25					30		
Gly	Ile	Leu	Phe	Leu	Pro	Ile	Arg	Ala	Gly	Gly	His	Gly	Val	Trp	Ala
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Ile	Val	Val	Met	Ser	Ala	Ile	Ile	Phe	Pro	Leu	Thr	Tyr	Leu	Gly	His
	50					55					60				
Arg	Ala	Leu	Ala	Tyr	Phe	Ile	Gly	Ser	Lys	Asp	Lys	Glu	Asp	Ile	Thr
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Met	Val	Val	Arg	Ser	His	Phe	Gly	Ala	Gln	Trp	Gly	Phe	Leu	Ile	Thr
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Leu	Leu	Tyr	Phe	Leu	Ala	Ile	Tyr	Pro	Ile	Cys	Leu	Val	Tyr	Gly	Val
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Gly	Ile	Thr	Asn	Val	Phe	Asp	His	Phe	Phe	Thr	Asn	Gln	Leu	His	Leu
	115						120					125			
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			165						170					175	
Leu	Ile	Pro	Tyr	Trp	Gln	Gly	Ala	Asn	Leu	Phe	Val	Val	Pro	Ser	Phe
		180						185					190		
Lys	Glu	Phe	Val	Leu	Ala	Ile	Trp	Leu	Thr	Leu	Pro	Val	Leu	Val	Phe
	195						200					205			
Ala	Phe	Asp	His	Ser	Pro	Ile	Ile	Ser	Thr	Phe	Thr	Gln	Asn	Val	Gly
	210					215					220				
Lys	Glu	Tyr	Gly	Val	Phe	Lys	Glu	Tyr	Lys	Leu	Asn	Gln	Ile	Glu	Leu
225					230					235				240	
Gly	Thr	Ser	Leu	Met	Leu	Leu	Gly	Phe	Val	Met	Phe	Phe	Val	Phe	Ser
			245						250					255	
Cys	Val	Met	Cys	Leu	Asn	Ala	Asp	Asp	Phe	Val	Lys	Ala	Arg	Glu	Gln
			260					265					270		
Asn	Ile	Pro	Ile	Leu	Ser	Tyr	Leu	Ala	Asn	Thr	Leu	Asn	Asn	Pro	Leu
		275					280					285			
Ile	Asn	Tyr	Ala	Gly	Pro	Val	Val	Ala	Phe	Leu	Ala	Ile	Phe	Ser	Ser
	290					295					300				
Phe	Phe	Gly	His	Tyr	Tyr	Gly	Ala	Lys	Glu	Gly	Leu	Glu	Gly	Ile	Ile
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Ile	Gln	Ser	Leu	Lys	Leu	Lys	Lys	Ala	Ser	Lys	Pro	Leu	Ser	Val	Ser
			325						330					335	
Val	Thr	Ile	Phe	Leu	Trp	Leu	Thr	Ile	Thr	Leu	Val	Ala	Tyr	Ile	Asn
			340					345					350		
Pro	Asn	Ile	Leu	Asp	Phe	Ile	Glu	Asn	Leu	Gly	Gly	Pro	Ile	Ile	Ala
		355					360					365			
Leu	Ile	Leu	Phe	Val	Met	Pro	Met	Ile	Ala	Phe	Tyr	Ser	Val	Ser	Ser
	370					375					380				
Leu	Lys	Arg	Phe	Arg	Asn	Phe	Lys	Val	Asp	Ile	Phe	Val	Phe	Val	Phe
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Met Leu Asp Phe Ile Gln Glu Leu Ser Thr Pro His Val Arg Asp  
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ttt ttc ttg ttg ttt tta agg gtt agc ggc gtg ctg tct ttc ttc cct 155  
Phe Phe Leu Leu Phe Leu Arg Val Ser Gly Val Leu Ser Phe Phe Pro  
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50 55 60  
  
gct tac acg cca gag ggt ttt atc att gct tgc ttg tgc gaa ttg ttt 299  
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65 70 75  
  
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Leu Gly Val Cys Ala Ser Val Phe Leu Gln Ile Val Phe Ala Ser Leu  
80 85 90 95  
  
gtg ttt gca acc gat agc atc agc ttt tct atg ggg ctt acg atg gcg 395  
Val Phe Ala Thr Asp Ser Ile Ser Phe Ser Met Gly Leu Thr Met Ala  
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Ser Ala Tyr Asp Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln  
115 120 125  
  
gcc ctt tta ttg tta gcg att tta att tta ttg gat tta tgc ttc cac 491  
Ala Leu Leu Leu Leu Ala Ile Leu Ile Leu Leu Asp Leu Ser Phe His  
130 135 140  
  
cat caa atc att ttg ttt gtg gat cac agc tta aaa gcc gtc cct tta 539  
His Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu  
145 150 155

ggg caa ttt gtc ttt gag cca gcg ttg gct aaa aac atc gtt aaa gcc 587  
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 160 165 170 175  
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 Cys Leu Val Leu Leu Ser Asp Ile Ile Phe Gly Met Ile Met Lys Thr  
 195 200 205  
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 210 215 220  
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 Ile Gly Phe Val Gly Ile Ile Leu Ile Ala Ser Ala Ile Met Gly Arg  
 225 230 235  
 ttt aaa gaa gaa atc agc ctg gcc ttt agc gcc att agc aaa atc ttt 827  
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<210> 106

<211> 255

<212> PRT

<213> *Helicobacter pylori*

<400> 106

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 35 40 45  
 Tyr Val Ser Ala Ile Phe Tyr Pro Thr Leu Glu Phe Ser Asn Ala Ala  
 50 55 60  
 Tyr Thr Pro Glu Gly Phe Ile Ile Ala Cys Leu Cys Glu Leu Phe Leu  
 65 70 75 80  
 Gly Val Cys Ala Ser Val Phe Leu Gln Ile Val Phe Ala Ser Leu Val  
 85 90 95  
 Phe Ala Thr Asp Ser Ile Ser Phe Ser Met Gly Leu Thr Met Ala Ser  
 100 105 110  
 Ala Tyr Asp Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln Ala  
 115 120 125  
 Leu Leu Leu Leu Ala Ile Leu Ile Leu Leu Asp Leu Ser Phe His His  
 130 135 140  
 Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu Gly  
 145 150 155 160  
 Gln Phe Val Phe Glu Pro Ala Leu Ala Lys Asn Ile Val Lys Ala Phe  
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 Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu Cys



gta ttt ttg cac gat ctc acc ctt atc att gac aag aat caa agt gtt 747  
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 110 115 120 125  
  
 ata ggg att ctt ttt ggc ttg ctc gtg ttt ttc ccc tgt caa aga gaa 795  
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 130 135 140  
  
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 His Ser Pro Asn Leu Val Phe Leu Thr Ser Phe Ser Lys Asp Arg Gly  
 145 150 155  
  
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 Phe Phe Ser Arg Asn Ala Cys Gly Cys Ile Lys His Phe Leu Ser Val  
 160 165 170  
  
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 Pro Arg Gln Thr Leu Phe Asp Pro Thr Asn His Leu Ser Asp Ile Ala  
 190 195 200 205  
  
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 Thr Ile Phe Gln His Leu Ile Leu Ser Val Glu Ser Arg His Leu Ile  
 210 215 220  
  
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 225 230 235  
  
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 Pro Arg His Ser Phe Tyr Tyr Cys Asn Leu Leu Leu Ser Arg Ile  
 35 40 45  
 His Val Thr Leu Thr Ala His Asn Glu Phe Cys Pro Thr His Arg Ala  
 50 55 60  
 Ile Ala Pro Asn Phe Arg Val Val Ser Ile Ile Ala Asn Asn Gln Arg  
 65 70 75 80  
 Asn Phe Gln Ala Leu Arg Pro Ile Asn His Ile Ser Phe Ile Pro Arg





Asp	Phe	Ser	Leu	Leu	Lys	Gln	Ser	Val	Asn	Leu	Asn	Tyr	His	Ile	Asp	
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Ile	Lys	Asp	Leu	Arg	Ser	Phe	Lys	Glu	Trp	Ile	Pro	Tyr	Pro	Leu	Arg	
			95					100					105			
ggg	gct	gtt	atc	act	tct	ggg	aat	att	aaa	ggg	cat	aga	aaa	gcc	ctt	447
Gly	Ala	Val	Ile	Thr	Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	
		110					115					120				
atg	att	caa	ggc	gtc	tct	aat	gtg	gct	caa	tcc	cac	act	gcc	tac	aat	495
Met	Ile	Gln	Gly	Val	Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	
	125					130					135					
gcc	ctt	tta	gat	gat	ttc	aag	ctt	tct	cgc	tta	aat	ttg	aac	gca	caa	543
Ala	Leu	Leu	Asp	Asp	Phe	Lys	Leu	Ser	Arg	Leu	Asn	Leu	Asn	Ala	Gln	
140					145				150						155	
gac	gcc	aat	tta	gaa	gat	ttg	ctt	tat	tta	atc	aat	cgc	ccc	gct	tat	591
Asp	Ala	Asn	Leu	Glu	Asp	Leu	Leu	Tyr	Leu	Ile	Asn	Arg	Pro	Ala	Tyr	
			160					165						170		
gcg	aac	gca	aaa	gtg	tcc	tta	cag	gcg	gat	ttt	aac	tct	cta	aag	cct	639
Ala	Asn	Ala	Lys	Val	Ser	Leu	Gln	Ala	Asp	Phe	Asn	Ser	Leu	Lys	Pro	
			175					180					185			
tta	gag	ggg	cat	ttg	atc	cta	aca	gct	aat	aac	gct	tta	atc	aat	aac	687
Leu	Glu	Gly	His	Leu	Ile	Leu	Thr	Ala	Asn	Asn	Ala	Leu	Ile	Asn	Asn	
	190						195					200				
gcc	cta	atc	aat	caa	att	ttt	cat	tta	aac	ctt	aaa	gac	acg	ctt	gtt	735
Ala	Leu	Ile	Asn	Gln	Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	
	205				210						215					
ttc	agc	ctc	tcg	cat	tca	agc	gac	ttt	aaa	gga	aac	aaa	gcc	atc	agc	783
Phe	Ser	Leu	Ser	His	Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	
220				225					230					235		
gat	acc	acc	ctg	act	agc	cct	tta	gcc	aat	ttc	aaa	gcc	cta	aaa	agc	831
Asp	Thr	Thr	Leu	Thr	Ser	Pro	Leu	Ala	Asn	Phe	Lys	Ala	Leu	Lys	Ser	
			240					245						250		
gaa	tac	ctt	ttc	tct	att	tta	aaa	ctc	aac	gcc	ccc	tac	act	tta	gaa	879
Glu	Tyr	Leu	Phe	Ser	Ile	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	
		255						260					265			
atc	ccc	aat	cta	gcc	aaa	ctc	tat	aac	att	acc	aac	cac	ccc	tta	aaa	927
Ile	Pro	Asn	Leu	Ala	Lys	Leu	Tyr	Asn	Ile	Thr	Asn	His	Pro	Leu	Lys	
		270					275					280				
ggg	agc	ttg	act	tta	aaa	ggc	gct	ata	gaa	caa	agc	ccc	aaa	ctt	tta	975
Gly	Ser	Leu	Thr	Leu	Lys	Gly	Ala	Ile	Glu	Gln	Ser	Pro	Lys	Leu	Leu	
	285					290					295					

aaa gtc agc ggc cat tca aat tta cta gac ggc gcg ctg gat ttc acg	1023
Lys Val Ser Gly His Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr	
300 305 310 315	
ctt tta aat aaa gat ttg aaa ggg cgt ttt tcc aat att tcc act tta	1071
Leu Leu Asn Lys Asp Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu	
320 325 330	
aaa gct tta gat tta ttc cat tac cct aag ttt ttc caa tcc gtt gca	1119
Lys Ala Leu Asp Leu Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala	
335 340 345	
gac gct aat ttg gat tat gat ctt atc gct aag caa ggc gta ttg aaa	1167
Asp Ala Asn Leu Asp Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys	
350 355 360	
gcc cgc cta aaa aac gca aga ttc ctc aaa aat gca ttc agc gat ttt	1215
Ala Arg Leu Lys Asn Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe	
365 370 375	
ctc tac tcc att tct aaa ttt gat att aca aaa gaa att tat aac gat	1263
Leu Tyr Ser Ile Ser Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp	
380 385 390 395	
gcc aat ctg gta agc caa atc aac cag caa cgc ctg ctc tct gat ctg	1311
Ala Asn Leu Val Ser Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu	
400 405 410	
agt tta aaa agc ccc aaa acc caa ttg aaa atc cat aac ggt ttg ttg	1359
Ser Leu Lys Ser Pro Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu	
415 420 425	
gat tta aac acc aaa caa atg aac atg ctc atg gat gcg gaa att tta	1407
Asp Leu Asn Thr Lys Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu	
430 435 440	
aaa ttc att ttt aaa atg aaa ctt caa ggc aac atg cac cag cca aaa	1455
Lys Phe Ile Phe Lys Met Lys Leu Gln Gly Asn Met His Gln Pro Lys	
445 450 455	
ttt tct ctc att tta aac gaa aaa gcc att cag caa aac ttg caa caa	1503
Phe Ser Leu Ile Leu Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln	
460 465 470 475	
ggc ttg aaa gaa atc tta aaa aac gac acc ctt aaa aaa ggt tta gat	1551
Gly Leu Lys Glu Ile Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp	
480 485 490	
cat ttg ctt aaa gat gat aag ctc aaa gaa aag ctt gaa aaa ggg ctt	1599
His Leu Leu Lys Asp Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu	
495 500 505	
aag ggg ctt ttt taaaatttta aaggatagaa atggcgcaca ttttagttag	1651
Lys Gly Leu Phe	
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1661

<210> 110

<211> 511

<212> PRT

<213> Helicobacter pylori

<400> 110

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		20					25					30			
Ala	Ser	Tyr	Ile	Glu	Lys	Lys	Ile	Asn	Pro	Asn	Glu	His	Tyr	Leu	Ser
		35					40					45			
Val	Lys	Thr	Phe	Lys	Leu	Arg	Phe	Asn	Ser	Leu	Asp	Phe	Lys	Ala	Gln
	50					55					60				
Ala	Asn	Asp	Asp	Ser	Thr	Leu	Ile	Leu	Lys	Gly	Asp	Phe	Ser	Leu	Leu
65					70					75					80
Lys	Gln	Ser	Val	Asn	Leu	Asn	Tyr	His	Ile	Asp	Ile	Lys	Asp	Leu	Arg
			85						90					95	
Ser	Phe	Lys	Glu	Trp	Ile	Pro	Tyr	Pro	Leu	Arg	Gly	Ala	Val	Ile	Thr
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Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	Met	Ile	Gln	Gly	Val
		115					120					125			
Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	Ala	Leu	Leu	Asp	Asp
	130					135					140				
Phe	Lys	Leu	Ser	Arg	Leu	Asn	Leu	Asn	Ala	Gln	Asp	Ala	Asn	Leu	Glu
145					150					155					160
Asp	Leu	Leu	Tyr	Leu	Ile	Asn	Arg	Pro	Ala	Tyr	Ala	Asn	Ala	Lys	Val
			165						170					175	
Ser	Leu	Gln	Ala	Asp	Phe	Asn	Ser	Leu	Lys	Pro	Leu	Glu	Gly	His	Leu
		180						185					190		
Ile	Leu	Thr	Ala	Asn	Asn	Ala	Leu	Ile	Asn	Asn	Ala	Leu	Ile	Asn	Gln
	195						200					205			
Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	Phe	Ser	Leu	Ser	His
	210					215					220				
Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	Asp	Thr	Thr	Leu	Thr
225				230					235					240	
Ser	Pro	Leu	Ala	Asn	Phe	Lys	Ala	Leu	Lys	Ser	Glu	Tyr	Leu	Phe	Ser
			245						250					255	
Ile	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	Ile	Pro	Asn	Leu	Ala
		260						265					270		
Lys	Leu	Tyr	Asn	Ile	Thr	Asn	His	Pro	Leu	Lys	Gly	Ser	Leu	Thr	Leu
	275						280					285			
Lys	Gly	Ala	Ile	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Lys	Val	Ser	Gly	His
	290					295					300				
Ser	Asn	Leu	Leu	Asp	Gly	Ala	Leu	Asp	Phe	Thr	Leu	Leu	Asn	Lys	Asp
305				310					315					320	
Leu	Lys	Gly	Arg	Phe	Ser	Asn	Ile	Ser	Thr	Leu	Lys	Ala	Leu	Asp	Leu
			325						330					335	
Phe	His	Tyr	Pro	Lys	Phe	Phe	Gln	Ser	Val	Ala	Asp	Ala	Asn	Leu	Asp
		340					345						350		
Tyr	Asp	Leu	Ile	Ala	Lys	Gln	Gly	Val	Leu	Lys	Ala	Arg	Leu	Lys	Asn
		355					360						365		

Ala	Arg	Phe	Leu	Lys	Asn	Ala	Phe	Ser	Asp	Phe	Leu	Tyr	Ser	Ile	Ser
370						375					380				
Lys	Phe	Asp	Ile	Thr	Lys	Glu	Ile	Tyr	Asn	Asp	Ala	Asn	Leu	Val	Ser
385					390					395					400
Gln	Ile	Asn	Gln	Gln	Arg	Leu	Leu	Ser	Asp	Leu	Ser	Leu	Lys	Ser	Pro
			405						410					415	
Lys	Thr	Gln	Leu	Lys	Ile	His	Asn	Gly	Leu	Leu	Asp	Leu	Asn	Thr	Lys
		420						425					430		
Gln	Met	Asn	Met	Leu	Met	Asp	Ala	Glu	Ile	Leu	Lys	Phe	Ile	Phe	Lys
	435					440						445			
Met	Lys	Leu	Gln	Gly	Asn	Met	His	Gln	Pro	Lys	Phe	Ser	Leu	Ile	Leu
450					455						460				
Asn	Glu	Lys	Ala	Ile	Gln	Asn	Leu	Gln	Gln	Gly	Leu	Lys	Glu	Ile	
465				470				475						480	
Leu	Lys	Asn	Asp	Thr	Leu	Lys	Lys	Gly	Leu	Asp	His	Leu	Leu	Lys	Asp
			485					490						495	
Asp	Lys	Leu	Lys	Glu	Lys	Leu	Glu	Lys	Gly	Leu	Lys	Gly	Leu	Phe	
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<211> 397

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (53)...(352)

<400> 111

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Thr	Lys	His	Lys	Gly	Ile	Arg	Met	Phe	Lys	Gln	Ile	Arg	Arg	Met	Met	
	5					10					15					

agt	ttg	gca	ata	tta	atg	cct	agt	ttt	tta	ttg	gcg	gca	cca	gat	tac	154
Ser	Leu	Ala	Ile	Leu	Met	Pro	Ser	Phe	Leu	Leu	Ala	Ala	Pro	Asp	Tyr	
	20				25					30						

aaa	caa	aaa	ttc	act	caa	ata	ttg	gat	ttc	ata	agc	aat	gac	ttt	atc	202
Lys	Gln	Lys	Phe	Thr	Gln	Ile	Leu	Asp	Phe	Ile	Ser	Asn	Asp	Phe	Ile	
	35				40				45					50		

aag	gct	att	ggg	ggt	cta	atc	att	ggt	ggg	act	tgc	att	tac	gcc	tat	250
Lys	Ala	Ile	Gly	Gly	Leu	Ile	Ile	Val	Gly	Thr	Cys	Ile	Tyr	Ala	Tyr	
			55					60						65		

aaa	aat	tgg	gac	agg	ctt	gga	gaa	att	ggt	tgg	aaa	tgc	ggt	ggg	att	298
Lys	Asn	Trp	Asp	Arg	Leu	Gly	Glu	Ile	Gly	Trp	Lys	Cys	Val	Gly	Ile	
		70						75					80			

atc	att	ata	acc	gct	gct	att	tct	aat	gct	aaa	act	tta	agt	caa	tgg	346
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Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser Gln Trp  
85 90 95

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Leu Phe  
100

<210> 112  
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<212> PRT  
<213> Helicobacter pylori

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Asp Tyr Lys Gln Lys Phe Thr Gln Ile Leu Asp Phe Ile Ser Asn Asp  
35 40 45  
Phe Ile Lys Ala Ile Gly Gly Leu Ile Ile Val Gly Thr Cys Ile Tyr  
50 55 60  
Ala Tyr Lys Asn Trp Asp Arg Leu Gly Glu Ile Gly Trp Lys Cys Val  
65 70 75 80  
Gly Ile Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser  
85 90 95  
Gln Trp Leu Phe  
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<210> 113  
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<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (52)...(318)

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caa agc gac gct gtc ttt aag ata aat ttc tgt ctt gcc ctt ctt gta 105  
Gln Ser Asp Ala Val Phe Lys Ile Asn Phe Cys Leu Ala Leu Leu Val  
5 10 15

ttt gta aag agg ggc ttg agc gat ata aac atg ccc ttg ttc aat cag 153  
Phe Val Lys Arg Gly Leu Ser Asp Ile Asn Met Pro Leu Phe Asn Gln  
20 25 30

cgg gcg caa ata acg ata gaa aaa agt cat cag caa ggt ttg gat atg 201  
Arg Ala Gln Ile Thr Ile Glu Lys Ser His Gln Gln Gly Leu Asp Met  
35 40 45 50

gct ccc atc cac atc agc atc ggt cat gat aat gat ttt atg ata gcg 249  
Ala Pro Ile His Ile Ser Ile Gly His Asp Asn Asp Phe Met Ile Ala  
55 60 65

gat cat gtt ttt aat ttc ttc tgattttagg atttttgata aatggctttt 348  
Asp His Val Phe Asn Phe Phe  
85

<210> 114

<212> PRT

<213> Helicobacter pylori

<400> 114

<210> 115

<212> DNA

<213> *Helicobacter pylori*

<220>

$\langle 222 \rangle$  (54) ... (344)

<400> 115

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5 10 15

20	25	30	
gcc cac aaa aat gag att ttc ttt tgc cct aga aat agc tac att caa			200
Ala His Lys Asn Glu Ile Phe Phe Cys Pro Arg Asn Ser Tyr Ile Gln			
35	40	45	
gcg ttt aga atc tat caa gaa aga aag att acc ata agt ttt cac ggt			248
Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His Gly			
50	55	60	65
gga ata aat aat aat atc tgc ctt ctc gcc ttg aaa ggc atc cac agt			296
Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His Ser			
70	75	80	
gtc tat ttt gag ctc atc aaa att ctt gaa gcc gta ttt ttc cac ttc			344
Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His Phe			
85	90	95	
tgatcgcaag catctttttt gggcattata aggtgtgata at			386
<210> 116			
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<212> PRT			
<213> Helicobacter pylori			
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Ala Lys Asp Ile Leu Leu Ile Ala Ser Gln Ile Leu Lys Glu Arg Leu			
20	25	30	
Phe Ala His Lys Asn Glu Ile Phe Phe Cys Pro Arg Asn Ser Tyr Ile			
35	40	45	
Gln Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His			
50	55	60	
Gly Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His			
65	70	75	80
Ser Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His			
85	90	95	
Phe			
<210> 117			
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<212> DNA			
<213> Helicobacter pylori			
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<222> (55)...(516)			
<400> 117			
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		Ala	
		1	



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Ser Glu Val Ala Pro Ser Glu Val Leu Leu Asp Ser Ser Cys Leu Ser	
5 10 15	
ttt tct ttg act ata tcc tta gtt gtt act tgt tta gga gcg ctt ttt	153
Phe Ser Leu Thr Ile Ser Leu Val Val Thr Cys Leu Gly Ala Leu Phe	
20 25 30	
tct tta gct tcc tct tta gct tct tct ttt ttg ggc tct tct tta ggc	201
Ser Leu Ala Ser Ser Leu Ala Ser Ser Phe Leu Gly Ser Ser Leu Gly	
35 40 45	
tct tct ttt tta acc tct tca act tta ggc tca ggc tta ggc tcg ggt	249
Ser Ser Phe Leu Thr Ser Ser Thr Leu Gly Ser Gly Leu Gly Ser Gly	
50 55 60 65	
ttt ggt tca ggt ttg ggt tca ggc tta ggt ttt ggt ttt ggc ttt ggc	297
Phe Gly Ser Gly Leu Gly Ser Gly Leu Gly Phe Gly Phe Gly Phe Gly	
70 75 80	
ttg ggt tta ggc tta ggt tta ggc ttt gta acc tcc ttt ttg ggt tct	345
Leu Gly Leu Gly Leu Gly Leu Gly Phe Val Thr Ser Phe Leu Gly Ser	
85 90 95	
tct ttt ttt ggc tct tct ttc ttg ggt ttt tct tta ggc tct tct ttg	393
Ser Phe Phe Gly Ser Ser Phe Leu Gly Phe Ser Leu Gly Ser Ser Leu	
100 105 110	
ggt tta gcc gac tca gca tta gtc ttt gta ttg gaa tta gtg ttg atg	441
Gly Leu Ala Asp Ser Ala Leu Val Phe Val Leu Glu Leu Val Leu Met	
115 120 125	
ctg gct aaa ctc atg gta acc tta gtg gtc ccg gct tgc gct aaa ggc	489
Leu Ala Lys Leu Met Val Thr Leu Val Val Pro Ala Cys Ala Lys Gly	
130 135 140 145	
tct ggg gcg tct tcg cgc agt aaa aaa tagccaaacc ctatagcgta	536
Ser Gly Ala Ser Ser Arg Ser Lys Lys	
150	
tagggcaaaa gagattaataa agctaacact cgt	569
<210> 118	
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<212> PRT	
<213> Helicobacter pylori	
<400> 118	
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Phe Ser Leu Ala Ser Ser Leu Ala Ser Ser Phe Leu Gly Ser Ser Leu	
35 40 45	

Gly Ser Ser Phe Leu Thr Ser Ser Thr Leu Gly Ser Gly Leu Gly Ser  
 50 55 60  
 Gly Phe Gly Ser Gly Leu Gly Ser Gly Leu Gly Phe Gly Phe Gly Phe  
 65 70 75 80  
 Gly Leu Gly Leu Gly Leu Gly Leu Gly Phe Val Thr Ser Phe Leu Gly  
 85 90 95  
 Ser Ser Phe Phe Gly Ser Ser Phe Leu Gly Phe Ser Leu Gly Ser Ser  
 100 105 110  
 Leu Gly Leu Ala Asp Ser Ala Leu Val Phe Val Leu Glu Leu Val Leu  
 115 120 125  
 Met Leu Ala Lys Leu Met Val Thr Leu Val Val Pro Ala Cys Ala Lys  
 130 135 140  
 Gly Ser Gly Ala Ser Ser Arg Ser Lys Lys  
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<210> 119  
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> (77)...(310)

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 Asn Glu His His Thr Pro Ala Gly Ser Leu Val Leu  
 1 5 10  
  
 gga tct ttt atc atc ggc tct ttt aaa ggc gtg ggt gct ata ggg ggc 160  
 Gly Ser Phe Ile Ile Gly Ser Phe Lys Gly Val Gly Ala Ile Gly Gly  
 15 20 25  
  
 gtg ggt gct gtg gtt ttt ggg att tct tta ttt tct ttt ggg ggt ttt 208  
 Val Gly Ala Val Val Phe Gly Ile Ser Leu Phe Ser Phe Gly Gly Phe  
 30 35 40  
  
 tgc cac aac tct gtc aaa gcc gcc gct ttt tta gga tcc att ttg gct 256  
 Cys His Asn Ser Val Lys Ala Ala Ala Phe Leu Gly Ser Ile Leu Ala  
 45 50 55 60  
  
 aaa att tta ccg agt tct tgg ggt ttt agc gcc att aaa att tct aat 304  
 Lys Ile Leu Pro Ser Ser Trp Gly Phe Ser Ala Ile Lys Ile Ser Asn  
 65 70 75  
  
 gcg ttt tgagtgggta aattttctaa aatcagagcc gatttagaat ctttcattt 359  
 Ala Phe

<210> 120  
 <211> 78  
 <212> PRT

<213> Helicobacter pylori

<400> 120

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Ile	Gly	Ser	Phe	Lys	Gly	Val	Gly	Ala	Ile	Gly	Gly	Val	Gly	Ala	Val
			20					25					30		
Val	Phe	Gly	Ile	Ser	Leu	Phe	Ser	Phe	Gly	Gly	Phe	Cys	His	Asn	Ser
		35					40					45			
Val	Lys	Ala	Ala	Ala	Phe	Leu	Gly	Ser	Ile	Leu	Ala	Lys	Ile	Leu	Pro
	50					55					60				
Ser	Ser	Trp	Gly	Phe	Ser	Ala	Ile	Lys	Ile	Ser	Asn	Ala	Phe		
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<210> 121

<211> 1051

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(998)

<400> 121

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tta	aat	act	ttc	ttg	gat	aca	tgt	ttt	ctt	tta	ttc	atc	agt	att	ctt	104
Leu	Asn	Thr	Phe	Leu	Asp	Thr	Cys	Phe	Leu	Leu	Phe	Ile	Ser	Ile	Leu	
		5					10					15				
ttt	tat	tta	agt	ata	cca	att	tat	cct	aac	aaa	gtg	gtg	gtt	gtc	ccg	152
Phe	Tyr	Leu	Ser	Ile	Pro	Ile	Tyr	Pro	Asn	Lys	Val	Val	Val	Val	Pro	
	20					25					30					
caa	ggt	tcg	ctc	aaa	aaa	gtg	ttt	ttt	tct	tta	aaa	gag	caa	ggc	gtg	200
Gln	Gly	Ser	Leu	Lys	Lys	Val	Phe	Phe	Ser	Leu	Lys	Glu	Gln	Gly	Val	
	35				40					45					50	
gat	atg	aac	gct	ttg	gat	ttg	ctt	ttt	tta	cgc	ctg	atg	ggc	atg	cct	248
Asp	Met	Asn	Ala	Leu	Asp	Leu	Leu	Phe	Leu	Arg	Leu	Met	Gly	Met	Pro	
				55					60					65		
aaa	aaa	ggt	tat	att	gat	atg	ggc	gat	ggg	gct	tta	agg	aag	ggg	gat	296
Lys	Lys	Gly	Tyr	Ile	Asp	Met	Gly	Asp	Gly	Ala	Leu	Arg	Lys	Gly	Asp	
			70					75					80			
ttt	tta	gtc	cgt	ttg	att	aag	gca	aaa	gcg	gca	caa	aaa	agt	gcg	act	344
Phe	Leu	Val	Arg	Leu	Ile	Lys	Ala	Lys	Ala	Ala	Gln	Lys	Ser	Ala	Thr	
		85					90					95				
cta	atc	cct	ggg	gaa	agc	cgc	tat	ttt	ttc	acg	caa	att	ttg	agc	gag	392
Leu	Ile	Pro	Gly	Glu	Ser	Arg	Tyr	Phe	Phe	Thr	Gln	Ile	Leu	Ser	Glu	

100	105	110	
act tac caa cta gaa aca agc gat ctc aat cag gct tat gaa agc atc			440
Thr Tyr Gln Leu Glu Thr Ser Asp Leu Asn Gln Ala Tyr Glu Ser Ile			
115	120	125	130
gct cca cga ttg aat ggc gaa gtg ata gaa gat ggg gtg ata tgg cca			488
Ala Pro Arg Leu Asn Gly Glu Val Ile Glu Asp Gly Val Ile Trp Pro			
	135	140	145
gac act tat cat ttg cct tta ggg gag gac gct ttt aaa atc atg caa			536
Asp Thr Tyr His Leu Pro Leu Gly Glu Asp Ala Phe Lys Ile Met Gln			
	150	155	160
act ttg att ggt caa tcc atg aaa aaa cac gaa gcc tta agc aaa caa			584
Thr Leu Ile Gly Gln Ser Met Lys Lys His Glu Ala Leu Ser Lys Gln			
	165	170	175
tgg ctt gga tac tac cat aaa gaa gag tgg ttt gaa aaa atc att ctc			632
Trp Leu Gly Tyr Tyr His Lys Glu Glu Trp Phe Glu Lys Ile Ile Leu			
	180	185	190
gct tct att gtg caa aaa gaa gcc gct aat gtt gaa gaa atg ccc ttg			680
Ala Ser Ile Val Gln Lys Glu Ala Ala Asn Val Glu Glu Met Pro Leu			
195	200	205	210
att gcg agc gtg att ttt aac cgc ttg aaa aaa ggc atg cct tta caa			728
Ile Ala Ser Val Ile Phe Asn Arg Leu Lys Lys Gly Met Pro Leu Gln			
	215	220	225
atg gat ggg gct ttg aat tat cag gaa ttt tca cac gct aaa gta acc			776
Met Asp Gly Ala Leu Asn Tyr Gln Glu Phe Ser His Ala Lys Val Thr			
	230	235	240
aaa gag cgc att aaa acc gat aac acc ccc tac aat acc tat aaa ttt			824
Lys Glu Arg Ile Lys Thr Asp Asn Thr Pro Tyr Asn Thr Tyr Lys Phe			
	245	250	255
aag ggt ttg cct aaa aat cct gta ggg agc gtg agc cta gaa gcg att			872
Lys Gly Leu Pro Lys Asn Pro Val Gly Ser Val Ser Leu Glu Ala Ile			
	260	265	270
aga gcc gtg atc ttc cct aaa aaa acg gat ttc ttg tat ttt gtg aaa			920
Arg Ala Val Ile Phe Pro Lys Lys Thr Asp Phe Leu Tyr Phe Val Lys			
275	280	285	290
atg ccg gat aaa aaa cat gct ttc agc gcg act tat aaa gag cat tta			968
Met Pro Asp Lys Lys His Ala Phe Ser Ala Thr Tyr Lys Glu His Leu			
	295	300	305
aaa aac att aat ctt tct aat aat cat ttt taagattaag gtaaatgggg			1018
Lys Asn Ile Asn Leu Ser Asn Asn His Phe			
	310	315	
cgtttttttct tttgaattga gtaaaaagtg ttt			1051

<210> 122  
 <211> 316  
 <212> PRT  
 <213> Helicobacter pylori

<400> 122  
 Met Thr Leu Asn Thr Phe Leu Asp Thr Cys Phe Leu Leu Phe Ile Ser  
 1 5 10 15  
 Ile Leu Phe Tyr Leu Ser Ile Pro Ile Tyr Pro Asn Lys Val Val Val  
 20 25 30  
 Val Pro Gln Gly Ser Leu Lys Lys Val Phe Phe Ser Leu Lys Glu Gln  
 35 40 45  
 Gly Val Asp Met Asn Ala Leu Asp Leu Leu Phe Leu Arg Leu Met Gly  
 50 55 60  
 Met Pro Lys Lys Gly Tyr Ile Asp Met Gly Asp Gly Ala Leu Arg Lys  
 65 70 75 80  
 Gly Asp Phe Leu Val Arg Leu Ile Lys Ala Lys Ala Ala Gln Lys Ser  
 85 90 95  
 Ala Thr Leu Ile Pro Gly Glu Ser Arg Tyr Phe Phe Thr Gln Ile Leu  
 100 105 110  
 Ser Glu Thr Tyr Gln Leu Glu Thr Ser Asp Leu Asn Gln Ala Tyr Glu  
 115 120 125  
 Ser Ile Ala Pro Arg Leu Asn Gly Glu Val Ile Glu Asp Gly Val Ile  
 130 135 140  
 Trp Pro Asp Thr Tyr His Leu Pro Leu Gly Glu Asp Ala Phe Lys Ile  
 145 150 155 160  
 Met Gln Thr Leu Ile Gly Gln Ser Met Lys Lys His Glu Ala Leu Ser  
 165 170 175  
 Lys Gln Trp Leu Gly Tyr Tyr His Lys Glu Glu Trp Phe Glu Lys Ile  
 180 185 190  
 Ile Leu Ala Ser Ile Val Gln Lys Glu Ala Ala Asn Val Glu Glu Met  
 195 200 205  
 Pro Leu Ile Ala Ser Val Ile Phe Asn Arg Leu Lys Lys Gly Met Pro  
 210 215 220  
 Leu Gln Met Asp Gly Ala Leu Asn Tyr Gln Glu Phe Ser His Ala Lys  
 225 230 235 240  
 Val Thr Lys Glu Arg Ile Lys Thr Asp Asn Thr Pro Tyr Asn Thr Tyr  
 245 250 255  
 Lys Phe Lys Gly Leu Pro Lys Asn Pro Val Gly Ser Val Ser Leu Glu  
 260 265 270  
 Ala Ile Arg Ala Val Ile Phe Pro Lys Lys Thr Asp Phe Leu Tyr Phe  
 275 280 285  
 Val Lys Met Pro Asp Lys Lys His Ala Phe Ser Ala Thr Tyr Lys Glu  
 290 295 300  
 His Leu Lys Asn Ile Asn Leu Ser Asn Asn His Phe  
 305 310 315

<210> 123  
 <211> 637  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS

<222> (51)...(584)

<400> 123

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gaaagttcgg gggcggattc tatgattaat ggctatgggtt ataccaaaga atg agt      56
                                     Met Ser
                                     1

caa aaa atc cta att cta ggt att ggc aat atc ctt ttt ggc gat gaa      104
Gln Lys Ile Leu Ile Leu Gly Ile Gly Asn Ile Leu Phe Gly Asp Glu
      5              10              15

ggg att ggg gtg cat tta gcc cac tac ctc aaa aaa aat ttt tct ttt      152
Gly Ile Gly Val His Leu Ala His Tyr Leu Lys Lys Asn Phe Ser Phe
      20              25              30

ttc cct agc gtg gat att ata gat ggg ggg aca atg gcc cag cag ctc      200
Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln Gln Leu
      35              40              45

att cct tta atc act tcg tat gaa aag gtt ttg att ttg gat tgc gtg      248
Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp Cys Val
      55              60              65

agc gct gaa ggc gtt gag ata gga tca gtc tat gct ttt gat ttt aag      296
Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp Phe Lys
      70              75              80

gac gct cct aaa gaa atc aca tgg gct ggg agc gct cat gaa gtg gaa      344
Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu Val Glu
      85              90              95

atg cta cac act tta agg ctc acg gag ttt tta ggg gat ttg cct aaa      392
Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu Pro Lys
      100             105             110

act ttt atc gtg ggg ctt gtg cct ttt gtg ata ggg agc gag acc act      440
Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu Thr Thr
      115             120             125             130

ttc aag ctt tca agc aaa att tta aac gct tta gaa acc gcc tta aaa      488
Phe Lys Leu Ser Ser Lys Ile Leu Asn Ala Leu Glu Thr Ala Leu Lys
      135             140             145

gcc ata gaa acc caa ctc aac gca tgg ggg gtt aaa atg caa cgc acc      536
Ala Ile Glu Thr Gln Leu Asn Ala Trp Gly Val Lys Met Gln Arg Thr
      150             155             160

gat cat atc gct tta gaa tgt atc gct gaa ctt tct tat aag ggt ttt      584
Asp His Ile Ala Leu Glu Cys Ile Ala Glu Leu Ser Tyr Lys Gly Phe
      165             170             175

tgaattgggtt tttgtttttc tttttaaatg cgттаатgaa gaaacaagcc tga      637
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<210> 124

<211> 178

<212> PRT

<213> Helicobacter pylori

<400> 124

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Met Ser Gln Lys Ile Leu Ile Leu Gly Ile Gly Asn Ile Leu Phe Gly
 1           5           10           15
Asp Glu Gly Ile Gly Val His Leu Ala His Tyr Leu Lys Lys Asn Phe
      20           25           30
Ser Phe Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln
      35           40           45
Gln Leu Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp
      50           55           60
Cys Val Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp
65           70           75           80
Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu
      85           90           95
Val Glu Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu
      100          105          110
Pro Lys Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu
      115          120          125
Thr Thr Phe Lys Leu Ser Ser Lys Ile Leu Asn Ala Leu Glu Thr Ala
      130          135          140
Leu Lys Ala Ile Glu Thr Gln Leu Asn Ala Trp Gly Val Lys Met Gln
145          150          155          160
Arg Thr Asp His Ile Ala Leu Glu Cys Ile Ala Glu Leu Ser Tyr Lys
      165          170          175
Gly Phe
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<210> 125

<211> 214

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(161)

<400> 125

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gcattgctaa tttgggaata cttgtttatg ccagtgaat aggagcggct atg atg      56
                                     Met Met
                                     1

tgg cgt agt ctc arg gtg gct ttt acg atc act gat att agt aaa acc      104
Trp Arg Ser Leu Xaa Val Ala Phe Thr Ile Thr Asp Ile Ser Lys Thr
      5           10           15

ttt caa tcc cag cct aag cac cat caa atc ggc act tta gaa ttg aat      152
Phe Gln Ser Gln Pro Lys His His Gln Ile Gly Thr Leu Glu Leu Asn
      20           25           30

ttc gcc ttt tgatttaata tcagtttaat atttttcttc ctatatgata      201
Phe Ala Phe
      35
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tttatatgat att

214

<210> 126

<211> 37

<212> PRT

<213> Helicobacter pylori

<220>

<221> VARIANT

<222> 7

<223> Xaa = Any Amino Acid

<400> 126

Met	Met	Trp	Arg	Ser	Leu	Xaa	Val	Ala	Phe	Thr	Ile	Thr	Asp	Ile	Ser
1				5					10					15	
Lys	Thr	Phe	Gln	Ser	Gln	Pro	Lys	His	His	Gln	Ile	Gly	Thr	Leu	Glu
			20					25					30		
Leu	Asn	Phe	Ala	Phe											
			35												

<210> 127

<211> 1576

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(1523)

<400> 127

ctgtattcgc	ttctgtggat	tactaccctc	aaagaaaaga	aagccacaga	atg aac	56
					Met Asn	
					1	
acc acc atc	tta gaa gct	tat gcg gct	gag cca agc	agg caa acc	ctc	104
Thr Thr Ile	Leu Glu Ala	Tyr Ala Ala	Glu Pro Ser	Arg Gln Thr	Leu	
	5		10		15	
tct aaa gtc	agc aac cga	ttc aaa gag	cat ggc gct	aaa ttt gat	ctt	152
Ser Lys Val	Ser Asn Arg	Phe Lys Glu	His Gly Ala	Lys Phe Asp	Leu	
	20		25		30	
cgt gtg atg	gca acg cat	gga ggc acc	att agt tgg	aaa gct aaa	gaa	200
Arg Val Met	Ala Thr His	Gly Gly Thr	Ile Ser Trp	Lys Ala Lys	Glu	
	35		40		45	50
ctc gct agg	act att gtg	agc ggc cct	att gga ggc	gtg att gga	tct	248
Leu Ala Arg	Thr Ile Val	Ser Gly Pro	Ile Gly Gly	Val Ile Gly	Ser	
	55		60		65	
aaa ttg cta	ggc gaa acg	ctt ggt tat	gac aat att	gca tgc agt	gat	296
Lys Leu Leu	Gly Glu Thr	Leu Gly Tyr	Asp Asn Ile	Ala Cys Ser	Asp	
	70		75		80	



att ggk ggc acg agc ttt gat atg gcg ctt atc gtt aag agc aat ttt	344
Ile Xaa Gly Thr Ser Phe Asp Met Ala Leu Ile Val Lys Ser Asn Phe	
85 90 95	
aac atc gct tct gac cct gat atg gca cgc ctt gtt tta tct cta ccg	392
Asn Ile Ala Ser Asp Pro Asp Met Ala Arg Leu Val Leu Ser Leu Pro	
100 105 110	
ctt gtg gct atg gat tct gtt ggc gca ggt gct ggg agt ttt gtg cgc	440
Leu Val Ala Met Asp Ser Val Gly Ala Gly Ala Gly Ser Phe Val Arg	
115 120 125 130	
att gat cca cac agc cga tct gtc aaa cta ggg cct gac agc gcg ggg	488
Ile Asp Pro His Ser Arg Ser Val Lys Leu Gly Pro Asp Ser Ala Gly	
135 140 145	
tat aga gtt ggc act tgt tgg aaa gac agc ggg tta gac acg gtt tca	536
Tyr Arg Val Gly Thr Cys Trp Lys Asp Ser Gly Leu Asp Thr Val Ser	
150 155 160	
gta acc gat tgc cat att gtt tta ggc tat ttg aac ccg gat aat ttc	584
Val Thr Asp Cys His Ile Val Leu Gly Tyr Leu Asn Pro Asp Asn Phe	
165 170 175	
tta ggc ggt ttg atc aaa tta gat gtg gat agg gct aaa aaa cac att	632
Leu Gly Gly Leu Ile Lys Leu Asp Val Asp Arg Ala Lys Lys His Ile	
180 185 190	
aaa gaa caa atc gct gat ccg cta ggc att agc gta gaa gat gcg gct	680
Lys Glu Gln Ile Ala Asp Pro Leu Gly Ile Ser Val Glu Asp Ala Ala	
195 200 205 210	
gct ggt gtg att gaa ttg ctt gat ttg gag ctt aaa gaa tac ttg cga	728
Ala Gly Val Ile Glu Leu Leu Asp Leu Glu Leu Lys Glu Tyr Leu Arg	
215 220 225	
tcc aac att agc gct aaa ggg tat agc cca tct gat ttt gtg tgc ttt	776
Ser Asn Ile Ser Ala Lys Gly Tyr Ser Pro Ser Asp Phe Val Cys Phe	
230 235 240	
tca tat ggt ggc gca gga cct gtg cat acc tat ggc tat aca gaa gga	824
Ser Tyr Gly Gly Ala Gly Pro Val His Thr Tyr Gly Tyr Thr Glu Gly	
245 250 255	
tta ggg ttt aag gat gtg gta gtg cct gcg tgg gcg gct gga ttt agc	872
Leu Gly Phe Lys Asp Val Val Val Pro Ala Trp Ala Ala Gly Phe Ser	
260 265 270	
gct ttt ggt tgt gct tgc gct gat ttt gaa tac aga tac gac aag agc	920
Ala Phe Gly Cys Ala Cys Ala Asp Phe Glu Tyr Arg Tyr Asp Lys Ser	
275 280 285 290	
gtg gat att gcc att ccg cag tat tct tca gac aag tca aaa ata gac	968
Val Asp Ile Ala Ile Pro Gln Tyr Ser Ser Asp Lys Ser Lys Ile Asp	

295	300	305	
gca tgc aaa atc att caa gac gca tgg gat gaa ttg act ttg aaa gtg			1016
Ala Cys Lys Ile Ile Gln Asp Ala Trp Asp Glu Leu Thr Leu Lys Val			
310	315	320	
att gaa gag ttc aag atc aat gga ttt tct caa aaa gat gtg atc tta			1064
Ile Glu Glu Phe Lys Ile Asn Gly Phe Ser Gln Lys Asp Val Ile Leu			
325	330	335	
aga cct gga tac agg atg cag tat atg ggg caa ttg aat gat tta gag			1112
Arg Pro Gly Tyr Arg Met Gln Tyr Met Gly Gln Leu Asn Asp Leu Glu			
340	345	350	
atc act tct cct gtg tca aaa gct gca agc gtg gct gat tgg gaa gag			1160
Ile Thr Ser Pro Val Ser Lys Ala Ala Ser Val Ala Asp Trp Glu Glu			
355	360	365	370
att gtc aaa gaa tat gaa aaa acc tac gct cgc gtt tat tct gaa tca			1208
Ile Val Lys Glu Tyr Glu Lys Thr Tyr Ala Arg Val Tyr Ser Glu Ser			
375	380	385	
gcg tgt tct cca gag ctt ggt ttt agc gtg act ggc gtg atc atg cgt			1256
Ala Cys Ser Pro Glu Leu Gly Phe Ser Val Thr Gly Val Ile Met Arg			
390	395	400	
ggt gtt gtg gct acg caa aaa cct gtg att ccg gtt gaa aaa gag cat			1304
Gly Val Val Ala Thr Gln Lys Pro Val Ile Pro Val Glu Lys Glu His			
405	410	415	
ggt gct acg ccc cca aaa gaa gcc aaa ata ggc gtt aga aaa ttc tat			1352
Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly Val Arg Lys Phe Tyr			
420	425	430	
cgg cat aaa aaa tgg gtg gat gca gat gtg tgg caa atg gaa aaa tta			1400
Arg His Lys Lys Trp Val Asp Ala Asp Val Trp Gln Met Glu Lys Leu			
435	440	445	450
ctg cct gga aat gaa gtc ata gga cct gcg atc gtg gaa tca gat gcg			1448
Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile Val Glu Ser Asp Ala			
455	460	465	
acc act ttc gtg ata ccc aaa ggc ttt gcg aca aga cta gac aaa cac			1496
Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr Arg Leu Asp Lys His			
470	475	480	
cga ttg ttc cac ttg aaa gaa att aaa taaaggagtt caaaatggca			1543
Arg Leu Phe His Leu Lys Glu Ile Lys			
485	490		
aattttattga aaaacggcaa aacttttaaaa caa			1576
<210> 128			
<211> 491			
<212> PRT			

<213> Helicobacter pylori

<220>

<221> VARIANT

<222> 84

<223> Xaa = Any Amino Acid

<400> 128

Met	Asn	Thr	Thr	Ile	Leu	Glu	Ala	Tyr	Ala	Ala	Glu	Pro	Ser	Arg	Gln
1				5					10					15	
Thr	Leu	Ser	Lys	Val	Ser	Asn	Arg	Phe	Lys	Glu	His	Gly	Ala	Lys	Phe
			20					25					30		
Asp	Leu	Arg	Val	Met	Ala	Thr	His	Gly	Gly	Thr	Ile	Ser	Trp	Lys	Ala
			35				40					45			
Lys	Glu	Leu	Ala	Arg	Thr	Ile	Val	Ser	Gly	Pro	Ile	Gly	Gly	Val	Ile
	50					55					60				
Gly	Ser	Lys	Leu	Leu	Gly	Glu	Thr	Leu	Gly	Tyr	Asp	Asn	Ile	Ala	Cys
65					70					75					80
Ser	Asp	Ile	Xaa	Gly	Thr	Ser	Phe	Asp	Met	Ala	Leu	Ile	Val	Lys	Ser
				85				90						95	
Asn	Phe	Asn	Ile	Ala	Ser	Asp	Pro	Asp	Met	Ala	Arg	Leu	Val	Leu	Ser
			100					105					110		
Leu	Pro	Leu	Val	Ala	Met	Asp	Ser	Val	Gly	Ala	Gly	Ala	Gly	Ser	Phe
			115				120					125			
Val	Arg	Ile	Asp	Pro	His	Ser	Arg	Ser	Val	Lys	Leu	Gly	Pro	Asp	Ser
	130					135					140				
Ala	Gly	Tyr	Arg	Val	Gly	Thr	Cys	Trp	Lys	Asp	Ser	Gly	Leu	Asp	Thr
145					150					155					160
Val	Ser	Val	Thr	Asp	Cys	His	Ile	Val	Leu	Gly	Tyr	Leu	Asn	Pro	Asp
				165				170						175	
Asn	Phe	Leu	Gly	Leu	Ile	Lys	Leu	Asp	Val	Asp	Arg	Ala	Lys	Lys	
			180				185					190			
His	Ile	Lys	Glu	Gln	Ile	Ala	Asp	Pro	Leu	Gly	Ile	Ser	Val	Glu	Asp
		195					200					205			
Ala	Ala	Ala	Gly	Val	Ile	Glu	Leu	Leu	Asp	Leu	Glu	Leu	Lys	Glu	Tyr
	210					215				220					
Leu	Arg	Ser	Asn	Ile	Ser	Ala	Lys	Gly	Tyr	Ser	Pro	Ser	Asp	Phe	Val
225				230						235					240
Cys	Phe	Ser	Tyr	Gly	Gly	Ala	Gly	Pro	Val	His	Thr	Tyr	Gly	Tyr	Thr
				245					250					255	
Glu	Gly	Leu	Gly	Phe	Lys	Asp	Val	Val	Val	Pro	Ala	Trp	Ala	Ala	Gly
			260				265					270			
Phe	Ser	Ala	Phe	Gly	Cys	Ala	Cys	Ala	Asp	Phe	Glu	Tyr	Arg	Tyr	Asp
		275				280						285			
Lys	Ser	Val	Asp	Ile	Ala	Ile	Pro	Gln	Tyr	Ser	Ser	Asp	Lys	Ser	Lys
	290					295					300				
Ile	Asp	Ala	Cys	Lys	Ile	Ile	Gln	Asp	Ala	Trp	Asp	Glu	Leu	Thr	Leu
305				310						315					320
Lys	Val	Ile	Glu	Glu	Phe	Lys	Ile	Asn	Gly	Phe	Ser	Gln	Lys	Asp	Val
				325					330					335	
Ile	Leu	Arg	Pro	Gly	Tyr	Arg	Met	Gln	Tyr	Met	Gly	Gln	Leu	Asn	Asp
			340				345						350		
Leu	Glu	Ile	Thr	Ser	Pro	Val	Ser	Lys	Ala	Ala	Ser	Val	Ala	Asp	Trp
		355				360						365			
Glu	Glu	Ile	Val	Lys	Glu	Tyr	Glu	Lys	Thr	Tyr	Ala	Arg	Val	Tyr	Ser

370		375		380
Glu Ser Ala Cys Ser Pro	Glu Leu Gly Phe Ser Val Thr Gly Val Ile			
385		390		400
Met Arg Gly Val Val Ala Thr Gln Lys Pro Val Ile Pro Val Glu Lys				
		405		415
Glu His Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly Val Arg Lys				
		420		430
Phe Tyr Arg His Lys Lys Trp Val Asp Ala Asp Val Trp Gln Met Glu				
		435		445
Lys Leu Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile Val Glu Ser				
		450		460
Asp Ala Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr Arg Leu Asp				
465		470		480
Lys His Arg Leu Phe His Leu Lys Glu Ile Lys				
		485		490

<210> 129  
 <211> 303  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (52)...(261)

<400> 129  
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 Met Ile  
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cag tta aaa tca aat ttg gat tgg tac gca gat tat ttg aat ttt tta 105  
 Gln Leu Lys Ser Asn Leu Asp Trp Tyr Ala Asp Tyr Leu Asn Phe Leu  
 5 10 15

gat cgc ttt ggg gaa aaa atg gaa gaa tcc aaa gag cga aaa caa ctc 153  
 Asp Arg Phe Gly Glu Lys Met Glu Glu Ser Lys Glu Arg Lys Gln Leu  
 20 25 30

ctg atc gct tcc ctt gca cct ctt gcg ggc ttt gct gca aga ata tcg 201  
 Leu Ile Ala Ser Leu Ala Pro Leu Ala Gly Phe Ala Ala Arg Ile Ser  
 35 40 45 50

ccg gga tta ttg agc tta ttg ggt ttg atg ctg gca atg ggg tgt gca 249  
 Pro Gly Leu Leu Ser Leu Leu Gly Leu Met Leu Ala Met Gly Cys Ala  
 55 60 65

aat ttt tgg att tagaaaccaa tctgtgcaag atttatgaat cgcgcccgtt 301  
 Asn Phe Trp Ile  
 70

aa 303

<210> 130  
 <211> 70

<212> PRT

<213> Helicobacter pylori

<400> 130

Met	Ile	Gln	Leu	Lys	Ser	Asn	Leu	Asp	Trp	Tyr	Ala	Asp	Tyr	Leu	Asn
1				5				10						15	
Phe	Leu	Asp	Arg	Phe	Gly	Glu	Lys	Met	Glu	Glu	Ser	Lys	Glu	Arg	Lys
			20					25					30		
Gln	Leu	Leu	Ile	Ala	Ser	Leu	Ala	Pro	Leu	Ala	Gly	Phe	Ala	Ala	Arg
		35					40					45			
Ile	Ser	Pro	Gly	Leu	Leu	Ser	Leu	Leu	Gly	Leu	Met	Leu	Ala	Met	Gly
	50					55					60				
Cys	Ala	Asn	Phe	Trp	Ile										
65					70										

<210> 131

<211> 826

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(773)

<400> 131

tggtttaatt	gttaagccgg	ctagaaaaag	agcggttattt	gcgccatatc	atg	cta	56
					Met	Leu	
					1		
gaa	gat	gtg	ggc	gaa	gag	ggg	104
Glu	Asp	Val	Gly	Glu	Glu	Gly	
		5				10	
						15	
tta	gtc	att	ggg	gct	ggg	ggg	152
Leu	Val	Ile	Gly	Ala	Gly	Gly	
		20				25	
						30	
tgt	gcc	gct	ggg	ata	gga	aaa	200
Cys	Ala	Ala	Gly	Ile	Gly	Lys	
		35				40	
						45	
						50	
gat	atg	agt	aat	ttg	caa	cgc	248
Asp	Met	Ser	Asn	Leu	Gln	Arg	
			55			60	
						65	
aac	caa	tct	aaa	gcc	tct	agc	296
Asn	Gln	Ser	Lys	Ala	Ser	Ser	
		70				75	
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gcg	ggg	att	gaa	ata	gag	gct	344
Ala	Gly	Ile	Glu	Ile	Glu	Ala	
		85				90	
						95	
gct	ctt	tct	ctc	ata	gag	cct	392
						tat	
						gat	
						ttt	
						atc	
						ata	
						gac	
						gcc	
						acg	
						gac	

Ala Leu Ser Leu Ile Glu Pro Tyr Asp Phe Ile Ile Asp Ala Thr Asp	
100 105 110	
aat ttt aac gct aaa ttt ttg atc aat gac gct tgc gtg tta gcc caa	440
Asn Phe Asn Ala Lys Phe Leu Ile Asn Asp Ala Cys Val Leu Ala Gln	
115 120 125 130	
aaa ccc tat tcg cat gcc ggg gtt tta gaa tac agg ggg caa agc atg	488
Lys Pro Tyr Ser His Ala Gly Val Leu Glu Tyr Arg Gly Gln Ser Met	
135 140 145	
agc gtt tta ccc cat agc gca tgc tta gcg tgc gtt ttt gat aag ccc	536
Ser Val Leu Pro His Ser Ala Cys Leu Ala Cys Val Phe Asp Lys Pro	
150 155 160	
cct aaa aag gga tta aat ccc att tca ggg ctt ttt ggg gtc tta ccc	584
Pro Lys Lys Gly Leu Asn Pro Ile Ser Gly Leu Phe Gly Val Leu Pro	
165 170 175	
gga gtt tta ggg tgt atc caa gcg agc gaa tgc ctt aaa tat ttt tta	632
Gly Val Leu Gly Cys Ile Gln Ala Ser Glu Cys Leu Lys Tyr Phe Leu	
180 185 190	
ggg ttt gaa act tta ctt ata aat act tta ctt ata gcc gat att aaa	680
Gly Phe Glu Thr Leu Leu Ile Asn Thr Leu Leu Ile Ala Asp Ile Lys	
195 200 205 210	
acg atg gat ttt aaa aaa att caa gca ccc aaa aac cct gaa tgt agg	728
Thr Met Asp Phe Lys Lys Ile Gln Ala Pro Lys Asn Pro Glu Cys Arg	
215 220 225	
gtt tgt ggc acg cat aaa atc acg cat tta cag gat tat gaa att	773
Val Cys Gly Thr His Lys Ile Thr His Leu Gln Asp Tyr Glu Ile	
230 235 240	
tagattaagg ggtaagtttt ggatttatca accatattag gcttggtatt ggc	826

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 <212> PRT  
 <213> *Helicobacter pylori*

<400> 132

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Ser Val Leu Val Ile Gly Ala Gly Gly Leu Gly Ser Ala Val Leu Met	
20 25 30	
Tyr Leu Cys Ala Ala Gly Ile Gly Lys Ile Gly Ile Val Asp Phe Asp	
35 40 45	
Val Val Asp Met Ser Asn Leu Gln Arg Gln Ile Ile His Ser Gln Asp	
50 55 60	
Phe Leu Asn Gln Ser Lys Ala Ser Ser Ala Lys Ala Arg Leu Lys Gln	
65 70 75 80	
Leu Asn Ala Gly Ile Glu Ile Glu Ala Phe Glu Glu Arg Phe Lys Ala	
85 90 95	

His	Asn	Ala	Leu	Ser	Leu	Ile	Glu	Pro	Tyr	Asp	Phe	Ile	Ile	Asp	Ala
			100					105					110		
Thr	Asp	Asn	Phe	Asn	Ala	Lys	Phe	Leu	Ile	Asn	Asp	Ala	Cys	Val	Leu
		115					120					125			
Ala	Gln	Lys	Pro	Tyr	Ser	His	Ala	Gly	Val	Leu	Glu	Tyr	Arg	Gly	Gln
	130					135					140				
Ser	Met	Ser	Val	Leu	Pro	His	Ser	Ala	Cys	Leu	Ala	Cys	Val	Phe	Asp
145					150					155				160	
Lys	Pro	Pro	Lys	Lys	Gly	Leu	Asn	Pro	Ile	Ser	Gly	Leu	Phe	Gly	Val
			165					170					175		
Leu	Pro	Gly	Val	Leu	Gly	Cys	Ile	Gln	Ala	Ser	Glu	Cys	Leu	Lys	Tyr
		180						185					190		
Phe	Leu	Gly	Phe	Glu	Thr	Leu	Leu	Ile	Asn	Thr	Leu	Leu	Ile	Ala	Asp
	195					200					205				
Ile	Lys	Thr	Met	Asp	Phe	Lys	Lys	Ile	Gln	Ala	Pro	Lys	Asn	Pro	Glu
	210					215					220				
Cys	Arg	Val	Cys	Gly	Thr	His	Lys	Ile	Thr	His	Leu	Gln	Asp	Tyr	Glu
225					230					235					240
Ile															

<210> 133  
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 <213> *Helicobacter pylori*

<220>  
 <221> CDS  
 <222> (51)...(494)

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cgc atg aat aaa aat tat ctt tta atc ttt ttg ttg tta gcg agt ctt															104		
Arg Met Asn Lys Asn Tyr Leu Leu Ile Phe Leu Leu Leu Ala Ser Leu																	
														5	10	15	
ggt gct aga gag aag gac gct tct tca aac ctt ttt gat ttg att gat															152		
Val Ala Arg Glu Lys Asp Ala Ser Ser Asn Leu Phe Asp Leu Ile Asp																	
														20	25	30	
aag ggg atc aac aga gaa caa gaa tta aaa gag cag gag caa aaa acg															200		
Lys Gly Ile Asn Arg Glu Gln Glu Leu Lys Glu Gln Glu Gln Lys Thr																	
														35	40	45	50
cgc tta aaa ctg gct caa agc cct tta gta gcg tta gag att gtc ccc															248		
Arg Leu Lys Leu Ala Gln Ser Pro Leu Val Ala Leu Glu Ile Val Pro																	
														55	60	65	
caa gaa acg ccc tat tta gaa tgg caa ggg gct agg gag tcg tat tat															296		
Gln Glu Thr Pro Tyr Leu Glu Trp Gln Gly Ala Arg Glu Ser Tyr Tyr																	
														70	75	80	

tta aag gtg agc gct gta gtg gag agc gtg gtt atc tta aaa att gac	344
Leu Lys Val Ser Ala Val Val Glu Ser Val Val Ile Leu Lys Ile Asp	
85 90 95	

atc aat caa ggg cgt tct tgc tgc ctc tac ccc acg cct aaa agc gtt	392
Ile Asn Gln Gly Arg Ser Cys Ser Leu Tyr Pro Thr Pro Lys Ser Val	
100 105 110	

tct tta gtg agg aat caa agc gta gcc tat gaa att tta tgc gaa aac	440
Ser Leu Val Arg Asn Gln Ser Val Ala Tyr Glu Ile Leu Cys Glu Asn	
115 120 125 130	

caa ccc cta tgg ata gaa gta agc acc aat tta ggc aaa cgc acc ttt	488
Gln Pro Leu Trp Ile Glu Val Ser Thr Asn Leu Gly Lys Arg Thr Phe	
135 140 145	

cag ttt taacctgcaa ccaacattaa agaatgcctt tagcatttta aaaccccttt	544
Gln Phe	

atc	547
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<210> 134  
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 <212> PRT  
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Met Asn Arg Met Asn Lys Asn Tyr Leu Leu Ile Phe Leu Leu Leu Ala	
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20 25 30	
Ile Asp Lys Gly Ile Asn Arg Glu Gln Glu Leu Lys Glu Gln Glu Gln	
35 40 45	
Lys Thr Arg Leu Lys Leu Ala Gln Ser Pro Leu Val Ala Leu Glu Ile	
50 55 60	
Val Pro Gln Glu Thr Pro Tyr Leu Glu Trp Gln Gly Ala Arg Glu Ser	
65 70 75 80	
Tyr Tyr Leu Lys Val Ser Ala Val Val Glu Ser Val Val Ile Leu Lys	
85 90 95	
Ile Asp Ile Asn Gln Gly Arg Ser Cys Ser Leu Tyr Pro Thr Pro Lys	
100 105 110	
Ser Val Ser Leu Val Arg Asn Gln Ser Val Ala Tyr Glu Ile Leu Cys	
115 120 125	
Glu Asn Gln Pro Leu Trp Ile Glu Val Ser Thr Asn Leu Gly Lys Arg	
130 135 140	
Thr Phe Gln Phe	
145	

<210> 135  
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<220>

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<222> (51)...(1631)

<400> 135

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                                     Met Leu
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gct tcc atc atc tca att tta agg gtt ttt gtt ttg tta ttc aac acg      104
Ala Ser Ile Ile Ser Ile Leu Arg Val Phe Val Leu Leu Phe Asn Thr
      5                      10                      15

ccg tta ttc atc ttt gct ttt ttg cct gtt ggt ttt tta ggg tat ttt      152
Pro Leu Phe Ile Phe Ala Phe Leu Pro Val Gly Phe Leu Gly Tyr Phe
      20                      25                      30

atc ttg caa gct tat gct aaa aat ccc ctg ttc cct aaa cta tgg cta      200
Ile Leu Gln Ala Tyr Ala Lys Asn Pro Leu Phe Pro Lys Leu Trp Leu
      35                      40                      45                      50

gta ttg gct agt ttg ttt ttt tat gct ttt tgg aat gtg aag tat ttg      248
Val Leu Ala Ser Leu Phe Phe Tyr Ala Phe Trp Asn Val Lys Tyr Leu
      55                      60                      65

ccc tta ttg gtt ggc tct att gtt ttt aat tat ttt gtg gct ttg aaa      296
Pro Leu Leu Val Gly Ser Ile Val Phe Asn Tyr Phe Val Ala Leu Lys
      70                      75                      80

atc cat caa acc cag cca aat gca tat aaa aga tta tgg ctt att ttg      344
Ile His Gln Thr Gln Pro Asn Ala Tyr Lys Arg Leu Trp Leu Ile Leu
      85                      90                      95

ggc ttg atc gct aat gtt tca ctt tta gga ttt ttc aaa tac act gat      392
Gly Leu Ile Ala Asn Val Ser Leu Leu Gly Phe Phe Lys Tyr Thr Asp
      100                      105                      110

ttt ttc tta acc aat ttc aat cta ata tgg aag agc cat ttt gaa acc      440
Phe Phe Leu Thr Asn Phe Asn Leu Ile Trp Lys Ser His Phe Glu Thr
      115                      120                      125                      130

ttg cat tta atc ttg cct tta gcg atc agc ttt ttc act ttg caa caa      488
Leu His Leu Ile Leu Pro Leu Ala Ile Ser Phe Phe Thr Leu Gln Gln
      135                      140                      145

atc gct tac ttg atg gac act tat aag caa aat caa atc atg cag ccc      536
Ile Ala Tyr Leu Met Asp Thr Tyr Lys Gln Asn Gln Ile Met Gln Pro
      150                      155                      160

aaa atg aga gag aga gtg agt gaa aac gct cct att tta tta aat cct      584
Lys Met Arg Glu Arg Val Ser Glu Asn Ala Pro Ile Leu Leu Asn Pro
      165                      170                      175

ccc act tca ttt ttt tca ctt tcg cat ttt tta gat tac gct tta ttt      632
Pro Thr Ser Phe Phe Ser Leu Ser His Phe Leu Asp Tyr Ala Leu Phe
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180	185	190	
gtg agt ttc ttc cct caa ctc att gca ggg cct att gtg cat cat agc			680
Val Ser Phe Phe Pro Gln Leu Ile Ala Gly Pro Ile Val His His Ser			
195	200	205	210
gag atg atg cct caa ttt aaa gat aaa aac aat caa tat ttg aat tac			728
Glu Met Met Pro Gln Phe Lys Asp Lys Asn Asn Gln Tyr Leu Asn Tyr			
	215	220	225
aga aat atc gct tta ggc ttg ttt atc ttt tct atc ggt ttg ttt aaa			776
Arg Asn Ile Ala Leu Gly Leu Phe Ile Phe Ser Ile Gly Leu Phe Lys			
	230	235	240
aag gtc gtg att gca gat aat acc gct cat ttt gct gat ttt gga ttt			824
Lys Val Val Ile Ala Asp Asn Thr Ala His Phe Ala Asp Phe Gly Phe			
	245	250	255
gat aag gcg act agc tta agt ttt att caa gca tgg atg act tct tta			872
Asp Lys Ala Thr Ser Leu Ser Phe Ile Gln Ala Trp Met Thr Ser Leu			
	260	265	270
tct tat tcg ttc cag ctg tat ttt gat ttt agc ggt tat tgc gat atg			920
Ser Tyr Ser Phe Gln Leu Tyr Phe Asp Phe Ser Gly Tyr Cys Asp Met			
275	280	285	290
gct ata ggc att ggc ctc ttt ttt aac atc aaa ctc cct atc aat ttt			968
Ala Ile Gly Ile Gly Leu Phe Phe Asn Ile Lys Leu Pro Ile Asn Phe			
	295	300	305
aat agc ccc tat aag gct ttg aat atc caa gat ttt tgg agg agg tgg			1016
Asn Ser Pro Tyr Lys Ala Leu Asn Ile Gln Asp Phe Trp Arg Arg Trp			
	310	315	320
cat atc act ttg agc cgc ttc tta aaa gag tat ttg tat atc cct tta			1064
His Ile Thr Leu Ser Arg Phe Leu Lys Glu Tyr Leu Tyr Ile Pro Leu			
	325	330	335
ggg ggt aat agg gtg aaa gaa tta atc gtg tat agg aat tta att tta			1112
Gly Gly Asn Arg Val Lys Glu Leu Ile Val Tyr Arg Asn Leu Ile Leu			
	340	345	350
gtg ttt ttg att ggg ggg ttt tgg cat ggg gct ggt tgg act ttt atc			1160
Val Phe Leu Ile Gly Gly Phe Trp His Gly Ala Gly Trp Thr Phe Ile			
355	360	365	370
att tgg ggg cta ttg cat ggg att gct ttg agc gtt cat aga gcg tat			1208
Ile Trp Gly Leu Leu His Gly Ile Ala Leu Ser Val His Arg Ala Tyr			
	375	380	385
tct cat gcc act aga aaa ttc cat ttc act atg cca aag att tta gca			1256
Ser His Ala Thr Arg Lys Phe His Phe Thr Met Pro Lys Ile Leu Ala			
	390	395	400
tgg ctc atc act ttt aat ttt atc aat ctc gca tgg gtg ttt ttt aga			1304

Trp	Leu	Ile	Thr	Phe	Asn	Phe	Ile	Asn	Leu	Ala	Trp	Val	Phe	Phe	Arg	
	405						410					415				
gcc	aaa	aat	tta	gaa	agc	gct	ttg	aag	gtt	tta	aag	ggg	atg	gtt	ggg	1352
Ala	Lys	Asn	Leu	Glu	Ser	Ala	Leu	Lys	Val	Leu	Lys	Gly	Met	Val	Gly	
	420					425					430					
ttg	aat	ggg	gtt	tcg	ctt	tgt	cat	ctt	tca	aaa	gag	gca	tca	gag	ttt	1400
Leu	Asn	Gly	Val	Ser	Leu	Cys	His	Leu	Ser	Lys	Glu	Ala	Ser	Glu	Phe	
	435				440					445					450	
tta	aat	cgt	gtc	aat	gat	aac	atg	atc	atg	cac	acc	ata	atg	tat	gca	1448
Leu	Asn	Arg	Val	Asn	Asp	Asn	Met	Ile	Met	His	Thr	Ile	Met	Tyr	Ala	
			455					460						465		
tcc	ccc	aca	ttt	aaa	atg	tgt	gtt	ttg	atg	ata	atc	atc	tct	ttt	tgt	1496
Ser	Pro	Thr	Phe	Lys	Met	Cys	Val	Leu	Met	Ile	Ile	Ile	Ser	Phe	Cys	
			470					475					480			
tta	aaa	aat	agt	tcc	cat	tta	tac	caa	tcc	aat	caa	atg	gat	tgg	att	1544
Leu	Lys	Asn	Ser	Ser	His	Leu	Tyr	Gln	Ser	Asn	Gln	Met	Asp	Trp	Ile	
	485						490				495					
aaa	aca	aca	agc	gct	tgt	ttg	ttg	ctc	tct	ata	ggg	ttt	tta	ttt	att	1592
Lys	Thr	Thr	Ser	Ala	Cys	Leu	Leu	Leu	Ser	Ile	Gly	Phe	Leu	Phe	Ile	
	500					505					510					
ttt	gcc	agt	tct	caa	tcg	gta	ttt	ttg	tat	ttt	aat	ttt	taggacactg			1641
Phe	Ala	Ser	Ser	Gln	Ser	Val	Phe	Leu	Tyr	Phe	Asn	Phe				
	515				520					525						
ctatggaatt ttataaaaaa caaacttttaa tcattgtttc ttt																1684
<210> 136																
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<212> PRT																
<213> Helicobacter pylori																
<400> 136																
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Asn	Thr	Pro	Leu	Phe	Ile	Phe	Ala	Phe	Leu	Pro	Val	Gly	Phe	Leu	Gly	
			20					25					30			
Tyr	Phe	Ile	Leu	Gln	Ala	Tyr	Ala	Lys	Asn	Pro	Leu	Phe	Pro	Lys	Leu	
	35						40					45				
Trp	Leu	Val	Leu	Ala	Ser	Leu	Phe	Phe	Tyr	Ala	Phe	Trp	Asn	Val	Lys	
	50					55					60					
Tyr	Leu	Pro	Leu	Leu	Val	Gly	Ser	Ile	Val	Phe	Asn	Tyr	Phe	Val	Ala	
	65				70					75					80	
Leu	Lys	Ile	His	Gln	Thr	Gln	Pro	Asn	Ala	Tyr	Lys	Arg	Leu	Trp	Leu	
			85					90						95		
Ile	Leu	Gly	Leu	Ile	Ala	Asn	Val	Ser	Leu	Leu	Gly	Phe	Phe	Lys	Tyr	
			100				105					110				
Thr	Asp	Phe	Phe	Leu	Thr	Asn	Phe	Asn	Leu	Ile	Trp	Lys	Ser	His	Phe	
		115					120					125				

Glu	Thr	Leu	His	Leu	Ile	Leu	Pro	Leu	Ala	Ile	Ser	Phe	Phe	Thr	Leu
130						135					140				
Gln	Gln	Ile	Ala	Tyr	Leu	Met	Asp	Thr	Tyr	Lys	Gln	Asn	Gln	Ile	Met
145					150					155					160
Gln	Pro	Lys	Met	Arg	Glu	Arg	Val	Ser	Glu	Asn	Ala	Pro	Ile	Leu	Leu
			165						170					175	
Asn	Pro	Pro	Thr	Ser	Phe	Phe	Ser	Leu	Ser	His	Phe	Leu	Asp	Tyr	Ala
			180					185					190		
Leu	Phe	Val	Ser	Phe	Phe	Pro	Gln	Leu	Ile	Ala	Gly	Pro	Ile	Val	His
	195						200					205			
His	Ser	Glu	Met	Met	Pro	Gln	Phe	Lys	Asp	Lys	Asn	Asn	Gln	Tyr	Leu
210						215					220				
Asn	Tyr	Arg	Asn	Ile	Ala	Leu	Gly	Leu	Phe	Ile	Phe	Ser	Ile	Gly	Leu
225				230					235						240
Phe	Lys	Lys	Val	Val	Ile	Ala	Asp	Asn	Thr	Ala	His	Phe	Ala	Asp	Phe
			245						250					255	
Gly	Phe	Asp	Lys	Ala	Thr	Ser	Leu	Ser	Phe	Ile	Gln	Ala	Trp	Met	Thr
		260					265						270		
Ser	Leu	Ser	Tyr	Ser	Phe	Gln	Leu	Tyr	Phe	Asp	Phe	Ser	Gly	Tyr	Cys
	275						280					285			
Asp	Met	Ala	Ile	Gly	Ile	Gly	Leu	Phe	Phe	Asn	Ile	Lys	Leu	Pro	Ile
290						295					300				
Asn	Phe	Asn	Ser	Pro	Tyr	Lys	Ala	Leu	Asn	Ile	Gln	Asp	Phe	Trp	Arg
305				310						315					320
Arg	Trp	His	Ile	Thr	Leu	Ser	Arg	Phe	Leu	Lys	Glu	Tyr	Leu	Tyr	Ile
			325						330					335	
Pro	Leu	Gly	Gly	Asn	Arg	Val	Lys	Glu	Leu	Ile	Val	Tyr	Arg	Asn	Leu
		340						345					350		
Ile	Leu	Val	Phe	Leu	Ile	Gly	Gly	Phe	Trp	His	Gly	Ala	Gly	Trp	Thr
	355					360						365			
Phe	Ile	Ile	Trp	Gly	Leu	Leu	His	Gly	Ile	Ala	Leu	Ser	Val	His	Arg
370					375						380				
Ala	Tyr	Ser	His	Ala	Thr	Arg	Lys	Phe	His	Phe	Thr	Met	Pro	Lys	Ile
385				390						395					400
Leu	Ala	Trp	Leu	Ile	Thr	Phe	Asn	Phe	Ile	Asn	Leu	Ala	Trp	Val	Phe
			405						410					415	
Phe	Arg	Ala	Lys	Asn	Leu	Glu	Ser	Ala	Leu	Lys	Val	Leu	Lys	Gly	Met
		420						425					430		
Val	Gly	Leu	Asn	Gly	Val	Ser	Leu	Cys	His	Leu	Ser	Lys	Glu	Ala	Ser
	435						440					445			
Glu	Phe	Leu	Asn	Arg	Val	Asn	Asp	Asn	Met	Ile	Met	His	Thr	Ile	Met
450					455						460				
Tyr	Ala	Ser	Pro	Thr	Phe	Lys	Met	Cys	Val	Leu	Met	Ile	Ile	Ile	Ser
465				470						475					480
Phe	Cys	Leu	Lys	Asn	Ser	Ser	His	Leu	Tyr	Gln	Ser	Asn	Gln	Met	Asp
			485						490					495	
Trp	Ile	Lys	Thr	Ser	Ala	Cys	Leu	Leu	Leu	Ser	Ile	Gly	Phe	Leu	
		500					505					510			
Phe	Ile	Phe	Ala	Ser	Ser	Gln	Ser	Val	Phe	Leu	Tyr	Phe	Asn	Phe	
	515						520					525			

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 <211> 3973  
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<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(3920)

<400> 137

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Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser Leu Ala
      5                      10                      15

tta gta gga gcg tta gtc agc atc aca ccg caa caa agt cat gcc gcc      152
Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His Ala Ala
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ttt ttc aca acc gtg atc att cca gcc att gtt ggg ggg att gct aca      200
Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile Ala Thr
      35                      40                      45                      50

ggc gct gct gta gga acg gtc tca ggg ctt ctt ggc tgg ggg cta aaa      248
Gly Ala Ala Val Gly Thr Val Ser Gly Leu Leu Gly Trp Gly Leu Lys
                        55                      60                      65

caa gcc gaa gaa gcc aat aaa acc cca gat aaa ccc gat aaa gtt tgg      296
Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys Val Trp
                        70                      75                      80

cgc att caa gca gga aaa ggc ttt aat gaa ttc cct aac aag gaa tac      344
Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys Glu Tyr
      85                      90                      95

gac tta tac aga tcc cta cta tct agt aag att gat gga ggc tgg gat      392
Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly Trp Asp
      100                      105                      110

tgg ggg aat gcc gct acg cat tat tgg gtc aaa ggc ggg caa tgg aac      440
Trp Gly Asn Ala Ala Thr His Tyr Trp Val Lys Gly Gly Gln Trp Asn
      115                      120                      125                      130

aag ctt gaa gtg gat atg aaa gac gct gta ggg act tat aat ctc tca      488
Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Asn Leu Ser
                        135                      140                      145

ggg cta aga aac ttt act ggt ggg gat tta gat gtc aat atg caa aaa      536
Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met Gln Lys
                        150                      155                      160

gcc act ttg cgc ttg ggc caa ttc aat ggc aat tct ttc aca agc tat      584
Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr Ser Tyr
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Ile	Leu	Ser	Ala	Lys	Glu	Thr	Lys	Glu	Tyr	Met	Pro	Val	Val	Asn	Asp		
			165					170					175				
aat	atc	tgc	ggg	agc	gtg	ctt	tta	acc	gaa	aac	gcg	cat	gtg	gat	ccg	633	
Asn	Ile	Cys	Gly	Ser	Val	Leu	Leu	Thr	Glu	Asn	Ala	His	Val	Asp	Pro		
		180					185					190					
ggc	gaa	gtg	atg	cac	tct	ttg	caa	gaa	tat	tta	caa	aat	gtt	ggc	gtg	681	
Gly	Glu	Val	Met	His	Ser	Leu	Gln	Glu	Tyr	Leu	Gln	Asn	Val	Gly	Val		
	195					200					205						
gag	ttc	ctt	tat	aat	gaa	gaa	gtg	atc	gat	ttt	gag	ttt	aaa	aat	aac	729	
Glu	Phe	Leu	Tyr	Asn	Glu	Glu	Val	Ile	Asp	Phe	Glu	Phe	Lys	Asn	Asn		
210					215					220					225		
ctc	att	gag	ggc	gtt	atc	acg	cac	aag	gaa	aaa	atc	caa	gca	gaa	aca	777	
Leu	Ile	Glu	Gly	Val	Ile	Thr	His	Lys	Glu	Lys	Ile	Gln	Ala	Glu	Thr		
				230					235					240			
atc	att	cta	gcc	act	ggg	gct	aac	ccc	act	ctc	att	aaa	aaa	acc	aag	825	
Ile	Ile	Leu	Ala	Thr	Gly	Ala	Asn	Pro	Thr	Leu	Ile	Lys	Lys	Thr	Lys		
			245					250					255				
aac	gat	ttt	tta	atg	atg	ggg	gct	aaa	gga	tat	agc	atc	acc	ttt	aaa	873	
Asn	Asp	Phe	Leu	Met	Met	Gly	Ala	Lys	Gly	Tyr	Ser	Ile	Thr	Phe	Lys		
		260					265					270					
atg	cct	gaa	gaa	tta	aaa	ccc	aaa	acc	tct	tct	tta	ttt	gcg	gat	att	921	
Met	Pro	Glu	Glu	Leu	Lys	Pro	Lys	Thr	Ser	Ser	Leu	Phe	Ala	Asp	Ile		
	275					280					285						
ttc	atg	gcg	atg	acc	cca	cga	aga	gac	act	gta	agg	atc	act	tct	aaa	969	
Phe	Met	Ala	Met	Thr	Pro	Arg	Arg	Asp	Thr	Val	Arg	Ile	Thr	Ser	Lys		
290					295					300					305		
tta	gaa	tta	aac	acc	aac	aac	gct	ctc	att	gat	aaa	gag	caa	atc	gct	1017	
Leu	Glu	Leu	Asn	Thr	Asn	Asn	Ala	Leu	Ile	Asp	Lys	Glu	Gln	Ile	Ala		
			310					315						320			
aac	atg	aaa	aag	aat	tta	gcc	gct	ttc	acg	cag	cct	ttt	gaa	atg	aaa	1065	
Asn	Met	Lys	Lys	Asn	Leu	Ala	Ala	Phe	Thr	Gln	Pro	Phe	Glu	Met	Lys		
			325					330					335				

gac gcc ata gag tgg tgc ggt ttc aga ccc tta acc cct aat gat att 1113  
Asp Ala Ile Glu Trp Cys Gly Phe Arg Pro Leu Thr Pro Asn Asp Ile  
340 345 350

cct tat ttg ggc tat gac aaa cgc tat aaa aac tta atc cat gcg aca 1161  
Pro Tyr Leu Gly Tyr Asp Lys Arg Tyr Lys Asn Leu Ile His Ala Thr  
355 360 365

ggg cta ggg tgg ctt ggc atc act ttt ggc cca gcc att ggt aaa atc 1209  
Gly Leu Gly Trp Leu Gly Ile Thr Phe Gly Pro Ala Ile Gly Lys Ile  
370 375 380 385

atc gcc aat ttg agc caa gac gga gcg aat gaa aaa aat gcc gat att 1257  
Ile Ala Asn Leu Ser Gln Asp Gly Ala Asn Glu Lys Asn Ala Asp Ile  
390 395 400

atg ctt ttt tct gca ttt ttt agg gat taaggaattt cttttttaaa 1304  
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405 410

ccctagttta ttaaggagtt tttatggaaa c 1335

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<211> 410  
<212> PRT  
<213> Helicobacter pylori

<400> 140  
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Cys Ala Tyr Ser Met His Lys Leu Gly His Lys Val Cys Val Ile Glu  
20 25 30  
Lys Asn Asp Gly Ala Asn Gly Thr Ser Phe Gly Asn Ala Gly Leu Ile  
35 40 45  
Ser Ala Phe Lys Lys Ala Pro Leu Ser Cys Pro Gly Val Val Leu Asp  
50 55 60  
Thr Leu Lys Leu Met Leu Lys Asn Gln Ala Pro Leu Lys Phe His Phe  
65 70 75 80  
Gly Leu Asn Leu Lys Leu Tyr Gln Trp Ile Leu Lys Phe Val Lys Ser  
85 90 95  
Ala Asn Ala Lys Ser Thr His Arg Thr Met Ala Leu Phe Glu Arg Tyr  
100 105 110  
Gly Trp Leu Ser Ile Asp Met Tyr His Gln Met Leu Lys Asp Gly Met  
115 120 125  
Asp Phe Trp Tyr Lys Glu Asp Gly Leu Leu Met Ile Tyr Thr Leu Glu  
130 135 140  
Glu Ser Phe Glu Lys Lys Leu Lys Thr Cys Asp Asn Ser Gly Ala Tyr  
145 150 155 160  
Lys Ile Leu Ser Ala Lys Glu Thr Lys Glu Tyr Met Pro Val Val Asn  
165 170 175  
Asp Asn Ile Cys Gly Ser Val Leu Leu Thr Glu Asn Ala His Val Asp  
180 185 190  
Pro Gly Glu Val Met His Ser Leu Gln Glu Tyr Leu Gln Asn Val Gly  
195 200 205  
Val Glu Phe Leu Tyr Asn Glu Glu Val Ile Asp Phe Glu Phe Lys Asn



210	215	220
Asn Leu Ile Glu Gly Val	Ile Thr His Lys Glu	Lys Ile Gln Ala Glu
225	230	235
Thr Ile Ile Leu Ala Thr	Gly Ala Asn Pro Thr	Leu Ile Lys Lys Thr
	245	250
Lys Asn Asp Phe Leu Met	Met Gly Ala Lys Gly	Tyr Ser Ile Thr Phe
	260	265
Lys Met Pro Glu Glu Leu	Lys Pro Lys Thr Ser	Ser Leu Phe Ala Asp
	275	280
Ile Phe Met Ala Met Thr	Pro Arg Arg Asp Thr	Val Arg Ile Thr Ser
	290	295
Lys Leu Glu Leu Asn Thr	Asn Asn Ala Leu Ile	Asp Lys Glu Gln Ile
305	310	315
Ala Asn Met Lys Lys Asn	Leu Ala Ala Phe Thr	Gln Pro Phe Glu Met
	325	330
Lys Asp Ala Ile Glu Trp	Cys Gly Phe Arg Pro	Leu Thr Pro Asn Asp
	340	345
Ile Pro Tyr Leu Gly Tyr	Asp Lys Arg Tyr Lys	Asn Leu Ile His Ala
	355	360
Thr Gly Leu Gly Trp Leu	Gly Ile Thr Phe Gly	Pro Ala Ile Gly Lys
	370	375
Ile Ile Ala Asn Leu Ser	Gln Asp Gly Ala Asn	Glu Lys Asn Ala Asp
385	390	395
Ile Met Leu Phe Ser Ala	Phe Phe Arg Asp	
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 <211> 1579  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (51)...(1526)

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	Met Glu
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cat aaa gaa atc gtt ata ggg gtt gat cta ggc tct aga aag att tgc	104
His Lys Glu Ile Val Ile Gly Val Asp Leu Gly Ser Arg Lys Ile Cys	
	5 10 15
gcg ata gtg gct gaa ttt aaa gaa ggg att ttg cgc atc att ggc acg	152
Ala Ile Val Ala Glu Phe Lys Glu Gly Ile Leu Arg Ile Ile Gly Thr	
	20 25 30
gcc cat caa gac tcc aaa gaa atc aat tca aaa gcc att aaa aga ggg	200
Ala His Gln Asp Ser Lys Glu Ile Asn Ser Lys Ala Ile Lys Arg Gly	
	35 40 45 50
cgt atc aat agc ctt gct cac gct tcc aac gcc att aaa gaa gtg att	248
Arg Ile Asn Ser Leu Ala His Ala Ser Asn Ala Ile Lys Glu Val Ile	

55										60										65										
aat	agc	gct	aaa	aaa	atg	gca	ggg	ttg	aac	gct	gat	gaa	gac	aga	aat	296														
Asn	Ser	Ala	Lys	Lys	Met	Ala	Gly	Leu	Asn	Ala	Asp	Glu	Asp	Arg	Asn															
			70					75						80																
aac	ccc	atg	ccc	cat	ttt	ggg	gaa	tac	cac	cct	aaa	act	aag	gcg	att	344														
Asn	Pro	Met	Pro	His	Phe	Gly	Glu	Tyr	His	Pro	Lys	Thr	Lys	Ala	Ile															
		85					90					95																		
gtt	tct	ttt	tct	ggg	gct	tat	act	gaa	agc	att	aga	gat	gtt	acc	ggg	392														
Val	Ser	Phe	Ser	Gly	Ala	Tyr	Thr	Glu	Ser	Ile	Arg	Asp	Val	Thr	Gly															
	100					105					110																			
gta	gcg	agc	acc	aaa	gat	aat	gtg	gta	acc	att	gat	gaa	atc	aat	cg	440														
Val	Ala	Ser	Thr	Lys	Asp	Asn	Val	Val	Thr	Ile	Asp	Glu	Ile	Asn	Arg															
115					120					125					130															
gct	atc	aat	agt	gca	tgc	gct	aaa	gca	ggc	tta	gat	aac	gac	aaa	cat	488														
Ala	Ile	Asn	Ser	Ala	Cys	Ala	Lys	Ala	Gly	Leu	Asp	Asn	Asp	Lys	His															
				135					140					145																
att	ttg	cat	gct	ctc	ccc	tat	cgc	ttc	act	tta	gac	aaa	caa	gaa	gtg	536														
Ile	Leu	His	Ala	Leu	Pro	Tyr	Arg	Phe	Thr	Leu	Asp	Lys	Gln	Glu	Val															
			150					155					160																	
aat	gac	cct	tta	ggg	atg	agc	ggg	act	cgc	ttg	gaa	gtc	ttt	atc	cac	584														
Asn	Asp	Pro	Leu	Gly	Met	Ser	Gly	Thr	Arg	Leu	Glu	Val	Phe	Ile	His															
		165					170					175																		
att	gtc	tat	aca	gaa	aaa	aac	aac	att	gaa	aat	tta	gaa	aaa	atc	atg	632														
Ile	Val	Tyr	Thr	Glu	Lys	Asn	Asn	Ile	Glu	Asn	Leu	Glu	Lys	Ile	Met															
	180					185					190																			
atc	caa	tct	ggg	gta	gag	att	gaa	aac	atc	gtg	atc	aat	tct	tat	gca	680														
Ile	Gln	Ser	Gly	Val	Glu	Ile	Glu	Asn	Ile	Val	Ile	Asn	Ser	Tyr	Ala															
195					200					205					210															
gcc	tcg	att	gcc	acc	tta	tct	aat	gat	gaa	agg	gaa	ttg	ggc	gtg	gct	728														
Ala	Ser	Ile	Ala	Thr	Leu	Ser	Asn	Asp	Glu	Arg	Glu	Leu	Gly	Val	Ala															
				215					220					225																
tgc	gtg	gat	atg	ggc	gga	gag	aca	tgc	aac	ctt	acg	att	tat	agc	ggc	776														
Cys	Val	Asp	Met	Gly	Gly	Glu	Thr	Cys	Asn	Leu	Thr	Ile	Tyr	Ser	Gly															
			230					235					240																	
aat	tcc	ata	cgc	tat	aac	aaa	tat	ttg	ccc	gta	ggc	tct	cac	cat	tta	824														
Asn	Ser	Ile	Arg	Tyr	Asn	Lys	Tyr	Leu	Pro	Val	Gly	Ser	His	His	Leu															
		245					250					255																		
acc	acg	gat	tta	tcg	cac	atg	ctc	aac	acc	cca	ttc	cct	tac	gct	gaa	872														
Thr	Thr	Asp	Leu	Ser	His	Met	Leu	Asn	Thr	Pro	Phe	Pro	Tyr	Ala	Glu															
	260					265					270																			
gaa	gtt	aag	atc	aaa	tac	ggg	gat	ctt	tct	ttt	gaa	ggc	ggc	gaa	gaa	920														

Glu Val Lys Ile Lys Tyr Gly Asp Leu Ser Phe Glu Gly Gly Glu Glu	
275 280 285 290	
acg ccc tct caa aat gtc caa atc cct acc acc ggc tcg gat ggc cat	968
Thr Pro Ser Gln Asn Val Gln Ile Pro Thr Thr Gly Ser Asp Gly His	
295 300 305	
gaa agc cat att gtg ccg ctt agt gaa atc caa act atc atg aga gaa	1016
Glu Ser His Ile Val Pro Leu Ser Glu Ile Gln Thr Ile Met Arg Glu	
310 315 320	
agg gct tta gaa act ttt aaa atc atc cac agg agc att caa gat agc	1064
Arg Ala Leu Glu Thr Phe Lys Ile Ile His Arg Ser Ile Gln Asp Ser	
325 330 335	
ggc tta gaa gag cat ttg ggc gga ggc gtt gtg tta acc ggt ggg atg	1112
Gly Leu Glu Glu His Leu Gly Gly Gly Val Val Leu Thr Gly Gly Met	
340 345 350	
gct tta atg aaa ggg atc aaa gaa tta gcc aga acc cat ttc act aat	1160
Ala Leu Met Lys Gly Ile Lys Glu Leu Ala Arg Thr His Phe Thr Asn	
355 360 365 370	
tac ccg gtg cgt ttg gca gcc cct gtg gaa aaa tac aat atc atg ggc	1208
Tyr Pro Val Arg Leu Ala Ala Pro Val Glu Lys Tyr Asn Ile Met Gly	
375 380 385	
atg ttt gaa gat ttg aaa gac cct cgc ttt tca gtc gta gtt ggc ttg	1256
Met Phe Glu Asp Leu Lys Asp Pro Arg Phe Ser Val Val Val Gly Leu	
390 395 400	
att tta tac aaa gca ggg ggg cat acc aat tat gaa aga gac tct aaa	1304
Ile Leu Tyr Lys Ala Gly Gly His Thr Asn Tyr Glu Arg Asp Ser Lys	
405 410 415	
ggg gtt atc cgc tac cat gaa agc gat gat tac aca aga aca gcc cat	1352
Gly Val Ile Arg Tyr His Glu Ser Asp Asp Tyr Thr Arg Thr Ala His	
420 425 430	
caa tca agc cct acc ccc cat atc cat tca tcg ccc aca gaa agg aat	1400
Gln Ser Ser Pro Thr Pro His Ile His Ser Ser Pro Thr Glu Arg Asn	
435 440 445 450	
ttg agc gat tta aaa gcc cct agt gct cct tta aac acc gct aaa aac	1448
Leu Ser Asp Leu Lys Ala Pro Ser Ala Pro Leu Asn Thr Ala Lys Asn	
455 460 465	
gat gac ttt tta cct ata aaa ccc acc gaa caa aaa ggt ttt ttt aaa	1496
Asp Asp Phe Leu Pro Ile Lys Pro Thr Glu Gln Lys Gly Phe Phe Lys	
470 475 480	
agt ttc ctt gat aag att tct aaa ttc ttt taagatacag ccatttcttt	1546
Ser Phe Leu Asp Lys Ile Ser Lys Phe Phe	
485 490	

atgcgataaa aacgccttga tggttatcaa aag

1579

<210> 142

<211> 492

<212> PRT

<213> Helicobacter pylori

<400> 142

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Ile	Cys	Ala	Ile	Val	Ala	Glu	Phe	Lys	Glu	Gly	Ile	Leu	Arg	Ile	Ile
		20					25					30			
Gly	Thr	Ala	His	Gln	Asp	Ser	Lys	Glu	Ile	Asn	Ser	Lys	Ala	Ile	Lys
	35					40					45				
Arg	Gly	Arg	Ile	Asn	Ser	Leu	Ala	His	Ala	Ser	Asn	Ala	Ile	Lys	Glu
	50				55					60					
Val	Ile	Asn	Ser	Ala	Lys	Lys	Met	Ala	Gly	Leu	Asn	Ala	Asp	Glu	Asp
65				70					75					80	
Arg	Asn	Asn	Pro	Met	Pro	His	Phe	Gly	Glu	Tyr	His	Pro	Lys	Thr	Lys
		85						90					95		
Ala	Ile	Val	Ser	Phe	Ser	Gly	Ala	Tyr	Thr	Glu	Ser	Ile	Arg	Asp	Val
		100					105						110		
Thr	Gly	Val	Ala	Ser	Thr	Lys	Asp	Asn	Val	Val	Thr	Ile	Asp	Glu	Ile
	115					120						125			
Asn	Arg	Ala	Ile	Asn	Ser	Ala	Cys	Ala	Lys	Ala	Gly	Leu	Asp	Asn	Asp
	130				135						140				
Lys	His	Ile	Leu	His	Ala	Leu	Pro	Tyr	Arg	Phe	Thr	Leu	Asp	Lys	Gln
145				150					155					160	
Glu	Val	Asn	Asp	Pro	Leu	Gly	Met	Ser	Gly	Thr	Arg	Leu	Glu	Val	Phe
		165						170					175		
Ile	His	Ile	Val	Tyr	Thr	Glu	Lys	Asn	Asn	Ile	Glu	Asn	Leu	Glu	Lys
	180						185					190			
Ile	Met	Ile	Gln	Ser	Gly	Val	Glu	Ile	Glu	Asn	Ile	Val	Ile	Asn	Ser
	195					200						205			
Tyr	Ala	Ala	Ser	Ile	Ala	Thr	Leu	Ser	Asn	Asp	Glu	Arg	Glu	Leu	Gly
	210				215						220				
Val	Ala	Cys	Val	Asp	Met	Gly	Gly	Glu	Thr	Cys	Asn	Leu	Thr	Ile	Tyr
225				230					235					240	
Ser	Gly	Asn	Ser	Ile	Arg	Tyr	Asn	Lys	Tyr	Leu	Pro	Val	Gly	Ser	His
		245						250					255		
His	Leu	Thr	Thr	Asp	Leu	Ser	His	Met	Leu	Asn	Thr	Pro	Phe	Pro	Tyr
	260						265					270			
Ala	Glu	Glu	Val	Lys	Ile	Lys	Tyr	Gly	Asp	Leu	Ser	Phe	Glu	Gly	Gly
	275					280						285			
Glu	Glu	Thr	Pro	Ser	Gln	Asn	Val	Gln	Ile	Pro	Thr	Thr	Gly	Ser	Asp
	290				295						300				
Gly	His	Glu	Ser	His	Ile	Val	Pro	Leu	Ser	Glu	Ile	Gln	Thr	Ile	Met
305				310					315					320	
Arg	Glu	Arg	Ala	Leu	Glu	Thr	Phe	Lys	Ile	Ile	His	Arg	Ser	Ile	Gln
		325						330					335		
Asp	Ser	Gly	Leu	Glu	Glu	His	Leu	Gly	Gly	Gly	Val	Val	Leu	Thr	Gly
	340					345						350			
Gly	Met	Ala	Leu	Met	Lys	Gly	Ile	Lys	Glu	Leu	Ala	Arg	Thr	His	Phe
	355					360					365				
Thr	Asn	Tyr	Pro	Val	Arg	Leu	Ala	Ala	Pro	Val	Glu	Lys	Tyr	Asn	Ile

370		375		380
Met Gly Met Phe Glu Asp Leu Lys Asp Pro Arg Phe Ser Val Val Val				
385		390		395
Gly Leu Ile Leu Tyr Lys Ala Gly Gly His Thr Asn Tyr Glu Arg Asp				400
		405		410
Ser Lys Gly Val Ile Arg Tyr His Glu Ser Asp Asp Tyr Thr Arg Thr				415
		420		425
Ala His Gln Ser Ser Pro Thr Pro His Ile His Ser Ser Pro Thr Glu				430
		435		440
Arg Asn Leu Ser Asp Leu Lys Ala Pro Ser Ala Pro Leu Asn Thr Ala				445
		450		455
Lys Asn Asp Asp Phe Leu Pro Ile Lys Pro Thr Glu Gln Lys Gly Phe				460
465		470		475
Phe Lys Ser Phe Leu Asp Lys Ile Ser Lys Phe Phe				480
		485		490

<210> 143  
 <211> 1987  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1934)

<400> 143	
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Arg Val Ala Gly Leu Lys Gln Leu Tyr Glu His Lys Ile Ala Ser Lys	
5 10 15	
ggc att gat ggc gca agc cct gaa gaa caa tta gaa aaa atc aag cat	152
Gly Ile Asp Gly Ala Ser Pro Glu Glu Gln Leu Glu Lys Ile Lys His	
20 25 30	
tat tta gcg cat gaa att gaa gaa agg gag tta gaa ttc caa aaa atc	200
Tyr Leu Ala His Glu Ile Glu Glu Arg Glu Leu Glu Phe Gln Lys Ile	
35 40 45 50	
caa gcc cta ctc ttt aaa aaa ggg ctt tgt atc acc ccc tat aat gaa	248
Gln Ala Leu Leu Phe Lys Lys Gly Leu Cys Ile Thr Pro Tyr Asn Glu	
55 60 65	
ttg aat tta gag caa aaa gcg aag gct aaa acc tat ttt aaa gag cag	296
Leu Asn Leu Glu Gln Lys Ala Lys Ala Lys Thr Tyr Phe Lys Glu Gln	
70 75 80	
ctt tac gcg tta gtt ttg cct ttt aaa ttg gat tct tca cac act ttc	344
Leu Tyr Ala Leu Val Leu Pro Phe Lys Leu Asp Ser Ser His Thr Phe	
85 90 95	

ccg cct tta gcg aat ttg act ttc gcg ctt ttt gcc cgc atc aaa gac	392
Pro Pro Leu Ala Asn Leu Thr Phe Ala Leu Phe Ala Arg Ile Lys Asp	
100 105 110	
aaa gaa acc caa att atc tcc tat gcg ctc atc aaa ctc ccc tct ttt	440
Lys Glu Thr Gln Ile Ile Ser Tyr Ala Leu Ile Lys Leu Pro Ser Phe	
115 120 125 130	
atc ttc cgt ttt gta gag cta gaa aaa ggc ttg ttt gtg tta gct gaa	488
Ile Phe Arg Phe Val Glu Leu Glu Lys Gly Leu Phe Val Leu Ala Glu	
135 140 145	
gaa atc gtg gaa gcg cat tta gaa gaa ttg ttt tta gag cat gag att	536
Glu Ile Val Glu Ala His Leu Glu Glu Leu Phe Leu Glu His Glu Ile	
150 155 160	
tta gat tgc atg gcg ttt agg gta act tgc gat gcg gat att gct atc	584
Leu Asp Cys Met Ala Phe Arg Val Thr Cys Asp Ala Asp Ile Ala Ile	
165 170 175	
act gaa gat gaa gcg cat gat tat gca gat ttg atg agt aag agt ttg	632
Thr Glu Asp Glu Ala His Asp Tyr Ala Asp Leu Met Ser Lys Ser Leu	
180 185 190	
agg aaa cgc aat caa ggc gaa atc gtg cgc ttg caa acc caa aaa ggg	680
Arg Lys Arg Asn Gln Gly Glu Ile Val Arg Leu Gln Thr Gln Lys Gly	
195 200 205 210	
agt caa gag ctt tta aaa acc ctc tta gcg tct tta agg agt ttt caa	728
Ser Gln Glu Leu Leu Lys Thr Leu Leu Ala Ser Leu Arg Ser Phe Gln	
215 220 225	
acc cac tct tac aaa aag cac aaa ctc acc ggc atg cat atc tat aaa	776
Thr His Ser Tyr Lys Lys His Lys Leu Thr Gly Met His Ile Tyr Lys	
230 235 240	
agc gcg atc atg ctc aat tta ggg gat ttg tgg gaa tta gtc aat cat	824
Ser Ala Ile Met Leu Asn Leu Gly Asp Leu Trp Glu Leu Val Asn His	
245 250 255	
agc gat ttt aaa gcg ctc aaa tcg ccc aat ttc aca ccc aaa atc cac	872
Ser Asp Phe Lys Ala Leu Lys Ser Pro Asn Phe Thr Pro Lys Ile His	
260 265 270	
cct cat ttc aat gaa aac gat ctt ttc aaa tct ata gaa aaa cag gat	920
Pro His Phe Asn Glu Asn Asp Leu Phe Lys Ser Ile Glu Lys Gln Asp	
275 280 285 290	
ctg ttg ctg ttt cat cct tat gaa agt ttt gag cct gtg att gat tta	968
Leu Leu Leu Phe His Pro Tyr Glu Ser Phe Glu Pro Val Ile Asp Leu	
295 300 305	
ata gag caa gcc gct agc gat cca gcc acc ctt tct atc aaa atg acg	1016
Ile Glu Gln Ala Ala Ser Asp Pro Ala Thr Leu Ser Ile Lys Met Thr	
310 315 320	

ctt tat cgt gtg ggc aag cat tcc ccc att gtc aaa gct ttg att gaa	1064
Leu Tyr Arg Val Gly Lys His Ser Pro Ile Val Lys Ala Leu Ile Glu	
325 330 335	
gcg gcg agc aag att caa gtg agc gtt tta gtg gaa tta aaa gcg cgc	1112
Ala Ala Ser Lys Ile Gln Val Ser Val Leu Val Glu Leu Lys Ala Arg	
340 345 350	
ttt gat gaa gag agc aat ctg cac tgg gca aaa gct tta gaa agg gcg	1160
Phe Asp Glu Glu Ser Asn Leu His Trp Ala Lys Ala Leu Glu Arg Ala	
355 360 365 370	
ggc gcg tta gtc gtt tat ggc gtt ttc aaa ctc aaa gtg cat gct aaa	1208
Gly Ala Leu Val Val Tyr Gly Val Phe Lys Leu Lys Val His Ala Lys	
375 380 385	
atg cta ttg atc act aaa aaa aca gac aac caa tta cgc cat ttc acc	1256
Met Leu Leu Ile Thr Lys Lys Thr Asp Asn Gln Leu Arg His Phe Thr	
390 395 400	
cat tta agc acg ggc aat tac aac cct ttg agc gct aaa gtc tat acc	1304
His Leu Ser Thr Gly Asn Tyr Asn Pro Leu Ser Ala Lys Val Tyr Thr	
405 410 415	
gat gtg agt ttt ttt agc gct aaa aat gaa atc gct aac gac att atc	1352
Asp Val Ser Phe Phe Ser Ala Lys Asn Glu Ile Ala Asn Asp Ile Ile	
420 425 430	
aag ctt ttc cat tcc ttg ctc act agc agc gcg act aat agc gca tta	1400
Lys Leu Phe His Ser Leu Leu Thr Ser Ser Ala Thr Asn Ser Ala Leu	
435 440 445 450	
gaa acg ctt ttt atg gca ccc aaa caa atc aag cct aaa atc att gaa	1448
Glu Thr Leu Phe Met Ala Pro Lys Gln Ile Lys Pro Lys Ile Ile Glu	
455 460 465	
ctc att caa aat gaa atg aat cac caa caa gaa ggc tat atc att tta	1496
Leu Ile Gln Asn Glu Met Asn His Gln Gln Glu Gly Tyr Ile Ile Leu	
470 475 480	
aaa gcc aac gcc cta gtg gat agc gaa atc att gaa tgg ctc tat caa	1544
Lys Ala Asn Ala Leu Val Asp Ser Glu Ile Ile Glu Trp Leu Tyr Gln	
485 490 495	
gcc tct caa aaa ggg gtt aaa att gat ctc att att aga ggg att tgc	1592
Ala Ser Gln Lys Gly Val Lys Ile Asp Leu Ile Ile Arg Gly Ile Cys	
500 505 510	
tgt tta aag ccc caa gtc aag ggc ttg agc gaa aat atc agg gtg tat	1640
Cys Leu Lys Pro Gln Val Lys Gly Leu Ser Glu Asn Ile Arg Val Tyr	
515 520 525 530	
tct atc gtg ggg aaa tat tta gaa cat gca cgc att tat tat ttt aaa	1688
Ser Ile Val Gly Lys Tyr Leu Glu His Ala Arg Ile Tyr Tyr Phe Lys	

535	540	545	
cat gaa aat att tat ttt tct agc gcg gat tta atg ccc agg aat tta			1736
His Glu Asn Ile Tyr Phe Ser Ser Ala Asp Leu Met Pro Arg Asn Leu			
550	555	560	
gaa agg cgc gtg gaa ttg ctc att cca gcc aca aac cca aag atc gct			1784
Glu Arg Arg Val Glu Leu Leu Ile Pro Ala Thr Asn Pro Lys Ile Ala			
565	570	575	
cat aaa ttg ttg cat att tta gaa atc caa ctc aaa gac acc tta aaa			1832
His Lys Leu Leu His Ile Leu Glu Ile Gln Leu Lys Asp Thr Leu Lys			
580	585	590	
cgc tac gag tta aat tct aaa ggc cgt tac att aaa gtt tca aac cct			1880
Arg Tyr Glu Leu Asn Ser Lys Gly Arg Tyr Ile Lys Val Ser Asn Pro			
595	600	605	610
aac gat cct tta aat tcg cag gat tat ttt gaa aaa caa gcc ctt aaa			1928
Asn Asp Pro Leu Asn Ser Gln Asp Tyr Phe Glu Lys Gln Ala Leu Lys			
615	620	625	
acc ttt taagggttat cgttcaaatc ataaaagata aggatttaaa tgctttattc			1984
Thr Phe			
att			1987
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<213> Helicobacter pylori			
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1 5 10 15			
Ser Lys Gly Ile Asp Gly Ala Ser Pro Glu Glu Gln Leu Glu Lys Ile			
20 25 30			
Lys His Tyr Leu Ala His Glu Ile Glu Glu Arg Glu Leu Glu Phe Gln			
35 40 45			
Lys Ile Gln Ala Leu Leu Phe Lys Lys Gly Leu Cys Ile Thr Pro Tyr			
50 55 60			
Asn Glu Leu Asn Leu Glu Gln Lys Ala Lys Ala Lys Thr Tyr Phe Lys			
65 70 75 80			
Glu Gln Leu Tyr Ala Leu Val Leu Pro Phe Lys Leu Asp Ser Ser His			
85 90 95			
Thr Phe Pro Pro Leu Ala Asn Leu Thr Phe Ala Leu Phe Ala Arg Ile			
100 105 110			
Lys Asp Lys Glu Thr Gln Ile Ile Ser Tyr Ala Leu Ile Lys Leu Pro			
115 120 125			
Ser Phe Ile Phe Arg Phe Val Glu Leu Glu Lys Gly Leu Phe Val Leu			
130 135 140			
Ala Glu Glu Ile Val Glu Ala His Leu Glu Glu Leu Phe Leu Glu His			
145 150 155 160			
Glu Ile Leu Asp Cys Met Ala Phe Arg Val Thr Cys Asp Ala Asp Ile			





Asn Pro Asn Asp Pro Leu Asn Ser Gln Asp Tyr Phe Glu Lys Gln Ala  
610 615 620  
Leu Lys Thr Phe  
625

<210> 145  
<211> 616  
<212> DNA  
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Met Gly  
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ttg aaa aat ctc tca aca ctt ctg gtg ttt tta ttc ttt tgt tta ggg 104  
Leu Lys Asn Leu Ser Thr Leu Leu Val Phe Leu Phe Phe Cys Leu Gly  
5 10 15  
  
tgt gtg agc aat ttt aat gaa gac act tac acg cta gac tta gtt tta 152  
Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu Asp Leu Val Leu  
20 25 30  
  
gaa aaa aag atc caa gcc agc agg aaa ggt gaa atc acc caa gat aat 200  
Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln Asp Asn  
35 40 45 50  
  
gtg cct atc atc acg gct atc gct acg cat tta aac gat gtg gat agc 248  
Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val Asp Ser  
55 60 65  
  
ggc act tac tat gac cat gag tat ttt tta gtg gag att ttc acg caa 296  
Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe Thr Gln  
70 75 80  
  
aat aac gac tgg ata gat gat ggc tat att tct tat gaa ctt ttt ggc 344  
Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr Glu Leu Phe Gly  
85 90 95  
  
aca aaa cct ata ggc tca gag cct tta tgg gtg cga gaa atc aca aaa 392  
Thr Lys Pro Ile Gly Ser Glu Pro Leu Trp Val Arg Glu Ile Thr Lys  
100 105 110  
  
gat gaa ttt gat ggc att tta gaa acc acg aac agg tgg agc aga gct 440  
Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg Trp Ser Arg Ala  
115 120 125 130  
  
ttt ttg ctc gct ttt aac aaa ttg gat tat tta gcg gtt caa gaa gcc 488  
Phe Leu Leu Ala Phe Asn Lys Leu Asp Tyr Leu Ala Val Gln Glu Ala  
135 140 145

aaa cta gag ctt gat gcc tat agt ttg ggc aag att gtt ttt aat ttc 536  
 Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile Val Phe Asn Phe  
                   150                                  155                                  160

gct tat caa gtc ccc cta cct caa ttt taatgcgctt agattacgcc 583  
 Ala Tyr Gln Val Pro Leu Pro Gln Phe  
                   165                                  170

ttattcagtc agcatttagt aaatagcaga gaa 616

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 <211> 171  
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   1                                  5                                  10                                  15  
 Leu Gly Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu Asp Leu  
                                   20                                  25                                  30  
 Val Leu Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln  
                                   35                                  40                                  45  
 Asp Asn Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val  
   50                                  55                                  60  
 Asp Ser Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe  
  65                                  70                                  75                                  80  
 Thr Gln Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr Glu Leu  
                                   85                                  90                                  95  
 Phe Gly Thr Lys Pro Ile Gly Ser Glu Pro Leu Trp Val Arg Glu Ile  
                                  100                                 105                                 110  
 Thr Lys Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg Trp Ser  
                                  115                                 120                                 125  
 Arg Ala Phe Leu Leu Ala Phe Asn Lys Leu Asp Tyr Leu Ala Val Gln  
                                  130                                 135                                 140  
 Glu Ala Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile Val Phe  
  145                                 150                                 155                                 160  
 Asn Phe Ala Tyr Gln Val Pro Leu Pro Gln Phe  
                                  165                                 170

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 cgagttttga gaattttaa tctatcaact ttatttatgg ggctaattggg agcggtaaga 180  
 caaccacttc tagtttttta aaaaatctag ctgaaaatgg gattgaagac aagtttgcta 240

atagtaaaat agcatggtat aacaatgaga gtttaaagat tgaagtttat aacaagcaat 300  
 ttaaagaaga gcaattgaga aactctcaag ttaaaggcat ttttacgctc ggtaaaaaaa 360  
 cgaacgagaa tttagaaaaa attgaaagca agaaagaatc aataaacaaa gagaatgaaa 420  
 agaaaataaa aaatgaagca agcttgcaag ttttaacaca aaaaaaggaa aaggaagaaa 480  
 aggattttgc tgataggtgt tgggaaaaac tttataagaa aaatgaagag gattttaaag 540  
 aaacgctaga aggctttaag cgtaaagaga agtttaaaga aaaaatcctt aaggaatttg 600  
 aaaacgataa atacaatcaa agcgaaatag taggggttaga aaaattaaag gaaaaaattg 660  
 agattgtttt tggtgaaaac caaacagaat tggcactatt ggaatgcaat ttaacagatt 720  
 ttgattttat tgaaaatcat tctatttggg aacaaaaaat tgtagggagt ggtgatgcag 780  
 ccattgcaga ttttaataaaa agattaagca atgaagattg ggtagctcaa ggtagagaat 840  
 atataaaaga taatagtata tgccctttct gtcaaaaaga aaccattacc gaagaattta 900  
 aaaaacaact agaattcttat tttgatacaa gttatcaaga atctattgaa acgatcaagg 960  
 aaaag atg gaa gac tac gca agc aga acc gct gga gca ctg gag cga ctt 1010  
 Met Glu Asp Tyr Ala Ser Arg Thr Ala Gly Ala Leu Glu Arg Leu  
 1 5 10 15

gat aag att gtt gaa aca gaa cag aag aat caa caa act aaa ttg gac 1058  
 Asp Lys Ile Val Glu Thr Glu Gln Lys Asn Gln Gln Thr Lys Leu Asp  
 20 25 30

aca gaa aat ttg aaa ata att att gaa act ttg aga agt aaa atc aat 1106  
 Thr Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn  
 35 40 45

ggg aat cag caa aag atg ctt gat aaa agt aaa gaa atg agc aga aat 1154  
 Gly Asn Gln Gln Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn  
 50 55 60

ttt aag ctt gat agc act aaa aac gag ata gac gca att aaa gat ttg 1202  
 Phe Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu  
 65 70 75

att aaa aag gct aat gag caa ata gcc aat tat aat gag atg ata aag 1250  
 Ile Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys  
 80 85 90 95

gat att gaa aaa cag aaa aag agt tgt aag gaa caa act tgg aaa ttt 1298  
 Asp Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe  
 100 105 110

cta gtc aat gaa ttt aaa agt gat ata caa gaa tat aat aaa aag tat 1346  
 Leu Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr  
 115 120 125

tgc ggt ttg gag aaa gga ata aac aat tta gag aaa gca att agt gaa 1394  
 Cys Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu  
 130 135 140

aat caa gaa gag gta aag aaa tta gaa aat gaa att aag gaa tta gaa 1442  
 Asn Gln Glu Glu Val Lys Lys Leu Glu Asn Glu Ile Lys Glu Leu Glu  
 145 150 155

aaa act atg gta agc ata aag ccc att gtc aat gaa atc aat acg ctt 1490  
 Lys Thr Met Val Ser Ile Lys Pro Ile Val Asn Glu Ile Asn Thr Leu  
 160 165 170 175

tta aaa ggg tat gga ttc gcg aat ttt agt ttg gca tgc act gaa gat	1538
Leu Lys Gly Tyr Gly Phe Ala Asn Phe Ser Leu Ala Cys Thr Glu Asp	
180 185 190	
gaa aaa ttt tat cgt att caa aga gaa gat ggt caa tta gta gga gaa	1586
Glu Lys Phe Tyr Arg Ile Gln Arg Glu Asp Gly Gln Leu Val Gly Glu	
195 200 205	
aca ctg agc gag ggt gaa gtt act ttc atc act ttc tta tat tat tat	1634
Thr Leu Ser Glu Gly Glu Val Thr Phe Ile Thr Phe Leu Tyr Tyr Tyr	
210 215 220	
cat tta gca aaa ggc tct tta gaa gag aac gat ata tca aaa aat aag	1682
His Leu Ala Lys Gly Ser Leu Glu Glu Asn Asp Ile Ser Lys Asn Lys	
225 230 235	
gtt tta gtg att gat gac ccc att tca agt ttg gat agc aat ata ttg	1730
Val Leu Val Ile Asp Asp Pro Ile Ser Ser Leu Asp Ser Asn Ile Leu	
240 245 250 255	
ttt ata gtg agt gtt tta gtt aaa gat ctt atg aaa gaa gcc atg gaa	1778
Phe Ile Val Ser Val Leu Val Lys Asp Leu Met Lys Glu Ala Met Glu	
260 265 270	
gaa aaa aca aac atc aag caa gtt att ata cta acc cac aac aca tat	1826
Glu Lys Thr Asn Ile Lys Gln Val Ile Ile Leu Thr His Asn Thr Tyr	
275 280 285	
ttt tac aag gaa att aca tta gaa tgt gat tta aaa cgc tat caa ggg	1874
Phe Tyr Lys Glu Ile Thr Leu Glu Cys Asp Leu Lys Arg Tyr Gln Gly	
290 295 300	
aaa tat tct ttt tgg ata att aaa aag gat aat aat gtt tca aaa att	1922
Lys Tyr Ser Phe Trp Ile Ile Lys Lys Asp Asn Asn Val Ser Lys Ile	
305 310 315	
aaa gat tat aaa gaa aat ccc att aaa aat tcc tat gaa ttg cta tgg	1970
Lys Asp Tyr Lys Glu Asn Pro Ile Lys Asn Ser Tyr Glu Leu Leu Trp	
320 325 330 335	
caa gaa gta aaa caa gca aaa gaa aat aat gct tct tgg gta tct tta	2018
Gln Glu Val Lys Gln Ala Lys Glu Asn Asn Ala Ser Trp Val Ser Leu	
340 345 350	
caa aat gtt atg cga aga att att gag tat tac ttt agg att tta ggc	2066
Gln Asn Val Met Arg Arg Ile Ile Glu Tyr Tyr Phe Arg Ile Leu Gly	
355 360 365	
ggt ttt aaa cat aat gat agc ttg agt gaa tgt ttt gaa aat att gaa	2114
Gly Phe Lys His Asn Asp Ser Leu Ser Glu Cys Phe Glu Asn Ile Glu	
370 375 380	
gaa aaa cga gtg tgt aat tct ttc att tca tgg ttt aat gat ggc tct	2162
Glu Lys Arg Val Cys Asn Ser Phe Ile Ser Trp Phe Asn Asp Gly Ser	

385	390	395	
cat ggg att tca gat gat ttg ttt atg caa agt caa gat aca agt att	2210		
His Gly Ile Ser Asp Asp Leu Phe Met Gln Ser Gln Asp Thr Ser Ile			
400 405 410 415			
gag aca tat tta aaa gtt ttt gaa aaa ata ttt aaa gaa acc ggt cat	2258		
Glu Thr Tyr Leu Lys Val Phe Glu Lys Ile Phe Lys Glu Thr Gly His			
420 425 430			
gaa gct cat tat aaa atg atg atg aga atg aag taattgaatt aaaaacaagg	2311		
Glu Ala His Tyr Lys Met Met Met Arg Met Lys			
435 440			
aataacatgc gaatcgtatt tatgggaacg	2341		
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1 5 10 15			
Lys Ile Val Glu Thr Glu Gln Lys Asn Gln Gln Thr Lys Leu Asp Thr			
20 25 30			
Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn Gly			
35 40 45			
Asn Gln Lys Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn Phe			
50 55 60			
Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu Ile			
65 70 75 80			
Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys Asp			
85 90 95			
Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe Leu			
100 105 110			
Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr Cys			
115 120 125			
Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu Asn			
130 135 140			
Gln Glu Glu Val Lys Lys Leu Glu Asn Glu Ile Lys Glu Leu Glu Lys			
145 150 155 160			
Thr Met Val Ser Ile Lys Pro Ile Val Asn Glu Ile Asn Thr Leu Leu			
165 170 175			
Lys Gly Tyr Gly Phe Ala Asn Phe Ser Leu Ala Cys Thr Glu Asp Glu			
180 185 190			
Lys Phe Tyr Arg Ile Gln Arg Glu Asp Gly Gln Leu Val Gly Glu Thr			
195 200 205			
Leu Ser Glu Gly Glu Val Thr Phe Ile Thr Phe Leu Tyr Tyr Tyr His			
210 215 220			
Leu Ala Lys Gly Ser Leu Glu Glu Asn Asp Ile Ser Lys Asn Lys Val			
225 230 235 240			
Leu Val Ile Asp Asp Pro Ile Ser Ser Leu Asp Ser Asn Ile Leu Phe			
245 250 255			
Ile Val Ser Val Leu Val Lys Asp Leu Met Lys Glu Ala Met Glu Glu			



ggc ctt atc act tta agc tct caa acc gtc att gac gct tta ggc tat	296
Gly Leu Ile Thr Leu Ser Ser Gln Thr Val Ile Asp Ala Leu Gly Tyr	
70 75 80	
ggc gtg agt aac act gtt ggc aac caa tta gag ggc att tct aat atc	344
Gly Val Ser Asn Thr Val Gly Asn Gln Leu Glu Gly Ile Ser Asn Ile	
85 90 95	
ttg aat caa att ggc aaa aga aaa gac ttt tat tct agc cgt caa atc	392
Leu Asn Gln Ile Gly Lys Arg Lys Asp Phe Tyr Ser Ser Arg Gln Ile	
100 105 110	
tct agc att tcc caa caa atc ata ggg ctt aaa gga agc tct gat ccc	440
Ser Ser Ile Ser Gln Gln Ile Ile Gly Leu Lys Gly Ser Ser Asp Pro	
115 120 125 130	
tta aaa gcc cat tct tca cag atc aca gcc aaa ctc ctt tcc aac acc	488
Leu Lys Ala His Ser Ser Gln Ile Thr Ala Lys Leu Leu Ser Asn Thr	
135 140 145	
caa agc gcg ttt gat cag ggc atc gcg cta agc act aac atc att agc	536
Gln Ser Ala Phe Asp Gln Gly Ile Ala Leu Ser Thr Asn Ile Ile Ser	
150 155 160	
tct atc aat agc cta aac cct agc aac aac acc caa gag gtt aaa aaa	584
Ser Ile Asn Ser Leu Asn Pro Ser Asn Asn Thr Gln Glu Val Lys Lys	
165 170 175	
cag ctc caa aac acc gcg caa tcc atg aca gaa ttg ttg caa caa att	632
Gln Leu Gln Asn Thr Ala Gln Ser Met Thr Glu Leu Leu Gln Gln Ile	
180 185 190	
gaa cac agc atc act aaa acc act agc acc act tac gcg caa tcc tta	680
Glu His Ser Ile Thr Lys Thr Thr Ser Thr Thr Tyr Ala Gln Ser Leu	
195 200 205 210	
ctc tcc aat cta acc gat gcg gtg aat gcc tct agc aat aat acc gct	728
Leu Ser Asn Leu Thr Asp Ala Val Asn Ala Ser Ser Asn Asn Thr Ala	
215 220 225	
tat gtg agc gct ctt gtt aac gct tta aac act tta ggg gta ggg gtt	776
Tyr Val Ser Ala Leu Val Asn Ala Leu Asn Thr Leu Gly Val Gly Val	
230 235 240	
ttc ccc acc aca acc aca acg cat gtg gtg tta aac cca ccg gga caa	824
Phe Pro Thr Thr Thr Thr Thr His Val Val Leu Asn Pro Pro Gly Gln	
245 250 255	
gtc gta ttc tat cca acc aat tcc att tta ggc tct act tct tca aac	872
Val Val Phe Tyr Pro Thr Asn Ser Ile Leu Gly Ser Thr Ser Ser Asn	
260 265 270	
agc aat aac caa caa caa tac aac aac acc ctt tta atg aac acc tta	920
Ser Asn Asn Gln Gln Gln Tyr Asn Asn Thr Leu Leu Met Asn Thr Leu	
275 280 285 290	



caa ggg aca tta agc gct aat act caa aat aac ccc aat ggt tgc gcc	968
Gln Gly Thr Leu Ser Ala Asn Thr Gln Asn Asn Pro Asn Gly Cys Ala	
295 300 305	
aat caa gtc cag tgt ttg gag caa ttc atc caa aat tta gcc cct tta	1016
Asn Gln Val Gln Cys Leu Glu Gln Phe Ile Gln Asn Leu Ala Pro Leu	
310 315 320	
gcc gca acc ccc act tca aac aac cag gcc aac cag caa gtc caa gcc	1064
Ala Ala Thr Pro Thr Ser Asn Asn Gln Ala Asn Gln Val Gln Ala	
325 330 335	
atc gct caa aag ctt caa agc gtt gct atc aac act tta gac aac aat	1112
Ile Ala Gln Lys Leu Gln Ser Val Ala Ile Asn Thr Leu Asp Asn Asn	
340 345 350	
gcg atc aac aac acc acc tat aat tta aac aat ttg cac aac gct ttg	1160
Ala Ile Asn Asn Thr Thr Tyr Asn Leu Asn Asn Leu His Asn Ala Leu	
355 360 365 370	
aat ttc caa gcc tat gaa agc acg ata gaa caa tac aat aac gct tta	1208
Asn Phe Gln Ala Tyr Glu Ser Thr Ile Glu Gln Tyr Asn Asn Ala Leu	
375 380 385	
aaa caa att tct tgg atc agt ttt act gag cct aaa aac tta ctc aaa	1256
Lys Gln Ile Ser Trp Ile Ser Phe Thr Glu Pro Lys Asn Leu Leu Lys	
390 395 400	
aac act tcc aat aac tac caa atc ggc acc gtt acc aac gct caa ggg	1304
Asn Thr Ser Asn Asn Tyr Gln Ile Gly Thr Val Thr Asn Ala Gln Gly	
405 410 415	
caa aat atc agc gcc tat gat tgc atg act gct acc gga agc ctt tct	1352
Gln Asn Ile Ser Ala Tyr Asp Cys Met Thr Ala Thr Gly Ser Leu Ser	
420 425 430	
agc aat gct tct agc ggg att tca tgc tca gcc aca agc tcc aca agt	1400
Ser Asn Ala Ser Ser Gly Ile Ser Cys Ser Ala Thr Ser Ser Thr Ser	
435 440 445 450	
tcc aca aat agc ttt gac aat tct tta gtc gct acc tcc aaa gtc caa	1448
Ser Thr Asn Ser Phe Asp Asn Ser Leu Val Ala Thr Ser Lys Val Gln	
455 460 465	
acc atc aac ggc aaa gag cag atc ggc gtg aat tct ttt aac ctt gtc	1496
Thr Ile Asn Gly Lys Glu Gln Ile Gly Val Asn Ser Phe Asn Leu Val	
470 475 480	
tct caa gtg tgg agc gtt tat aat tct tta aaa act tca gaa gaa aat	1544
Ser Gln Val Trp Ser Val Tyr Asn Ser Leu Lys Thr Ser Glu Glu Asn	
485 490 495	
ttg caa aaa aac gcc aat att tta tgc gct aat ggg acg caa tct ggg	1592
Leu Gln Lys Asn Ala Asn Ile Leu Cys Ala Asn Gly Thr Gln Ser Gly	

500	505	510	
aca agc tca tgc aat agc tct tca ggg ggt ttg agc atc agc ggg aac Thr Ser Ser Cys Asn Ser Ser Ser Gly Gly Leu Ser Ile Ser Gly Asn 515 520 525 530			1640
gcc caa ttg caa aat att tta agc cct act agt ggg act acc act aat Ala Gln Leu Gln Asn Ile Leu Ser Pro Thr Ser Gly Thr Thr Thr Asn 535 540 545			1688
act caa gct aaa agc aac gct ccc aaa cta aaa gcg atg gtg gtg gtg Thr Gln Ala Lys Ser Asn Ala Pro Lys Leu Lys Ala Met Val Val Val 550 555 560			1736
aat aat gaa gaa gaa gct aaa acg gcc aat tta gcc caa agc agc ggg Asn Asn Glu Glu Glu Ala Lys Thr Ala Asn Leu Ala Gln Ser Ser Gly 565 570 575			1784
aca acc aca caa tct cct aac agc acg gtg atg gga gct tta aac acc Thr Thr Thr Gln Ser Pro Asn Ser Thr Val Met Gly Ala Leu Asn Thr 580 585 590			1832
gtg ttg caa aat gtc agc aat ttc caa caa agc att caa aac gct ttt Val Leu Gln Asn Val Ser Asn Phe Gln Gln Ser Ile Gln Asn Ala Phe 595 600 605 610			1880
caa aac caa gaa agt aat atc caa gct tgg gcg aat gcg att tat aac Gln Asn Gln Glu Ser Asn Ile Gln Ala Trp Ala Asn Ala Ile Tyr Asn 615 620 625			1928
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Val Gly Leu Gly Tyr Lys Tyr Phe Phe Gly Lys Ala Arg Lys Leu Gly	
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 Gln Ile Ser Ser Ile Ser Gln Gln Ile Ile Gly Leu Lys Gly Ser Ser  
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 Asp Pro Leu Lys Ala His Ser Ser Gln Ile Thr Ala Lys Leu Leu Ser  
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 Asn Thr Gln Ser Ala Phe Asp Gln Gly Ile Ala Leu Ser Thr Asn Ile  
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 Gln Ile Glu His Ser Ile Thr Lys Thr Thr Ser Thr Thr Tyr Ala Gln  
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 Thr Ala Tyr Val Ser Ala Leu Val Asn Ala Leu Asn Thr Leu Gly Val  
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Tyr	Asn	Thr	Asn	Gly	Ser	Gln	Ser	Gln	Glu	Met	Thr	Pro	Asn	Asn	Asn		
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Gln	Asp	Leu	Arg	Ile	Gln	Leu	Arg	Ala	Asn	Phe	Tyr	Gln	Leu	Ile	Asn		
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Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Ile	Phe	Ser	Ala	Phe	Leu	
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Gly Leu Gly Leu Glu Thr Asn Lys His Gly Ala Thr Leu Asn Lys Gly				
	260		265	270
Arg Val Gly Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp				
	275		280	285
Glu Gly Gln Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr				
	290		295	300
Pro Gly Val Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala				
305		310		315
Val Tyr Glu Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu				
	325		330	335
Leu Cys Gln Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala				
	340		345	350
Leu Ala Tyr Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile				
	355		360	365
Ile Val Val Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val				
	370		375	380
Tyr Asn Ala Leu Lys Gly Gly Leu Lys				
385		390		

<210> 153  
 <211> 601  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (197)...(547)

<221> misc\_feature  
 <222> 159  
 <223> n = A,T,C or G

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 gtgggggtgat cccccctatt ttgcgttcag ctttgctcgt gttcccttct acgattttgc 120  
 agcaagccac aagcaacaaa accttgcaag cggttgcgna ttttttaagc ccgcaaggta 180  
 tgcgtataat attttg atg ttc ttg ctc atc atc ttt ttt gct tac ttt tat 232  
 Met Phe Leu Leu Ile Ile Phe Phe Ala Tyr Phe Tyr  
 1 5 10  
 tct tct att gtg ttc aat tct aag gat att gcg gat aat ttg agg cgt 280  
 Ser Ser Ile Val Phe Asn Ser Lys Asp Ile Ala Asp Asn Leu Arg Arg  
 15 20 25  
 aat ggc ggg tat att cca ggg ctt agg cct gga gag ggg act tca tcg 328  
 Asn Gly Gly Tyr Ile Pro Gly Leu Arg Pro Gly Glu Gly Thr Ser Ser  
 30 35 40  
 ttt tta aat tct gta gcg agt aag ctc act ttg tgg ggt tca ttg tat 376

Phe Leu Asn Ser Val Ala Ser Lys Leu Thr Leu Trp Gly Ser Leu Tyr  
45 50 55 60  
tta gcg ctc att tct acc gtg cct tgg att ttg gtt aag gct atg ggc 424  
Leu Ala Leu Ile Ser Thr Val Pro Trp Ile Leu Val Lys Ala Met Gly  
65 70 75  
gtg cct ttt tac ttt gga ggc aca gcg gtg ctg att gtg gtt caa gtc 472  
Val Pro Phe Tyr Phe Gly Gly Thr Ala Val Leu Ile Val Val Gln Val  
80 85 90  
gct att gac acc atg aaa aag att gaa gcg caa att tat atg agc aag 520  
Ala Ile Asp Thr Met Lys Lys Ile Glu Ala Gln Ile Tyr Met Ser Lys  
95 100 105  
tat aaa act tta agc gcg gta ggc ttt taatggcaat ctctattaaa 567  
Tyr Lys Thr Leu Ser Ala Val Gly Phe  
110 115  
agcccaaaag aaatcaaagc tctaagaaaa gccg 601  
<210> 154  
<211> 117  
<212> PRT  
<213> Helicobacter pylori  
<400> 154  
Met Phe Leu Leu Ile Ile Phe Phe Ala Tyr Phe Tyr Ser Ser Ile Val  
1 5 10 15  
Phe Asn Ser Lys Asp Ile Ala Asp Asn Leu Arg Arg Asn Gly Gly Tyr  
20 25 30  
Ile Pro Gly Leu Arg Pro Gly Glu Gly Thr Ser Ser Phe Leu Asn Ser  
35 40 45  
Val Ala Ser Lys Leu Thr Leu Trp Gly Ser Leu Tyr Leu Ala Leu Ile  
50 55 60  
Ser Thr Val Pro Trp Ile Leu Val Lys Ala Met Gly Val Pro Phe Tyr  
65 70 75 80  
Phe Gly Gly Thr Ala Val Leu Ile Val Val Gln Val Ala Ile Asp Thr  
85 90 95  
Met Lys Lys Ile Glu Ala Gln Ile Tyr Met Ser Lys Tyr Lys Thr Leu  
100 105 110  
Ser Ala Val Gly Phe  
115  
<210> 155  
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<212> DNA  
<213> Helicobacter pylori  
<220>  
<221> CDS  
<222> (64)...(675)  
<400> 155

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tca atg act cta ggc att gat gaa gcg ggt agg ggg tgt ttg gcc ggt	108
Met Thr Leu Gly Ile Asp Glu Ala Gly Arg Gly Cys Leu Ala Gly	
1 5 10 15	
tcg ctt ttt gtg gct ggg gtg gcg tgt aat gaa aaa aca gcc tta gaa	156
Ser Leu Phe Val Ala Gly Val Ala Cys Asn Glu Lys Thr Ala Leu Glu	
20 25 30	
ttt cta aaa atg ggt tta aaa gac agc aag aag ctc agc cta aaa aag	204
Phe Leu Lys Met Gly Leu Lys Asp Ser Lys Lys Leu Ser Leu Lys Lys	
35 40 45	
cgc ttt ttc tta gaa tat aag atc aaa acg cat ggt gag gtg ggg ttt	252
Arg Phe Phe Leu Glu Tyr Lys Ile Lys Thr His Gly Glu Val Gly Phe	
50 55 60	
ttc gtg gtt aaa aaa agc gca aat gaa att gat agc ttg ggc tta ggg	300
Phe Val Val Lys Lys Ser Ala Asn Glu Ile Asp Ser Leu Gly Leu Gly	
65 70 75	
gcg tgt ttg aaa ctc gct gtg caa gaa att tta gaa aat ggt tgc tct	348
Ala Cys Leu Lys Leu Ala Val Gln Glu Ile Leu Glu Asn Gly Cys Ser	
80 85 90 95	
tta gtt gat gaa ata aaa ata gac ggc aac acg gcg ttt ggc ttg aac	396
Leu Val Asp Glu Ile Lys Ile Asp Gly Asn Thr Ala Phe Gly Leu Asn	
100 105 110	
aaa cgc tac ccc cat ata caa acc atc atc aag ggc gat gaa aca atc	444
Lys Arg Tyr Pro His Ile Gln Thr Ile Ile Lys Gly Asp Glu Thr Ile	
115 120 125	
gct caa atc gct atg gcg tct gtt ttg gcg aaa gct ttt aag gac aga	492
Ala Gln Ile Ala Met Ala Ser Val Leu Ala Lys Ala Phe Lys Asp Arg	
130 135 140	
gaa atg cta gag ttg cac gct ttg ttt aag gaa tac ggc tgg gat aag	540
Glu Met Leu Glu Leu His Ala Leu Phe Lys Glu Tyr Gly Trp Asp Lys	
145 150 155	
aat tgc ggg tat ggg act aaa caa cat ata gaa gcg atc att aag cta	588
Asn Cys Gly Tyr Gly Thr Lys Gln His Ile Glu Ala Ile Ile Lys Leu	
160 165 170 175	
ggg gct acg cct ttt cat cgg cat agc ttc acg ctt aaa aac cgc atc	636
Gly Ala Thr Pro Phe His Arg His Ser Phe Thr Leu Lys Asn Arg Ile	
180 185 190	
tta aat ccc aaa ctc tta gag gtg gaa caa cgc ctt att taaaagggcg	685
Leu Asn Pro Lys Leu Leu Glu Val Glu Gln Arg Leu Ile	
195 200	
ctgagatggg tagcgctcgc tgaagaaagg tcgatgcgtt	725

<210> 156  
 <211> 204  
 <212> PRT  
 <213> Helicobacter pylori

<400> 156  
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 1 5 10 15  
 Leu Phe Val Ala Gly Val Ala Cys Asn Glu Lys Thr Ala Leu Glu Phe  
 20 25 30  
 Leu Lys Met Gly Leu Lys Asp Ser Lys Lys Leu Ser Leu Lys Lys Arg  
 35 40 45  
 Phe Phe Leu Glu Tyr Lys Ile Lys Thr His Gly Glu Val Gly Phe Phe  
 50 55 60  
 Val Val Lys Lys Ser Ala Asn Glu Ile Asp Ser Leu Gly Leu Gly Ala  
 65 70 75 80  
 Cys Leu Lys Leu Ala Val Gln Glu Ile Leu Glu Asn Gly Cys Ser Leu  
 85 90 95  
 Val Asp Glu Ile Lys Ile Asp Gly Asn Thr Ala Phe Gly Leu Asn Lys  
 100 105 110  
 Arg Tyr Pro His Ile Gln Thr Ile Ile Lys Gly Asp Glu Thr Ile Ala  
 115 120 125  
 Gln Ile Ala Met Ala Ser Val Leu Ala Lys Ala Phe Lys Asp Arg Glu  
 130 135 140  
 Met Leu Glu Leu His Ala Leu Phe Lys Glu Tyr Gly Trp Asp Lys Asn  
 145 150 155 160  
 Cys Gly Tyr Gly Thr Lys Gln His Ile Glu Ala Ile Ile Lys Leu Gly  
 165 170 175  
 Ala Thr Pro Phe His Arg His Ser Phe Thr Leu Lys Asn Arg Ile Leu  
 180 185 190  
 Asn Pro Lys Leu Leu Glu Val Glu Gln Arg Leu Ile  
 195 200

<210> 157  
 <211> 2821  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (58)...(2769)

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 1  
 aag ggg aat ttg agc gtt aat gag cct aaa act tac gcc aaa tgg caa 108  
 Lys Gly Asn Leu Ser Val Asn Glu Pro Lys Thr Tyr Ala Lys Trp Gln  
 5 10 15  
 gag caa caa gcg ttt aaa cgc atg caa gct agg aaa gac aac cat ggg 156  
 Glu Gln Gln Ala Phe Lys Arg Met Gln Ala Arg Lys Asp Asn His Gly  
 20 25 30

gat ttc act ttg cat gac ggg ccg cct tat gcg aac ggg cat ttg cat	204
Asp Phe Thr Leu His Asp Gly Pro Pro Tyr Ala Asn Gly His Leu His	
35 40 45	
ttg ggg cat gcc tta aat aaa att tta aaa gac att gtc gtt aaa aga	252
Leu Gly His Ala Leu Asn Lys Ile Leu Lys Asp Ile Val Val Lys Arg	
50 55 60 65	
gaa tat ttt aag ggg aag aaa atc tat tac acg ccc ggt tgg gat tgc	300
Glu Tyr Phe Lys Gly Lys Lys Ile Tyr Tyr Thr Pro Gly Trp Asp Cys	
70 75 80	
cat ggt ttg ccc att gag cag caa att tta gag cga tta gaa aaa gaa	348
His Gly Leu Pro Ile Glu Gln Gln Ile Leu Glu Arg Leu Glu Lys Glu	
85 90 95	
aaa aca agc cta gaa aac ccc acg ctg ttt aga gaa aag tgc cga gat	396
Lys Thr Ser Leu Glu Asn Pro Thr Leu Phe Arg Glu Lys Cys Arg Asp	
100 105 110	
cat gcg aag aaa ttt tta gaa atc caa aag aat gaa ttt ttg caa ttg	444
His Ala Lys Lys Phe Leu Glu Ile Gln Lys Asn Glu Phe Leu Gln Leu	
115 120 125	
ggt gtt ttg ggg gat ttt gaa gat cct tat aaa acc atg gat ttt aaa	492
Gly Val Leu Gly Asp Phe Glu Asp Pro Tyr Lys Thr Met Asp Phe Lys	
130 135 140 145	
ttt gaa gcg agc att tat aga gcc tta gtg gaa gtg gct aaa aaa ggg	540
Phe Glu Ala Ser Ile Tyr Arg Ala Leu Val Glu Val Ala Lys Lys Gly	
150 155 160	
ctt ttg aaa gag cgc cac aag cct att tat tgg agt tat gca tgc gag	588
Leu Leu Lys Glu Arg His Lys Pro Ile Tyr Trp Ser Tyr Ala Cys Glu	
165 170 175	
agc gct tta gcg gaa gct gaa gtg gaa tac aaa atg aaa aaa tcg ccc	636
Ser Ala Leu Ala Glu Ala Glu Val Glu Tyr Lys Met Lys Lys Ser Pro	
180 185 190	
tcc att ttc gtg gcg ttt ggt ttg aaa aag gag agt tta gaa aaa tta	684
Ser Ile Phe Val Ala Phe Gly Leu Lys Lys Glu Ser Leu Glu Lys Leu	
195 200 205	
aaa gtc aaa aaa gcg agc ttg gtg att tgg acg acc acg cct tgg act	732
Lys Val Lys Lys Ala Ser Leu Val Ile Trp Thr Thr Thr Pro Trp Thr	
210 215 220 225	
ttg tat gcg aat gta gcg atc gct ttg aaa aaa gac gct gtt tat gcg	780
Leu Tyr Ala Asn Val Ala Ile Ala Leu Lys Lys Asp Ala Val Tyr Ala	
230 235 240	
ctc acc caa aaa ggc tat tta gtc gct aaa gcc ttg cat gaa aaa tta	828
Leu Thr Gln Lys Gly Tyr Leu Val Ala Lys Ala Leu His Glu Lys Leu	

245	250	255	
gcc gct tta ggg gtg gtg gat aat gag atc aca cat gaa ttc aat tcc			876
Ala Ala Leu Gly Val Val Asp Asn Glu Ile Thr His Glu Phe Asn Ser			
260	265	270	
aat gat tta gaa tat tta gtg gct aca aac ccg ctc aat caa agg gat			924
Asn Asp Leu Glu Tyr Leu Val Ala Thr Asn Pro Leu Asn Gln Arg Asp			
275	280	285	
tcg ctg gtg gct tta gga gag cat gtc ggt tta gaa gat ggc aca gga			972
Ser Leu Val Ala Leu Gly Glu His Val Gly Leu Glu Asp Gly Thr Gly			
290	295	300	305
gcc gtg cat acc gca cct ggg cat ggt gaa gag gac tat tat tta ggc			1020
Ala Val His Thr Ala Pro Gly His Gly Glu Glu Asp Tyr Tyr Leu Gly			
310	315	320	
tta aga tat aat tta gaa gtg tta atg tct gta gat gag aaa ggt tgc			1068
Leu Arg Tyr Asn Leu Glu Val Leu Met Ser Val Asp Glu Lys Gly Cys			
325	330	335	
tat gat gag ggc att atc cat aac caa cta tta gat gaa agc tat ctg			1116
Tyr Asp Glu Gly Ile Ile His Asn Gln Leu Leu Asp Glu Ser Tyr Leu			
340	345	350	
ggc gag cat gtt ttt aag gct caa aaa cgc att ata gag caa ttg ggc			1164
Gly Glu His Val Phe Lys Ala Gln Lys Arg Ile Ile Glu Gln Leu Gly			
355	360	365	
gat tct tta ttg cta gag caa gag att gag cat tct tat ccg cat tgc			1212
Asp Ser Leu Leu Leu Glu Gln Glu Ile Glu His Ser Tyr Pro His Cys			
370	375	380	385
tgg agg acg cac aag cct gtg att tac aga gcg act acg caa tgg ttt			1260
Trp Arg Thr His Lys Pro Val Ile Tyr Arg Ala Thr Thr Gln Trp Phe			
390	395	400	
att tta atg gat gag cct ttt atc caa aat gat ggc tct caa aaa acc			1308
Ile Leu Met Asp Glu Pro Phe Ile Gln Asn Asp Gly Ser Gln Lys Thr			
405	410	415	
tta aga gaa gtg gct tta gat gcg att gaa aag gtg gaa ttt gtg cca			1356
Leu Arg Glu Val Ala Leu Asp Ala Ile Glu Lys Val Glu Phe Val Pro			
420	425	430	
agc agc ggg aaa aac cgc cta aaa acc atg ata gaa aac cgc cct gat			1404
Ser Ser Gly Lys Asn Arg Leu Lys Thr Met Ile Glu Asn Arg Pro Asp			
435	440	445	
tgg tgc ttg agc cgg caa aga aaa tgg ggc gtg cca ctg gcc ttt ttc			1452
Trp Cys Leu Ser Arg Gln Arg Lys Trp Gly Val Pro Leu Ala Phe Phe			
450	455	460	465
ata gac aaa cgc acg aat aag cct tgt ttt gaa agc gaa gtt tta gag			1500



Ile	Asp	Lys	Arg	Thr	Asn	Lys	Pro	Cys	Phe	Glu	Ser	Glu	Val	Leu	Glu	
				470					475					480		
cat	gtg	gcc	aat	ctt	ttt	gag	aaa	aaa	ggc	tgt	gat	gtg	tgg	tgg	gag	1548
His	Val	Ala	Asn	Leu	Phe	Glu	Lys	Lys	Gly	Cys	Asp	Val	Trp	Trp	Glu	
			485					490					495			
tat	agc	gtg	aaa	gat	tta	ttg	ccc	cct	agc	tat	caa	gag	gac	gcc	aag	1596
Tyr	Ser	Val	Lys	Asp	Leu	Leu	Pro	Pro	Ser	Tyr	Gln	Glu	Asp	Ala	Lys	
		500					505					510				
cat	tat	gag	aaa	atc	atg	cac	att	tta	gac	gtg	tgg	ttt	gat	agt	ggc	1644
His	Tyr	Glu	Lys	Ile	Met	His	Ile	Leu	Asp	Val	Trp	Phe	Asp	Ser	Gly	
	515					520				525						
agc	acc	ttt	aag	gcg	ggt	tta	gaa	gac	tat	cat	gga	gaa	aaa	ggg	caa	1692
Ser	Thr	Phe	Lys	Ala	Val	Leu	Glu	Asp	Tyr	His	Gly	Glu	Lys	Gly	Gln	
530					535				540						545	
agc	cct	agc	gat	gtg	atc	tta	gaa	ggg	agc	gat	cag	cat	agg	ggg	tgg	1740
Ser	Pro	Ser	Asp	Val	Ile	Leu	Glu	Gly	Ser	Asp	Gln	His	Arg	Gly	Trp	
				550					555					560		
ttt	caa	agc	tcg	ctt	cta	atc	ggc	tgt	ggt	tta	aac	aac	caa	gcc	cct	1788
Phe	Gln	Ser	Ser	Leu	Leu	Ile	Gly	Cys	Val	Leu	Asn	Asn	Gln	Ala	Pro	
			565					570					575			
ttt	aaa	aag	gtc	att	acg	cat	ggc	ttt	atc	gta	gat	gaa	aag	ggc	gaa	1836
Phe	Lys	Lys	Val	Ile	Thr	His	Gly	Phe	Ile	Val	Asp	Glu	Lys	Gly	Glu	
		580					585					590				
aaa	atg	agt	aaa	tct	aag	ggc	aat	gtg	gtg	tct	ttg	gac	aag	ctg	ctc	1884
Lys	Met	Ser	Lys	Ser	Lys	Gly	Asn	Val	Val	Ser	Leu	Asp	Lys	Leu	Leu	
	595					600					605					
aaa	acg	cat	ggg	agc	gat	gtg	gtg	cgt	ttg	tgg	gta	gcg	ttt	aat	gac	1932
Lys	Thr	His	Gly	Ser	Asp	Val	Val	Arg	Leu	Trp	Val	Ala	Phe	Asn	Asp	
610					615				620						625	
tat	caa	aac	gat	ttg	aga	gtc	tct	caa	acc	ttt	ttc	act	caa	aca	gaa	1980
Tyr	Gln	Asn	Asp	Leu	Arg	Val	Ser	Gln	Thr	Phe	Phe	Thr	Gln	Thr	Glu	
				630				635						640		
caa	cat	tat	aaa	aaa	ttc	cgc	aac	acc	ctg	aaa	ttc	tta	ctc	gct	aat	2028
Gln	His	Tyr	Lys	Lys	Phe	Arg	Asn	Thr	Leu	Lys	Phe	Leu	Leu	Ala	Asn	
			645					650					655			
ttt	agc	gat	atg	gat	ctc	aag	aat	tta	gaa	cgc	ccc	cat	aac	ttc	agc	2076
Phe	Ser	Asp	Met	Asp	Leu	Lys	Asn	Leu	Glu	Arg	Pro	His	Asn	Phe	Ser	
		660					665					670				
cct	tta	gat	cat	ttt	atg	tta	gag	act	tta	gaa	acc	ata	agc	gct	gga	2124
Pro	Leu	Asp	His	Phe	Met	Leu	Glu	Thr	Leu	Glu	Thr	Ile	Ser	Ala	Gly	
		675				680					685					

gtc aat agc gcg ttt gaa gag cat gat ttt gtg aaa ggc ttg aat att	2172
Val Asn Ser Ala Phe Glu Glu His Asp Phe Val Lys Gly Leu Asn Ile	
690 695 700 705	
tta atg gcg ttt gtt acc aat gaa ttg agc ggg att tat tta gac gct	2220
Leu Met Ala Phe Val Thr Asn Glu Leu Ser Gly Ile Tyr Leu Asp Ala	
710 715 720	
tgc aag gat agc ttg tat tgc gat agc aaa aac aat gaa aaa cgc caa	2268
Cys Lys Asp Ser Leu Tyr Cys Asp Ser Lys Asn Asn Glu Lys Arg Gln	
725 730 735	
gcc att caa atg gtt tta ctc gct aca gct agt aag ttg tgc tac ttt	2316
Ala Ile Gln Met Val Leu Leu Ala Thr Ala Ser Lys Leu Cys Tyr Phe	
740 745 750	
tta gcc ccg att tta acg cac acg att gaa gaa gtt tta gag cat agc	2364
Leu Ala Pro Ile Leu Thr His Thr Ile Glu Glu Val Leu Glu His Ser	
755 760 765	
caa gcg ctt cgc att ttt tta caa gcc aaa gat gtg ttt gat tta aaa	2412
Gln Ala Leu Arg Ile Phe Leu Gln Ala Lys Asp Val Phe Asp Leu Lys	
770 775 780 785	
gac att agc gtt tca gaa aaa ctc cac ctc aaa gag ttt aaa aaa cca	2460
Asp Ile Ser Val Ser Glu Lys Leu His Leu Lys Glu Phe Lys Lys Pro	
790 795 800	
gaa aat ttt gaa gcc gtt tta gcc ttg cgt tct gcc ttt aat gaa gag	2508
Glu Asn Phe Glu Ala Val Leu Ala Leu Arg Ser Ala Phe Asn Glu Glu	
805 810 815	
tta gac cga ttg aaa aaa gaa ggc gtc att aaa aat tgc tta gag tgc	2556
Leu Asp Arg Leu Lys Lys Glu Gly Val Ile Lys Asn Ser Leu Glu Cys	
820 825 830	
gct att gaa gta aaa gaa aaa gcg ttg gat gaa aat tta gta gaa gag	2604
Ala Ile Glu Val Lys Glu Lys Ala Leu Asp Glu Asn Leu Val Glu Glu	
835 840 845	
ttg ctg atg gta agc ttt gtg ggg att gca aaa gaa aaa ttg agt gaa	2652
Leu Leu Met Val Ser Phe Val Gly Ile Ala Lys Glu Lys Leu Ser Glu	
850 855 860 865	
acg cca gca ttc acg ctc ttt aaa gcc ccc ttt tat aaa tgc ccc agg	2700
Thr Pro Ala Phe Thr Leu Phe Lys Ala Pro Phe Tyr Lys Cys Pro Arg	
870 875 880	
tgt tgg cgt ttt aaa agc gag cta gaa aac acc cct tgc aag cgt tgc	2748
Cys Trp Arg Phe Lys Ser Glu Leu Glu Asn Thr Pro Cys Lys Arg Cys	
885 890 895	
gaa cag gtt tta aaa gag cga tgataaaagg atagggcttt tgaaaacttt	2799
Glu Gln Val Leu Lys Glu Arg	
900	

acaaacccat agagttttac aa

2821

<210> 158

<211> 904

<212> PRT

<213> Helicobacter pylori

<400> 158

Met	Lys	Gly	Asn	Leu	Ser	Val	Asn	Glu	Pro	Lys	Thr	Tyr	Ala	Lys	Trp
1				5					10					15	
Gln	Glu	Gln	Gln	Ala	Phe	Lys	Arg	Met	Gln	Ala	Arg	Lys	Asp	Asn	His
			20					25					30		
Gly	Asp	Phe	Thr	Leu	His	Asp	Gly	Pro	Pro	Tyr	Ala	Asn	Gly	His	Leu
		35					40					45			
His	Leu	Gly	His	Ala	Leu	Asn	Lys	Ile	Leu	Lys	Asp	Ile	Val	Val	Lys
	50					55					60				
Arg	Glu	Tyr	Phe	Lys	Gly	Lys	Lys	Ile	Tyr	Tyr	Thr	Pro	Gly	Trp	Asp
65					70					75					80
Cys	His	Gly	Leu	Pro	Ile	Glu	Gln	Gln	Ile	Leu	Glu	Arg	Leu	Glu	Lys
				85				90						95	
Glu	Lys	Thr	Ser	Leu	Glu	Asn	Pro	Thr	Leu	Phe	Arg	Glu	Lys	Cys	Arg
			100					105					110		
Asp	His	Ala	Lys	Lys	Phe	Leu	Glu	Ile	Gln	Lys	Asn	Glu	Phe	Leu	Gln
	115						120					125			
Leu	Gly	Val	Leu	Gly	Asp	Phe	Glu	Asp	Pro	Tyr	Lys	Thr	Met	Asp	Phe
	130					135					140				
Lys	Phe	Glu	Ala	Ser	Ile	Tyr	Arg	Ala	Leu	Val	Glu	Val	Ala	Lys	Lys
145					150					155					160
Gly	Leu	Leu	Lys	Glu	Arg	His	Lys	Pro	Ile	Tyr	Trp	Ser	Tyr	Ala	Cys
			165					170						175	
Glu	Ser	Ala	Leu	Ala	Glu	Ala	Glu	Val	Glu	Tyr	Lys	Met	Lys	Lys	Ser
			180					185					190		
Pro	Ser	Ile	Phe	Val	Ala	Phe	Gly	Leu	Lys	Lys	Glu	Ser	Leu	Glu	Lys
	195						200					205			
Leu	Lys	Val	Lys	Lys	Ala	Ser	Leu	Val	Ile	Trp	Thr	Thr	Thr	Pro	Trp
	210					215					220				
Thr	Leu	Tyr	Ala	Asn	Val	Ala	Ile	Ala	Leu	Lys	Lys	Asp	Ala	Val	Tyr
225					230					235					240
Ala	Leu	Thr	Gln	Lys	Gly	Tyr	Leu	Val	Ala	Lys	Ala	Leu	His	Glu	Lys
				245					250					255	
Leu	Ala	Ala	Leu	Gly	Val	Val	Asp	Asn	Glu	Ile	Thr	His	Glu	Phe	Asn
			260					265					270		
Ser	Asn	Asp	Leu	Glu	Tyr	Leu	Val	Ala	Thr	Asn	Pro	Leu	Asn	Gln	Arg
	275						280					285			
Asp	Ser	Leu	Val	Ala	Leu	Gly	Glu	His	Val	Gly	Leu	Glu	Asp	Gly	Thr
	290					295					300				
Gly	Ala	Val	His	Thr	Ala	Pro	Gly	His	Gly	Glu	Glu	Asp	Tyr	Tyr	Leu
305					310					315					320
Gly	Leu	Arg	Tyr	Asn	Leu	Glu	Val	Leu	Met	Ser	Val	Asp	Glu	Lys	Gly
				325					330					335	
Cys	Tyr	Asp	Glu	Gly	Ile	Ile	His	Asn	Gln	Leu	Leu	Asp	Glu	Ser	Tyr
			340					345					350		
Leu	Gly	Glu	His	Val	Phe	Lys	Ala	Gln	Lys	Arg	Ile	Ile	Glu	Gln	Leu
			355				360						365		

Gly	Asp	Ser	Leu	Leu	Leu	Glu	Gln	Glu	Ile	Glu	His	Ser	Tyr	Pro	His	370	375	380
Cys	Trp	Arg	Thr	His	Lys	Pro	Val	Ile	Tyr	Arg	Ala	Thr	Thr	Gln	Trp	385	390	395
Phe	Ile	Leu	Met	Asp	Glu	Pro	Phe	Ile	Gln	Asn	Asp	Gly	Ser	Gln	Lys	405	410	415
Thr	Leu	Arg	Glu	Val	Ala	Leu	Asp	Ala	Ile	Glu	Lys	Val	Glu	Phe	Val	420	425	430
Pro	Ser	Ser	Gly	Lys	Asn	Arg	Leu	Lys	Thr	Met	Ile	Glu	Asn	Arg	Pro	435	440	445
Asp	Trp	Cys	Leu	Ser	Arg	Gln	Arg	Lys	Trp	Gly	Val	Pro	Leu	Ala	Phe	450	455	460
Phe	Ile	Asp	Lys	Arg	Thr	Asn	Lys	Pro	Cys	Phe	Glu	Ser	Glu	Val	Leu	465	470	475
Glu	His	Val	Ala	Asn	Leu	Phe	Glu	Lys	Lys	Gly	Cys	Asp	Val	Trp	Trp	485	490	495
Glu	Tyr	Ser	Val	Lys	Asp	Leu	Leu	Pro	Pro	Ser	Tyr	Gln	Glu	Asp	Ala	500	505	510
Lys	His	Tyr	Glu	Lys	Ile	Met	His	Ile	Leu	Asp	Val	Trp	Phe	Asp	Ser	515	520	525
Gly	Ser	Thr	Phe	Lys	Ala	Val	Leu	Glu	Asp	Tyr	His	Gly	Glu	Lys	Gly	530	535	540
Gln	Ser	Pro	Ser	Asp	Val	Ile	Leu	Glu	Gly	Ser	Asp	Gln	His	Arg	Gly	545	550	555
Trp	Phe	Gln	Ser	Ser	Leu	Leu	Ile	Gly	Cys	Val	Leu	Asn	Asn	Gln	Ala	565	570	575
Pro	Phe	Lys	Lys	Val	Ile	Thr	His	Gly	Phe	Ile	Val	Asp	Glu	Lys	Gly	580	585	590
Glu	Lys	Met	Ser	Lys	Ser	Lys	Gly	Asn	Val	Val	Ser	Leu	Asp	Lys	Leu	595	600	605
Leu	Lys	Thr	His	Gly	Ser	Asp	Val	Val	Arg	Leu	Trp	Val	Ala	Phe	Asn	610	615	620
Asp	Tyr	Gln	Asn	Asp	Leu	Arg	Val	Ser	Gln	Thr	Phe	Phe	Thr	Gln	Thr	625	630	635
Glu	Gln	His	Tyr	Lys	Lys	Phe	Arg	Asn	Thr	Leu	Lys	Phe	Leu	Leu	Ala	645	650	655
Asn	Phe	Ser	Asp	Met	Asp	Leu	Lys	Asn	Leu	Glu	Arg	Pro	His	Asn	Phe	660	665	670
Ser	Pro	Leu	Asp	His	Phe	Met	Leu	Glu	Thr	Leu	Glu	Thr	Ile	Ser	Ala	675	680	685
Gly	Val	Asn	Ser	Ala	Phe	Glu	Glu	His	Asp	Phe	Val	Lys	Gly	Leu	Asn	690	695	700
Ile	Leu	Met	Ala	Phe	Val	Thr	Asn	Glu	Leu	Ser	Gly	Ile	Tyr	Leu	Asp	705	710	715
Ala	Cys	Lys	Asp	Ser	Leu	Tyr	Cys	Asp	Ser	Lys	Asn	Asn	Glu	Lys	Arg	725	730	735
Gln	Ala	Ile	Gln	Met	Val	Leu	Leu	Ala	Thr	Ala	Ser	Lys	Leu	Cys	Tyr	740	745	750
Phe	Leu	Ala	Pro	Ile	Leu	Thr	His	Thr	Ile	Glu	Glu	Val	Leu	Glu	His	755	760	765
Ser	Gln	Ala	Leu	Arg	Ile	Phe	Leu	Gln	Ala	Lys	Asp	Val	Phe	Asp	Leu	770	775	780
Lys	Asp	Ile	Ser	Val	Ser	Glu	Lys	Leu	His	Leu	Lys	Glu	Phe	Lys	Lys	785	790	795
Pro	Glu	Asn	Phe	Glu	Ala	Val	Leu	Ala	Leu	Arg	Ser	Ala	Phe	Asn	Glu	800		

				805					810					815					
Glu	Leu	Asp	Arg	Leu	Lys	Lys	Glu	Gly	Val	Ile	Lys	Asn	Ser	Leu	Glu				
				820				825					830						
Cys	Ala	Ile	Glu	Val	Lys	Glu	Lys	Ala	Leu	Asp	Glu	Asn	Leu	Val	Glu				
				835				840					845						
Glu	Leu	Leu	Met	Val	Ser	Phe	Val	Gly	Ile	Ala	Lys	Glu	Lys	Leu	Ser				
				850				855					860						
Glu	Thr	Pro	Ala	Phe	Thr	Leu	Phe	Lys	Ala	Pro	Phe	Tyr	Lys	Cys	Pro				
								870					875						
Arg	Cys	Trp	Arg	Phe	Lys	Ser	Glu	Leu	Glu	Asn	Thr	Pro	Cys	Lys	Arg				
				885				890						895					
Cys	Glu	Gln	Val	Leu	Lys	Glu	Arg												
				900															

<210> 159  
 <211> 339  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (70)...(288)

<400> 159  
 tgtagaatga aatcctagcc agtgagctag aatttaaatt tttaaatcaaa ggagtcacatca 60  
 tggcacacc atg aag aac aac acg gcg ggc acc acc acc acc atc acc aca 111  
 Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Ile Thr Thr  
 1 5 10

cac acc acc acc act atc atg gcg gtg aac acc acc atc acc acc aca 159  
 His Thr Thr Thr Thr Ile Met Ala Val Asn Thr Thr Thr Thr Thr Thr  
 15 20 25 30

gct ctc atc atg aag aag gtt gtt gca gca cta gcg aca gtc atc atc 207  
 Ala Leu Ile Met Lys Lys Val Val Ala Ala Leu Ala Thr Val Ile Ile  
 35 40 45

aag aag aag gtt gct gcc acg ggc atc acg agt aat atc ggt gtg gct 255  
 Lys Lys Lys Val Ala Ala Thr Gly Ile Thr Ser Asn Ile Gly Val Ala  
 50 55 60

agg ggc aac ttg act agg gtt gtc tct ggc ttt tgactttaaa atacaatcat 308  
 Arg Gly Asn Leu Thr Arg Val Val Ser Gly Phe  
 65 70

tccattctaa cccattctga tcaaaccggt t 339

<210> 160  
 <211> 73  
 <212> PRT  
 <213> Helicobacter pylori

<400> 160  
 Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr

1	5	10	15
Thr Thr Thr	Ile Met Ala Val Asn Thr	Thr Thr Thr	Thr Thr Thr
	20	25	30
Ile Met Lys	Lys Val Val Ala Ala	Leu Ala Thr Val	Ile Ile Lys Lys
	35	40	45
Lys Val Ala	Ala Thr Gly Ile Thr Ser	Asn Ile Gly Val	Ala Arg Gly
	50	55	60
Asn Leu Thr	Arg Val Val Ser Gly Phe		
65	70		

<210> 161  
 <211> 787  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(734)

<400> 161  
 gttttctact tatgatttttg tggaagaata ttgcaaatta aaggaaatgc atg ctt 56  
 Met Leu  
 1

gaa aaa gtg ttt caa gaa att acc aat aaa aga aag ttt ttt gca agt 104  
 Glu Lys Val Phe Gln Glu Ile Thr Asn Lys Arg Lys Phe Phe Ala Ser  
 5 10 15

tct agc aca ggg gag cag ttt gaa aac caa ttt agg aat gaa tta aaa 152  
 Ser Ser Thr Gly Glu Gln Phe Glu Asn Gln Phe Arg Asn Glu Leu Lys  
 20 25 30

aaa cac ttt agc gaa atc aat ggc gat tta aca gaa gaa tta agc cat 200  
 Lys His Phe Ser Glu Ile Asn Gly Asp Leu Thr Glu Glu Leu Ser His  
 35 40 45 50

att gaa gaa aag cct aat aaa gaa atc aaa acc act ttt aac caa ctc 248  
 Ile Glu Glu Lys Pro Asn Lys Glu Ile Lys Thr Thr Phe Asn Gln Leu  
 55 60 65

aaa aag caa gtt tta gaa aaa aat cac ccg cac acc ctt aaa aac cct 296  
 Lys Lys Gln Val Leu Glu Lys Asn His Pro His Thr Leu Lys Asn Pro  
 70 75 80

ttt tca aac ctt aca agc cat ttt tta tac cag cct ttt ggc tca caa 344  
 Phe Ser Asn Leu Thr Ser His Phe Leu Tyr Gln Pro Phe Gly Ser Gln  
 85 90 95

aat tac cct gat ttt ttg gtt ttt att ttt gac tat gtg gtg ggg att 392  
 Asn Tyr Pro Asp Phe Leu Val Phe Ile Phe Asp Tyr Val Val Gly Ile  
 100 105 110

gaa atc aag ttt tct aaa aac gat aag ggt gaa aaa aat ctt caa aca 440  
 Glu Ile Lys Phe Ser Lys Asn Asp Lys Gly Glu Lys Asn Leu Gln Thr

115	120	125	130	
tct cgc ccc atg tgg aat tca aac ctg cct aaa ccc aat gcg att tat				488
Ser Arg Pro Met Trp Asn Ser Asn Leu Pro Lys Pro Asn Ala Ile Tyr				
	135	140	145	
gtg tat gga gtc gct aat gca aac atc act ttt ttt aaa ggc tca gat				536
Val Tyr Gly Val Ala Asn Ala Asn Ile Thr Phe Phe Lys Gly Ser Asp				
	150	155	160	
att ttg agt tat gaa acc aga gag gtc ttg ctc aag tat ttt gat att				584
Ile Leu Ser Tyr Glu Thr Arg Glu Val Leu Leu Lys Tyr Phe Asp Ile				
	165	170	175	
tta gat aaa gat gaa aga agt ttg aaa aac gcc tta aag gat tta gaa				632
Leu Asp Lys Asp Glu Arg Ser Leu Lys Asn Ala Leu Lys Asp Leu Glu				
	180	185	190	
aac cct ttt ggg ttt gcc ccc tac atc aga aaa gct tat gag cat aaa				680
Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu His Lys				
	195	200	205	210
agg aat ttt cta acc acc acc aga ttg aaa gct tct ttt cgc cca acc				728
Arg Asn Phe Leu Thr Thr Thr Arg Leu Lys Ala Ser Phe Arg Pro Thr				
	215	220	225	
aca ttt taagagagcg gaatgtcttg gaatttttga aaacgctcac tcattagcgt				784
Thr Phe				
att				787
<210> 162				
<211> 228				
<212> PRT				
<213> Helicobacter pylori				
<400> 162				
Met Leu Glu Lys Val Phe Gln Glu Ile Thr Asn Lys Arg Lys Phe Phe				
1 5 10 15				
Ala Ser Ser Ser Thr Gly Glu Gln Phe Glu Asn Gln Phe Arg Asn Glu				
	20	25	30	
Leu Lys Lys His Phe Ser Glu Ile Asn Gly Asp Leu Thr Glu Glu Leu				
	35	40	45	
Ser His Ile Glu Glu Lys Pro Asn Lys Glu Ile Lys Thr Thr Phe Asn				
	50	55	60	
Gln Leu Lys Lys Gln Val Leu Glu Lys Asn His Pro His Thr Leu Lys				
65 70 75 80				
Asn Pro Phe Ser Asn Leu Thr Ser His Phe Leu Tyr Gln Pro Phe Gly				
	85	90	95	
Ser Gln Asn Tyr Pro Asp Phe Leu Val Phe Ile Phe Asp Tyr Val Val				
	100	105	110	
Gly Ile Glu Ile Lys Phe Ser Lys Asn Asp Lys Gly Glu Lys Asn Leu				
	115	120	125	
Gln Thr Ser Arg Pro Met Trp Asn Ser Asn Leu Pro Lys Pro Asn Ala				

130	135	140
Ile Tyr Val Tyr Gly Val Ala Asn Ala Asn Ile Thr Phe Phe Lys Gly		
145	150	155
Ser Asp Ile Leu Ser Tyr Glu Thr Arg Glu Val Leu Leu Lys Tyr Phe		
	165	170
Asp Ile Leu Asp Lys Asp Glu Arg Ser Leu Lys Asn Ala Leu Lys Asp		
	180	185
Leu Glu Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu		
	195	200
His Lys Arg Asn Phe Leu Thr Thr Thr Arg Leu Lys Ala Ser Phe Arg		
	210	215
Pro Thr Thr Phe		220
225		

<210> 163  
 <211> 540  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (53)...(493)

<400> 163  
 ccaaaccctt ttgaaacact tgctcactaa cccattataa gccgcaaaaa cc atg ctc 58  
Met Leu  
1

tct tta aaa caa gat tcc ttt ttt ttc tta tgt tta gga atc ctg ggg	106
Ser Leu Lys Gln Asp Ser Phe Phe Leu Cys Leu Gly Ile Leu Gly	
5 10 15	
ttt tat ttt tat agc ctt ttg agg gat tta atg cct ttt tta ccc cca	154
Phe Tyr Phe Tyr Ser Leu Leu Arg Asp Leu Met Pro Phe Leu Pro Pro	
20 25 30	
atg att ggg ttt tta ttc ttg ttt tat gcg aaa aaa tac gat cat ttt	202
Met Ile Gly Phe Leu Phe Leu Phe Tyr Ala Lys Lys Tyr Asp His Phe	
35 40 45 50	
tta ccc agt ttg agc gtg ttt ggt tgt ttg ttt tgg ttt gag agc atg	250
Leu Pro Ser Leu Ser Val Phe Gly Cys Leu Phe Trp Phe Glu Ser Met	
55 60 65	
cat tta aag act tta ggc gtt tta gct tta ttg ttt tta atc tac cat	298
His Leu Lys Thr Leu Gly Val Leu Ala Leu Leu Phe Leu Ile Tyr His	
70 75 80	
caa atc gcc tat aaa aac tct tta aag ctt ttt aat gac ggc ttt tta	346
Gln Ile Ala Tyr Lys Asn Ser Leu Lys Leu Phe Asn Asp Gly Phe Leu	
85 90 95	
ttc aaa act ttg cat gtt ttt ttg gtt tat tac ctt tat tta tcg cgc	394
Phe Lys Thr Leu His Val Phe Leu Val Tyr Tyr Leu Tyr Leu Ser Arg	



100	105	110	
ttt ttt tcg atg tct ttg agt ttg aaa ata ctc ggc ttt ctc gct ctt			442
Phe Phe Ser Met Ser Leu Ser Leu Lys Ile Leu Gly Phe Leu Ala Leu			
115	120	125	130
ttt gct tta ata gaa agc gct ttg tgg ggt ttg tat gaa aaa tct tcg			490
Phe Ala Leu Ile Glu Ser Ala Leu Trp Gly Leu Tyr Glu Lys Ser Ser			
	135	140	145
cta taagcttttg ctctttgttt ttataggggtt ttgggggtta ctagcct			540
Leu			

<210> 164  
 <211> 147  
 <212> PRT  
 <213> Helicobacter pylori

<400> 164

Met Leu Ser Leu Lys Gln Asp Ser Phe Phe Phe Leu Cys Leu Gly Ile			
1	5	10	15
Leu Gly Phe Tyr Phe Tyr Ser Leu Leu Arg Asp Leu Met Pro Phe Leu			
	20	25	30
Pro Pro Met Ile Gly Phe Leu Phe Leu Phe Tyr Ala Lys Lys Tyr Asp			
	35	40	45
His Phe Leu Pro Ser Leu Ser Val Phe Gly Cys Leu Phe Trp Phe Glu			
	50	55	60
Ser Met His Leu Lys Thr Leu Gly Val Leu Ala Leu Leu Phe Leu Ile			
65	70	75	80
Tyr His Gln Ile Ala Tyr Lys Asn Ser Leu Lys Leu Phe Asn Asp Gly			
	85	90	95
Phe Leu Phe Lys Thr Leu His Val Phe Leu Val Tyr Tyr Leu Tyr Leu			
	100	105	110
Ser Arg Phe Phe Ser Met Ser Leu Ser Leu Lys Ile Leu Gly Phe Leu			
	115	120	125
Ala Leu Phe Ala Leu Ile Glu Ser Ala Leu Trp Gly Leu Tyr Glu Lys			
	130	135	140
Ser Ser Leu			
145			

<210> 165  
 <211> 1888  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1835)

<400> 165

cactaaagtc aatccaagcg caagttggat gaaaaaataa gaaggaagtt atg aaa	56
	Met Lys

aag tca ttc aaa aaa tta ggc ttt gtc tct tta gcg gct agt ggc gtg	104
Lys Ser Phe Lys Lys Leu Gly Phe Val Ser Leu Ala Ala Ser Gly Val	
5 10 15	
ctt tta ggg agc atg aac gct acc gat tta gaa acc tac gca gca ttg	152
Leu Leu Gly Ser Met Asn Ala Thr Asp Leu Glu Thr Tyr Ala Ala Leu	
20 25 30	
caa aaa tca tcg cat gtt ttt ggt aat tat gct gaa aag gat aag gat	200
Gln Lys Ser Ser His Val Phe Gly Asn Tyr Ala Glu Lys Asp Lys Asp	
35 40 45 50	
agt aaa tta aca agc gat tca cca acg caa caa caa gat caa aaa gta	248
Ser Lys Leu Thr Ser Asp Ser Pro Thr Gln Gln Gln Asp Gln Lys Val	
55 60 65	
gcc caa aac acc gct tca aac gac agc caa gaa gcg aca aca ctt gaa	296
Ala Gln Asn Thr Ala Ser Asn Asp Ser Gln Glu Ala Thr Thr Leu Glu	
70 75 80	
aac acc gct tct act gac aac aca acc gcc aca act gat gaa act tat	344
Asn Thr Ala Ser Thr Asp Asn Thr Thr Ala Thr Thr Asp Glu Thr Tyr	
85 90 95	
aca aaa agc act gac act act gta gct ggt gcg gct caa aaa gta gaa	392
Thr Lys Ser Thr Asp Thr Thr Val Ala Gly Ala Ala Gln Lys Val Glu	
100 105 110	
acc gat aac aca gcc gtt caa agc gct gaa caa act tta aaa aca gat	440
Thr Asp Asn Thr Ala Val Gln Ser Ala Glu Gln Thr Leu Lys Thr Asp	
115 120 125 130	
gta gct aaa gtt caa gct gat gct agt gct aaa gat ttt gat gaa acc	488
Val Ala Lys Val Gln Ala Asp Ala Ser Ala Lys Asp Phe Asp Glu Thr	
135 140 145	
act ttt caa gcc gat caa gca gca gag caa acc gct gaa aaa gct tta	536
Thr Phe Gln Ala Asp Gln Ala Ala Glu Gln Thr Ala Glu Lys Ala Leu	
150 155 160	
caa cag gct gag agc aaa ctc aac acc gat caa cag act tta aac aca	584
Gln Gln Ala Glu Ser Lys Leu Asn Thr Asp Gln Gln Thr Leu Asn Thr	
165 170 175	
gcg tta caa gat cag acg aaa aca cca acc cca tca acc cca cca act	632
Ala Leu Gln Asp Gln Thr Lys Thr Pro Thr Pro Ser Thr Pro Pro Thr	
180 185 190	
aaa gag gaa cca aaa cac acc gct tca agc ggc aca cca cca gct cca	680
Lys Glu Glu Pro Lys His Thr Ala Ser Ser Gly Thr Pro Pro Ala Pro	
195 200 205 210	
gaa agc cca cca gct aaa aaa gat gaa aca agt ggc aca cca agt gct	728

Glu	Ser	Pro	Pro	Ala	Lys	Lys	Asp	Glu	Thr	Ser	Gly	Thr	Pro	Ser	Ala	
				215					220						225	
agt	ggg	agt	tct	gtg	gca	agc	cag	cta	acc	aaa	gat	acc	act	atg	gtt	776
Ser	Gly	Ser	Ser	Val	Ala	Ser	Gln	Leu	Thr	Lys	Asp	Thr	Thr	Met	Val	
			230					235					240			
aat	aat	ctt	aag	agt	gtg	agc	gtg	agc	gcg	atg	aac	acc	act	tta	agt	824
Asn	Asn	Leu	Lys	Ser	Val	Ser	Val	Ser	Ala	Met	Asn	Thr	Thr	Leu	Ser	
		245					250					255				
gga	gta	gaa	acc	atg	tct	caa	caa	act	gca	acg	att	ggc	aac	ctt	ttg	872
Gly	Val	Glu	Thr	Met	Ser	Gln	Gln	Thr	Ala	Thr	Ile	Gly	Asn	Leu	Leu	
	260					265					270					
aat	agt	agc	acc	gat	tta	agc	agt	gtg	att	ccc	aac	gct	caa	ggg	cta	920
Asn	Ser	Ser	Thr	Asp	Leu	Ser	Ser	Val	Ile	Pro	Asn	Ala	Gln	Gly	Leu	
	275				280					285					290	
aac	agc	gcg	ttt	agc	aca	tta	gaa	agc	gct	caa	aac	act	cta	aaa	ggc	968
Asn	Ser	Ala	Phe	Ser	Thr	Leu	Glu	Ser	Ala	Gln	Asn	Thr	Leu	Lys	Gly	
			295						300					305		
tat	tta	aat	tct	tct	agc	gcg	acg	att	ggg	caa	ttg	aca	aac	gga	tct	1016
Tyr	Leu	Asn	Ser	Ser	Ser	Ala	Thr	Ile	Gly	Gln	Leu	Thr	Asn	Gly	Ser	
			310					315					320			
aat	gcg	gtt	gtg	ggc	gcg	tta	gat	aaa	gct	atc	aat	caa	gtg	gat	atg	1064
Asn	Ala	Val	Val	Gly	Ala	Leu	Asp	Lys	Ala	Ile	Asn	Gln	Val	Asp	Met	
		325					330					335				
gct	ttg	gcc	gat	ctt	agt	gca	gct	gat	acg	caa	aaa	acg	caa	gcc	gtt	1112
Ala	Leu	Ala	Asp	Leu	Ser	Ala	Ala	Asp	Thr	Gln	Lys	Thr	Gln	Ala	Val	
	340					345					350					
acg	ctt	gca	act	gct	agt	gat	agt	cca	acg	aca	acg	aca	gat	gcc	atc	1160
Thr	Leu	Ala	Thr	Ala	Ser	Asp	Ser	Pro	Thr	Thr	Thr	Thr	Asp	Ala	Ile	
	355				360				365						370	
aat	ttc	tta	aac	gcg	cta	aaa	agc	aat	cta	atg	gct	caa	aaa	gac	gct	1208
Asn	Phe	Leu	Asn	Ala	Leu	Lys	Ser	Asn	Leu	Met	Ala	Gln	Lys	Asp	Ala	
				375					380					385		
ttt	ttg	aat	gtg	cat	aaa	aac	att	caa	acc	gct	gtc	gct	caa	gcc	cag	1256
Phe	Leu	Asn	Val	His	Lys	Asn	Ile	Gln	Thr	Ala	Val	Ala	Gln	Ala	Gln	
			390					395					400			
gaa	acc	tac	acg	cca	agc	gtg	atc	aac	acc	aat	aat	tac	ggg	caa	atg	1304
Glu	Thr	Tyr	Thr	Pro	Ser	Val	Ile	Asn	Thr	Asn	Asn	Tyr	Gly	Gln	Met	
		405					410					415				
tat	ggg	gta	gat	gcg	atg	gca	ggg	tat	aag	tgg	ttc	ttt	ggc	aaa	acc	1352
Tyr	Gly	Val	Asp	Ala	Met	Ala	Gly	Tyr	Lys	Trp	Phe	Phe	Gly	Lys	Thr	
	420					425					430					

aaa cgc ttt ggc ttt agg tct tat gga tac tac agc tat aac cat gcg	1400
Lys Arg Phe Gly Phe Arg Ser Tyr Gly Tyr Tyr Ser Tyr Asn His Ala	
435 440 445 450	
aat tta agc ttt gtg ggg agc cag ctt gga atc atg gag ggc gcg tct	1448
Asn Leu Ser Phe Val Gly Ser Gln Leu Gly Ile Met Glu Gly Ala Ser	
455 460 465	
caa gtg aat aac ttc act tat ggc gtg ggc ttt gat gtg ctc tat aac	1496
Gln Val Asn Asn Phe Thr Tyr Gly Val Gly Phe Asp Val Leu Tyr Asn	
470 475 480	
ttc tat gaa agc aaa gag ggc tat aac aca gca ggg ttg ttc tta ggc	1544
Phe Tyr Glu Ser Lys Glu Gly Tyr Asn Thr Ala Gly Leu Phe Leu Gly	
485 490 495	
ttt ggg tta gga ggg gat tgc ttt atc gtt caa gga gag agc tac ttg	1592
Phe Gly Leu Gly Gly Asp Ser Phe Ile Val Gln Gly Glu Ser Tyr Leu	
500 505 510	
aaa tct caa atg cac att tgc aac aac acc gcc ggc tgt tca gcg agc	1640
Lys Ser Gln Met His Ile Cys Asn Asn Thr Ala Gly Cys Ser Ala Ser	
515 520 525 530	
atg aac aca agc tac ttc caa atg cct gtt gaa ttt ggt ttt agg agc	1688
Met Asn Thr Ser Tyr Phe Gln Met Pro Val Glu Phe Gly Phe Arg Ser	
535 540 545	
aat ttc tct aaa cac agc ggg att gaa gtg ggc ttt aaa ttg cct tta	1736
Asn Phe Ser Lys His Ser Gly Ile Glu Val Gly Phe Lys Leu Pro Leu	
550 555 560	
ttc acc aac caa ttc tat aaa gaa agg ggc gta gat gga tgc gta gat	1784
Phe Thr Asn Gln Phe Tyr Lys Glu Arg Gly Val Asp Gly Ser Val Asp	
565 570 575	
gtg ttc tat aaa agg aat ttc tct att tat ttt aac tac atg atc aac	1832
Val Phe Tyr Lys Arg Asn Phe Ser Ile Tyr Phe Asn Tyr Met Ile Asn	
580 585 590	
ttc taagcctttc tattctttcc aatagagggt tttctctctg ttggtttctt	1885
Phe	
595	
ttt	1888
<210> 166	
<211> 595	
<212> PRT	
<213> Helicobacter pylori	
<400> 166	
Met Lys Lys Ser Phe Lys Lys Leu Gly Phe Val Ser Leu Ala Ala Ser	
1 5 10 15	
Gly Val Leu Leu Gly Ser Met Asn Ala Thr Asp Leu Glu Thr Tyr Ala	

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Ala Ser Gln Val Asn Asn Phe Thr Tyr Gly Val Gly Phe Asp Val Leu  
465 470 475 480  
Tyr Asn Phe Tyr Glu Ser Lys Glu Gly Tyr Asn Thr Ala Gly Leu Phe  
485 490 495  
Leu Gly Phe Gly Leu Gly Gly Asp Ser Phe Ile Val Gln Gly Glu Ser  
500 505 510  
Tyr Leu Lys Ser Gln Met His Ile Cys Asn Asn Thr Ala Gly Cys Ser  
515 520 525  
Ala Ser Met Asn Thr Ser Tyr Phe Gln Met Pro Val Glu Phe Gly Phe  
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Arg Ser Asn Phe Ser Lys His Ser Gly Ile Glu Val Gly Phe Lys Leu  
545 550 555 560  
Pro Leu Phe Thr Asn Gln Phe Tyr Lys Glu Arg Gly Val Asp Gly Ser  
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Ile Asn Phe  
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Leu Val Val Phe Leu Phe Leu Phe Val Gly Cys Thr Lys Lys Asp Phe  
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acg ctc aaa gat tta tcc ttg ccc caa gag gct tca agc tat ctt gca 153  
Thr Leu Lys Asp Leu Ser Leu Pro Gln Glu Ala Ser Ser Tyr Leu Ala  
25 30 35

tct caa aat ggc agt aac aac aac caa agc att gac ccc caa gcg tta 201  
Ser Gln Asn Gly Ser Asn Asn Asn Gln Ser Ile Asp Pro Gln Ala Leu  
40 45 50

aga gaa aat ctg aaa gag agc tat ctc aaa gcg tgg tat tcc cca tgg 249  
Arg Glu Asn Leu Lys Glu Ser Tyr Leu Lys Ala Trp Tyr Ser Pro Trp  
55 60 65

cta gat atg aaa gtc aaa agc aat aaa aaa gaa gtg ttt tgg atc ctt 297  
Leu Asp Met Lys Val Lys Ser Asn Lys Lys Glu Val Phe Trp Ile Leu  
70 75 80

aag gag atg aat aaa tcc acc ggt tat ggc gaa gat cta aaa ccc aac 345

Lys	Glu	Met	Asn	Lys	Ser	Thr	Gly	Tyr	Gly	Glu	Asp	Leu	Lys	Pro	Asn		
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Ala	Lys	Ala	Phe	Asn	Asp	Ala	Leu	Ile	Lys	Ser	Met	Asp	Ile	Glu	His		
				105					110					115			
tac	cct	agc	gtt	aag	att	agg	gct	gtt	gta	gcg	cga	gat	agc	gat	gtg	441	
Tyr	Pro	Ser	Val	Lys	Ile	Arg	Ala	Val	Val	Ala	Arg	Asp	Ser	Asp	Val		
			120					125					130				
agg	gct	gtg	cct	act	aac	aaa	cct	tat	tat	ctt	tct	caa	aaa	ggc	tat	489	
Arg	Ala	Val	Pro	Thr	Asn	Lys	Pro	Tyr	Tyr	Leu	Ser	Gln	Lys	Gly	Tyr		
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cct	ttt	gat	agg	tat	caa	aat	tcg	ctg	att	ttt	caa	ggc	acg	ccg	gtt	537	
Pro	Phe	Asp	Arg	Tyr	Gln	Asn	Ser	Leu	Ile	Phe	Gln	Gly	Thr	Pro	Val		
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Leu	Ile	Thr	His	Phe	Asn	Leu	Asp	Lys	Thr	Tyr	Ala	His	Ile	Gln	Ser		
165					170					175					180		
agt	ttt	gtt	tat	ggc	tgg	atc	aaa	gtt	agc	gat	tta	gtc	tac	atg	cac	633	
Ser	Phe	Val	Tyr	Gly	Trp	Ile	Lys	Val	Ser	Asp	Leu	Val	Tyr	Met	His		
				185					190					195			
gat	aaa	gac	ata	gag	ctt	tta	acc	cat	ctt	aaa	gat	tat	gtc	atg	cct	681	
Asp	Lys	Asp	Ile	Glu	Leu	Leu	Thr	His	Leu	Lys	Asp	Tyr	Val	Met	Pro		
			200					205					210				
ata	aaa	gat	aaa	atc	ccc	ctt	tat	aca	gac	tat	ggg	gat	ttt	tac	acc	729	
Ile	Lys	Asp	Lys	Ile	Pro	Leu	Tyr	Thr	Asp	Tyr	Gly	Asp	Phe	Tyr	Thr		
		215					220					225					
aac	gcc	aga	gtg	ggc	gaa	ttg	ttc	gct	ctc	atc	ccc	caa	agt	caa	aaa	777	
Asn	Ala	Arg	Val	Gly	Glu	Leu	Phe	Ala	Leu	Ile	Pro	Gln	Ser	Gln	Lys		
	230					235					240						
aca	cct	caa	aaa	ccc	caa	aaa	aag	gaa	ttg	aaa	gcc	tat	ggc	ttt	ttg	825	
Thr	Pro	Gln	Lys	Pro	Gln	Lys	Lys	Glu	Leu	Lys	Ala	Tyr	Gly	Phe	Leu		
245					250					255					260		
aga	gac	gct	aag	ggc	tat	gca	gct	tta	caa	agc	gtg	atc	tta	gaa	gaa	873	
Arg	Asp	Ala	Lys	Gly	Tyr	Ala	Ala	Leu	Gln	Ser	Val	Ile	Leu	Glu	Glu		
				265				270					275				
aag	gat	ttt	ttt	gtt	ttc	cct	aag	gct	ttt	aac	agc	gag	aac	atg	gcg	921	
Lys	Asp	Phe	Phe	Val	Phe	Pro	Lys	Ala	Phe	Asn	Ser	Glu	Asn	Met	Ala		
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tat	ttt	ata	gac	acc	atg	tta	ggg	caa	aaa	tac	ggc	tggt	ggc	ggg	cta	969	
Tyr	Phe	Ile	Asp	Thr	Met	Leu	Gly	Gln	Lys	Tyr	Gly	Trp	Gly	Gly	Leu		
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Leu Gly Asn Arg Asp Cys Ser Ala Phe Thr Arg Asp Ser Phe Ala Asn	
310 315 320	
ttt ggt att ttg ctc ccc aga aat tcc tat gcg caa agc cgt tat gcg	1065
Phe Gly Ile Leu Leu Pro Arg Asn Ser Tyr Ala Gln Ser Arg Tyr Ala	
325 330 335 340	
aac aat tat gtg gat tta agc tct atg aaa gcc aaa gaa aaa gaa gac	1113
Asn Asn Tyr Val Asp Leu Ser Ser Met Lys Ala Lys Glu Lys Glu Asp	
345 350 355	
tac atc ctt aaa aac gcc acg cct ttt gga acg ctc atc tat tta aaa	1161
Tyr Ile Leu Lys Asn Ala Thr Pro Phe Gly Thr Leu Ile Tyr Leu Lys	
360 365 370	
ggg cat atc atg ctt tat tta ggc gca cac aac cat caa gcg ata gtc	1209
Gly His Ile Met Leu Tyr Leu Gly Ala His Asn His Gln Ala Ile Val	
375 380 385	
gct cac agc att tgg tcg gtg caa acc caa aag cat ttt aaa acc ttg	1257
Ala His Ser Ile Trp Ser Val Gln Thr Gln Lys His Phe Lys Thr Leu	
390 395 400	
agc cat aaa ata gga ggc gtg gtg atc act tcg tta tgg tta gct gaa	1305
Ser His Lys Ile Gly Gly Val Val Ile Thr Ser Leu Trp Leu Ala Glu	
405 410 415 420	
gag cat aat ggg gcg ttt tct aaa aag aaa tta ttg att gat agg gtg	1353
Glu His Asn Gly Ala Phe Ser Lys Lys Lys Leu Leu Ile Asp Arg Val	
425 430 435	
ctt gga atg agc gat ttg aaa gat ttt gtc aat aaa act tca agc cct	1401
Leu Gly Met Ser Asp Leu Lys Asp Phe Val Asn Lys Thr Ser Ser Pro	
440 445 450	
tta aat gcg aat tga tttttcttata ttatgattac gattttatcaa tttaaaacat	1456
Leu Asn Ala Asn *	
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<212> PRT

<213> Helicobacter pylori

<400> 168

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Ser Tyr Leu Ala Ser Ser Gln Asn Gly Ser Asn Asn Asn Gln Ser Ile	
35 40 45	
Asp Pro Gln Ala Leu Arg Glu Asn Leu Lys Glu Ser Tyr Leu Lys Ala	



50					55					60					
Trp	Tyr	Ser	Pro	Trp	Leu	Asp	Met	Lys	Val	Lys	Ser	Asn	Lys	Lys	Glu
65					70					75					80
Val	Phe	Trp	Ile	Leu	Lys	Glu	Met	Asn	Lys	Ser	Thr	Gly	Tyr	Gly	Glu
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Asp	Leu	Lys	Pro	Asn	Ala	Lys	Ala	Phe	Asn	Asp	Ala	Leu	Ile	Lys	Ser
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Met	Asp	Ile	Glu	His	Tyr	Pro	Ser	Val	Lys	Ile	Arg	Ala	Val	Val	Ala
	115						120					125			
Arg	Asp	Ser	Asp	Val	Arg	Ala	Val	Pro	Thr	Asn	Lys	Pro	Tyr	Tyr	Leu
	130					135					140				
Ser	Gln	Lys	Gly	Tyr	Pro	Phe	Asp	Arg	Tyr	Gln	Asn	Ser	Leu	Ile	Phe
145					150					155					160
Gln	Gly	Thr	Pro	Val	Leu	Ile	Thr	His	Phe	Asn	Leu	Asp	Lys	Thr	Tyr
			165						170						175
Ala	His	Ile	Gln	Ser	Ser	Phe	Val	Tyr	Gly	Trp	Ile	Lys	Val	Ser	Asp
			180					185					190		
Leu	Val	Tyr	Met	His	Asp	Lys	Asp	Ile	Glu	Leu	Leu	Thr	His	Leu	Lys
	195						200					205			
Asp	Tyr	Val	Met	Pro	Ile	Lys	Asp	Lys	Ile	Pro	Leu	Tyr	Thr	Asp	Tyr
	210					215					220				
Gly	Asp	Phe	Tyr	Thr	Asn	Ala	Arg	Val	Gly	Glu	Leu	Phe	Ala	Leu	Ile
225					230					235					240
Pro	Gln	Ser	Gln	Lys	Thr	Pro	Gln	Lys	Pro	Gln	Lys	Lys	Glu	Leu	Lys
			245						250					255	
Ala	Tyr	Gly	Phe	Leu	Arg	Asp	Ala	Lys	Gly	Tyr	Ala	Ala	Leu	Gln	Ser
		260					265						270		
Val	Ile	Leu	Glu	Glu	Lys	Asp	Phe	Phe	Val	Phe	Pro	Lys	Ala	Phe	Asn
	275						280					285			
Ser	Glu	Asn	Met	Ala	Tyr	Phe	Ile	Asp	Thr	Met	Leu	Gly	Gln	Lys	Tyr
	290					295					300				
Gly	Trp	Gly	Gly	Leu	Leu	Gly	Asn	Arg	Asp	Cys	Ser	Ala	Phe	Thr	Arg
305				310					315						320
Asp	Ser	Phe	Ala	Asn	Phe	Gly	Ile	Leu	Leu	Pro	Arg	Asn	Ser	Tyr	Ala
			325						330					335	
Gln	Ser	Arg	Tyr	Ala	Asn	Asn	Tyr	Val	Asp	Leu	Ser	Ser	Met	Lys	Ala
		340					345						350		
Lys	Glu	Lys	Glu	Asp	Tyr	Ile	Leu	Lys	Asn	Ala	Thr	Pro	Phe	Gly	Thr
	355						360					365			
Leu	Ile	Tyr	Leu	Lys	Gly	His	Ile	Met	Leu	Tyr	Leu	Gly	Ala	His	Asn
	370				375					380					
His	Gln	Ala	Ile	Val	Ala	His	Ser	Ile	Trp	Ser	Val	Gln	Thr	Gln	Lys
385				390					395						400
His	Phe	Lys	Thr	Leu	Ser	His	Lys	Ile	Gly	Gly	Val	Val	Ile	Thr	Ser
		405							410					415	
Leu	Trp	Leu	Ala	Glu	Glu	His	Asn	Gly	Ala	Phe	Ser	Lys	Lys	Lys	Leu
	420						425						430		
Leu	Ile	Asp	Arg	Val	Leu	Gly	Met	Ser	Asp	Leu	Lys	Asp	Phe	Val	Asn
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Lys	Thr	Ser	Ser	Pro	Leu	Asn	Ala	Asn							
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Ile Ser Leu Leu Ala Val Ile Leu Ala Leu Leu Phe Val Ala Cys His  
5 10 15  
  
gaa act aaa aaa caa atc tta caa aac gaa gcc gat agc acc cct tca 152  
Glu Thr Lys Lys Gln Ile Leu Gln Asn Glu Ala Asp Ser Thr Pro Ser  
20 25 30  
  
gaa aaa acc att tgg caa cct gaa caa aaa taaaaattgt aaaaatactc 202  
Glu Lys Thr Ile Trp Gln Pro Glu Gln Lys  
35 40  
  
aaaggcatttt tttaaaataa acgcaataaa aaa 235

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Pro Ser Glu Lys Thr Ile Trp Gln Pro Glu Gln Lys  
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<222> (51)...(1298)

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tat ttt tta gaa caa acg gat agt gaa att ttt gag ctt atc ttt gaa 104

Tyr	Phe	Leu	Glu	Gln	Thr	Asp	Ser	Glu	Ile	Phe	Glu	Leu	Ile	Phe	Glu		
		5					10					15					
gaa	tac	aag	cgg	caa	aat	gag	cat	tta	gaa	atg	ata	gcg	agc	gag	aat	152	
Glu	Tyr	Lys	Arg	Gln	Asn	Glu	His	Leu	Glu	Met	Ile	Ala	Ser	Glu	Asn		
	20					25					30						
tac	act	ttt	gca	agc	gtt	atg	gag	gct	atg	ggg	agt	gtt	tta	acg	aat	200	
Tyr	Thr	Phe	Ala	Ser	Val	Met	Glu	Ala	Met	Gly	Ser	Val	Leu	Thr	Asn		
	35				40				45						50		
aaa	tac	gct	gaa	ggc	tac	cct	aac	aag	cgc	tat	tat	gga	ggc	tgt	gaa	248	
Lys	Tyr	Ala	Glu	Gly	Tyr	Pro	Asn	Lys	Arg	Tyr	Tyr	Gly	Gly	Cys	Glu		
				55					60					65			
gtg	gtg	gat	aaa	ata	gaa	agc	cta	gcc	ata	gaa	agg	gct	aaa	aag	ctt	296	
Val	Val	Asp	Lys	Ile	Glu	Ser	Leu	Ala	Ile	Glu	Arg	Ala	Lys	Lys	Leu		
			70					75					80				
ttt	aat	tgc	cag	ttc	gct	aac	gtg	caa	gcg	cat	tca	ggc	tca	caa	gcc	344	
Phe	Asn	Cys	Gln	Phe	Ala	Asn	Val	Gln	Ala	His	Ser	Gly	Ser	Gln	Ala		
	85						90					95					
aat	aac	gct	gtc	tat	cac	gct	ctt	tta	aag	cct	tat	gac	aag	att	tta	392	
Asn	Asn	Ala	Val	Tyr	His	Ala	Leu	Leu	Lys	Pro	Tyr	Asp	Lys	Ile	Leu		
	100					105					110						
ggc	atg	gat	tta	agc	tgt	gga	ggg	cat	tta	acg	cat	ggc	gct	aaa	gtg	440	
Gly	Met	Asp	Leu	Ser	Cys	Gly	Gly	His	Leu	Thr	His	Gly	Ala	Lys	Val		
	115				120					125				130			
agt	tta	acc	ggc	aag	cat	tat	cag	agc	ttt	tct	tat	ggc	gtg	aat	ttg	488	
Ser	Leu	Thr	Gly	Lys	His	Tyr	Gln	Ser	Phe	Ser	Tyr	Gly	Val	Asn	Leu		
			135					140						145			
gat	ggc	tat	att	gat	tat	gaa	gag	gcg	cta	aaa	atc	gct	caa	agc	gtt	536	
Asp	Gly	Tyr	Ile	Asp	Tyr	Glu	Glu	Ala	Leu	Lys	Ile	Ala	Gln	Ser	Val		
			150					155					160				
aag	cca	gaa	atc	atc	gtg	tgc	ggg	ttt	tca	gcc	tat	cca	agg	gag	att	584	
Lys	Pro	Glu	Ile	Ile	Val	Cys	Gly	Phe	Ser	Ala	Tyr	Pro	Arg	Glu	Ile		
		165					170					175					
gat	ttt	aag	aaa	ttt	aga	gaa	atc	gct	gat	gaa	gtg	ggg	gcg	tta	cta	632	
Asp	Phe	Lys	Lys	Phe	Arg	Glu	Ile	Ala	Asp	Glu	Val	Gly	Ala	Leu	Leu		
	180					185					190						
tta	ggc	gat	ata	gcc	cat	gtg	gca	ggg	ctt	gtg	gta	acc	ggt	gag	cat	680	
Leu	Gly	Asp	Ile	Ala	His	Val	Ala	Gly	Leu	Val	Val	Thr	Gly	Glu	His		
	195				200				205					210			
gcc	cat	cct	ttc	ccg	cat	tgc	cat	gtg	gtt	tca	agc	acc	act	cat	aag	728	
Ala	His	Pro	Phe	Pro	His	Cys	His	Val	Val	Ser	Ser	Thr	Thr	His	Lys		
				215					220					225			

acc tta aga ggg cct aga ggg ggg att att tta act aat gat gaa gag	776
Thr Leu Arg Gly Pro Arg Gly Gly Ile Ile Leu Thr Asn Asp Glu Glu	
230 235 240	
ata gcg gct aag att gac aaa gcg att ttt cca gga act caa ggc ggg	824
Ile Ala Ala Lys Ile Asp Lys Ala Ile Phe Pro Gly Thr Gln Gly Gly	
245 250 255	
cct ttg atg cat gtg att gct gct aaa gcg gtg ggt ttt aaa gag aat	872
Pro Leu Met His Val Ile Ala Ala Lys Ala Val Gly Phe Lys Glu Asn	
260 265 270	
cta aaa cca gaa ttt aaa gct tat gca caa tta gtg aaa tct aac atg	920
Leu Lys Pro Glu Phe Lys Ala Tyr Ala Gln Leu Val Lys Ser Asn Met	
275 280 285 290	
caa gtt ttg gct aaa gcg tta aaa gaa aaa aac cat aag tta gtg agt	968
Gln Val Leu Ala Lys Ala Leu Lys Glu Lys Asn His Lys Leu Val Ser	
295 300 305	
ggt ggc act tct aac cat ttg ctt tta atg gat ttt tta gat aag cct	1016
Gly Gly Thr Ser Asn His Leu Leu Leu Met Asp Phe Leu Asp Lys Pro	
310 315 320	
tat agc ggg aaa gac gct gat att gca tta ggg aat gcc gga atc acc	1064
Tyr Ser Gly Lys Asp Ala Asp Ile Ala Leu Gly Asn Ala Gly Ile Thr	
325 330 335	
gtg aat aaa aac acc att cct ggt gaa acg cgc agc cct ttt gta acg	1112
Val Asn Lys Asn Thr Ile Pro Gly Glu Thr Arg Ser Pro Phe Val Thr	
340 345 350	
agc ggg ata agg att ggc tca gcg gca ttg agc gca agg ggc atg gga	1160
Ser Gly Ile Arg Ile Gly Ser Ala Ala Leu Ser Ala Arg Gly Met Gly	
355 360 365 370	
gct aag gaa ttt gaa atc ata ggg aat aaa ata tca gat att ttg aat	1208
Ala Lys Glu Phe Glu Ile Ile Gly Asn Lys Ile Ser Asp Ile Leu Asn	
375 380 385	
gat att aat aat gtt agt ttg caa ttg cat gtg aaa gaa gaa ttg aaa	1256
Asp Ile Asn Asn Val Ser Leu Gln Leu His Val Lys Glu Glu Leu Lys	
390 395 400	
gcc atg gtc aat caa ttc cct gtg tac cac caa cct att ttt	1298
Ala Met Val Asn Gln Phe Pro Val Tyr His Gln Pro Ile Phe	
405 410 415	
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<213> Helicobacter pylori	

<400> 172

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			20					25					30		
Glu	Asn	Tyr	Thr	Phe	Ala	Ser	Val	Met	Glu	Ala	Met	Gly	Ser	Val	Leu
			35					40					45		
Thr	Asn	Lys	Tyr	Ala	Glu	Gly	Tyr	Pro	Asn	Lys	Arg	Tyr	Tyr	Gly	Gly
			50					55					60		
Cys	Glu	Val	Val	Asp	Lys	Ile	Glu	Ser	Leu	Ala	Ile	Glu	Arg	Ala	Lys
65					70					75					80
Lys	Leu	Phe	Asn	Cys	Gln	Phe	Ala	Asn	Val	Gln	Ala	His	Ser	Gly	Ser
				85					90					95	
Gln	Ala	Asn	Asn	Ala	Val	Tyr	His	Ala	Leu	Leu	Lys	Pro	Tyr	Asp	Lys
				100					105					110	
Ile	Leu	Gly	Met	Asp	Leu	Ser	Cys	Gly	Gly	His	Leu	Thr	His	Gly	Ala
			115					120					125		
Lys	Val	Ser	Leu	Thr	Gly	Lys	His	Tyr	Gln	Ser	Phe	Ser	Tyr	Gly	Val
			130					135					140		
Asn	Leu	Asp	Gly	Tyr	Ile	Asp	Tyr	Glu	Glu	Ala	Leu	Lys	Ile	Ala	Gln
145					150					155					160
Ser	Val	Lys	Pro	Glu	Ile	Ile	Val	Cys	Gly	Phe	Ser	Ala	Tyr	Pro	Arg
				165					170					175	
Glu	Ile	Asp	Phe	Lys	Lys	Phe	Arg	Glu	Ile	Ala	Asp	Glu	Val	Gly	Ala
			180					185					190		
Leu	Leu	Leu	Gly	Asp	Ile	Ala	His	Val	Ala	Gly	Leu	Val	Val	Thr	Gly
			195					200					205		
Glu	His	Ala	His	Pro	Phe	Pro	His	Cys	His	Val	Val	Ser	Ser	Thr	Thr
			210					215					220		
His	Lys	Thr	Leu	Arg	Gly	Pro	Arg	Gly	Gly	Ile	Ile	Leu	Thr	Asn	Asp
225					230					235					240
Glu	Glu	Ile	Ala	Ala	Lys	Ile	Asp	Lys	Ala	Ile	Phe	Pro	Gly	Thr	Gln
				245					250					255	
Gly	Gly	Pro	Leu	Met	His	Val	Ile	Ala	Ala	Lys	Ala	Val	Gly	Phe	Lys
			260					265					270		
Glu	Asn	Leu	Lys	Pro	Glu	Phe	Lys	Ala	Tyr	Ala	Gln	Leu	Val	Lys	Ser
			275					280					285		
Asn	Met	Gln	Val	Leu	Ala	Lys	Ala	Leu	Lys	Glu	Lys	Asn	His	Lys	Leu
			290					295				300			
Val	Ser	Gly	Gly	Thr	Ser	Asn	His	Leu	Leu	Leu	Met	Asp	Phe	Leu	Asp
305					310					315					320
Lys	Pro	Tyr	Ser	Gly	Lys	Asp	Ala	Asp	Ile	Ala	Leu	Gly	Asn	Ala	Gly
				325					330					335	
Ile	Thr	Val	Asn	Lys	Asn	Thr	Ile	Pro	Gly	Glu	Thr	Arg	Ser	Pro	Phe
			340					345					350		
Val	Thr	Ser	Gly	Ile	Arg	Ile	Gly	Ser	Ala	Ala	Leu	Ser	Ala	Arg	Gly
			355					360					365		
Met	Gly	Ala	Lys	Glu	Phe	Glu	Ile	Ile	Gly	Asn	Lys	Ile	Ser	Asp	Ile
			370					375				380			
Leu	Asn	Asp	Ile	Asn	Asn	Val	Ser	Leu	Gln	Leu	His	Val	Lys	Glu	Glu
385					390					395					400
Leu	Lys	Ala	Met	Val	Asn	Gln	Phe	Pro	Val	Tyr	His	Gln	Pro	Ile	Phe
				405					410					415	

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<210> 173
<211> 1513
<212> DNA
<213> Helicobacter pylori
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<400> 173

Gln	Asn	Asn	Asn	Glu	Gln	Leu	Tyr	Glu	Asn	Ile	Met	Lys	Val	Met	Leu		
		165					170					175					
tta	ggc	gcg	ggc	ggg	act	aat	ggg	gcg	tat	aat	ggc	gtg	agt	gtg	ggc	632	
Leu	Gly	Ala	Gly	Gly	Thr	Asn	Gly	Ala	Tyr	Asn	Gly	Val	Ser	Val	Gly		
	180					185					190						
gac	att	gcc	acg	ggc	atg	caa	aat	ttt	tct	tcg	caa	acg	ggc	ttg	ata	680	
Asp	Ile	Ala	Thr	Gly	Met	Gln	Asn	Phe	Ser	Ser	Gln	Thr	Gly	Leu	Ile		
195					200					205					210		
ggg	gct	aat	tct	acg	gtt	agc	gag	ctg	aat	gct	ttg	att	aag	agc	ggg	728	
Gly	Ala	Asn	Ser	Thr	Val	Ser	Glu	Leu	Asn	Ala	Leu	Ile	Lys	Ser	Gly		
				215				220						225			
att	tct	ttg	gat	cgt	gag	act	ttg	ggg	tta	ggg	agt	ttt	att	gaa	aaa	776	
Ile	Ser	Leu	Asp	Arg	Glu	Thr	Leu	Gly	Leu	Gly	Ser	Phe	Ile	Glu	Lys		
			230					235					240				
aat	atc	tgt	agc	ggc	gca	tcg	tct	tgt	ttt	agt	ggg	aat	cag	ctt	atc	824	
Asn	Ile	Cys	Ser	Gly	Ala	Ser	Ser	Cys	Phe	Ser	Gly	Asn	Gln	Leu	Ile		
		245					250					255					
tat	aag	aaa	ggg	cta	gac	aga	acc	ata	aac	atc	att	aat	acg	gta	tta	872	
Tyr	Lys	Lys	Gly	Leu	Asp	Arg	Thr	Ile	Asn	Ile	Ile	Asn	Thr	Val	Leu		
	260					265					270						
ggc	cag	ttt	gaa	tct	tcg	gct	agt	tct	ctt	tat	aag	att	tct	tat	atc	920	
Gly	Gln	Phe	Glu	Ser	Ser	Ala	Ser	Ser	Leu	Tyr	Lys	Ile	Ser	Tyr	Ile		
275					280					285					290		
cct	aac	ctc	ttt	tcg	ctc	aag	gat	tac	cag	tca	gcg	agc	atg	aac	ggc	968	
Pro	Asn	Leu	Phe	Ser	Leu	Lys	Asp	Tyr	Gln	Ser	Ala	Ser	Met	Asn	Gly		
				295					300					305			
ttt	ggg	gct	aag	atg	ggc	tat	aaa	caa	ttt	ttc	acc	cat	aag	aaa	aat	1016	
Phe	Gly	Ala	Lys	Met	Gly	Tyr	Lys	Gln	Phe	Phe	Thr	His	Lys	Lys	Asn		
			310					315					320				
gtt	ggc	tta	agg	tat	tac	ggg	ttt	ttg	gat	tat	ggc	tat	gcg	aac	ttt	1064	
Val	Gly	Leu	Arg	Tyr	Tyr	Gly	Phe	Leu	Asp	Tyr	Gly	Tyr	Ala	Asn	Phe		
		325				330					335						
ggc	gat	acg	aat	tta	aaa	gtg	ggg	gcg	aat	ctt	gtt	act	tat	ggg	gta	1112	
Gly	Asp	Thr	Asn	Leu	Lys	Val	Gly	Ala	Asn	Leu	Val	Thr	Tyr	Gly	Val		
	340					345					350						
gga	acg	gat	ttt	tta	tac	aat	gtg	tat	gaa	cgc	tct	aga	agg	agg	gaa	1160	
Gly	Thr	Asp	Phe	Leu	Tyr	Asn	Val	Tyr	Glu	Arg	Ser	Arg	Arg	Arg	Glu		
355					360					365					370		
agg	act	acg	atc	ggc	ctt	ttc	ttt	ggc	gct	caa	att	gca	ggg	caa	act	1208	
Arg	Thr	Thr	Ile	Gly	Leu	Phe	Phe	Gly	Ala	Gln	Ile	Ala	Gly	Gln	Thr		
				375				380						385			

tgg agc act aat gta acg aac tta ttg agc ggg caa agg cct gat gtc	1256
Trp Ser Thr Asn Val Thr Asn Leu Leu Ser Gly Gln Arg Pro Asp Val	
390 395 400	
aag tcc agt tgc ttc caa ttc ttg ttt gat ttg ggc gtg cgc acc aac	1304
Lys Ser Ser Ser Phe Gln Phe Leu Phe Asp Leu Gly Val Arg Thr Asn	
405 410 415	
ttt gca aaa acc aat ttc aat aag cac agg cta gac caa ggg ata gaa	1352
Phe Ala Lys Thr Asn Phe Asn Lys His Arg Leu Asp Gln Gly Ile Glu	
420 425 430	
ttt ggg gtg aaa atc cct gtt atc gct cat aaa tat ttt gca acc caa	1400
Phe Gly Val Lys Ile Pro Val Ile Ala His Lys Tyr Phe Ala Thr Gln	
435 440 445 450	
ggc tca agc gcg agc tat atg agg aat ttt agc ttc tat gtg ggc tat	1448
Gly Ser Ser Ala Ser Tyr Met Arg Asn Phe Ser Phe Tyr Val Gly Tyr	
455 460 465	
tca gtc ggt ttt taaggaaggc tcttgatgaa aaataccaat acaaaagaga	1500
Ser Val Gly Phe	
470	
taaagaatac aag	1513

<210> 174  
 <211> 470  
 <212> PRT  
 <213> Helicobacter pylori

<400> 174

Met Ser Leu Cys Arg Ala Glu Glu Asp Gly Ala Phe Phe Val Ile Asp	
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Gln Ala Gln Glu Leu Arg Gln Leu Ile Arg Asp Gly Ala Val Arg Leu	
35 40 45	
Gln Thr Ser Ala Ile Pro Leu Ser Tyr Tyr Leu Asp Ile Leu Gly Asn	
50 55 60	
Lys Thr Ala Thr Leu Leu Arg Glu Ser Leu Lys Asn Asn Ala Gln Pro	
65 70 75 80	
Ser Gln Pro Asn Ala Gln Pro Pro Gln Gln Asn Gly Pro Ser Asn Gln	
85 90 95	
Ala Leu Ala Asn Leu Glu Gln Ser Leu Gly Ile Leu Gly Lys Leu Leu	
100 105 110	
Asp Leu Ser Gln Gln Tyr Ala Ser Gln Gly Val Ile Lys Pro Leu Val	
115 120 125	
Val Asp Val Gly Lys Glu Gln Ile Gly Ile Thr Asp Ser Met Leu Leu	
130 135 140	
Val Ala Gln Asn Ile Val Leu Ala Leu Gly Gln Val Asp Leu Ser Lys	
145 150 155 160	
Ile Gln Gln Asn Asn Asn Glu Gln Leu Tyr Glu Asn Ile Met Lys Val	
165 170 175	
Met Leu Leu Gly Ala Gly Gly Thr Asn Gly Ala Tyr Asn Gly Val Ser	





5	10	15	
atc atc gtt tat ttt ttc caa gca ttt caa ggg gtt ttg aat ttt gaa			152
Ile Ile Val Tyr Phe Phe Gln Ala Phe Gln Gly Val Leu Asn Phe Glu			
20	25	30	
ggg ggt ttt tta ggg ttt ttt atc gtg gcg ttg tct tcg tat tac ggc			200
Gly Gly Phe Leu Gly Phe Phe Ile Val Ala Leu Ser Ser Tyr Tyr Gly			
35	40	45	50
gtt aaa aag cgt ttg gat tta agg aaa caa aat tca ata gaa aaa gaa			248
Val Lys Lys Arg Leu Asp Leu Arg Lys Gln Asn Ser Ile Glu Lys Glu			
55	60	65	
gaa aag caa aaa ttc caa aaa ttc gcc ctg ggc ttg gaa atg tct ttc			296
Glu Lys Gln Lys Phe Gln Lys Phe Ala Leu Gly Leu Glu Met Ser Phe			
70	75	80	
aat gtg tgg cgt tta gga ggg tat ggg gtt tta cta ggc att tta gga			344
Asn Val Trp Arg Leu Gly Gly Tyr Gly Val Leu Leu Gly Ile Leu Gly			
85	90	95	
acg ctt tta ttc ttg cat ctt ttt aac ggg tta atc ttt ctt att ggc			392
Thr Leu Leu Phe Leu His Leu Phe Asn Gly Leu Ile Phe Leu Ile Gly			
100	105	110	
gtg ttt gtg agc tcg ctc tct agc gcg tta tta cga ttt ttg aat aat			440
Val Phe Val Ser Ser Leu Ser Ser Ala Leu Leu Arg Phe Leu Asn Asn			
115	120	125	130
aat ggt aag ttt tgacacaaac tcacatggat ttttaaccctt ttaatcctct			492
Asn Gly Lys Phe			
tttaattttt aat			505
<210> 176			
<211> 134			
<212> PRT			
<213> Helicobacter pylori			
<400> 176			
Met Cys Gln Ile Gln Cys Leu Leu Ile Leu Leu Ser Ile Asn Ile Val			
1	5	10	15
Ser Ala Ile Ile Val Tyr Phe Phe Gln Ala Phe Gln Gly Val Leu Asn			
20	25	30	
Phe Glu Gly Gly Phe Leu Gly Phe Ile Val Ala Leu Ser Ser Tyr			
35	40	45	
Tyr Gly Val Lys Lys Arg Leu Asp Leu Arg Lys Gln Asn Ser Ile Glu			
50	55	60	
Lys Glu Glu Lys Gln Lys Phe Gln Lys Phe Ala Leu Gly Leu Glu Met			
65	70	75	80
Ser Phe Asn Val Trp Arg Leu Gly Gly Tyr Gly Val Leu Leu Gly Ile			
85	90	95	
Leu Gly Thr Leu Leu Phe Leu His Leu Phe Asn Gly Leu Ile Phe Leu			

	100		105		110
Ile Gly Val Phe Val Ser Ser Leu Ser Ser Ala Leu Leu Arg Phe Leu					
	115		120		125
Asn Asn Asn Gly Lys Phe					
	130				

<210> 177  
 <211> 511  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(458)

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	Met Leu
	1
aag agt acc atc aaa gaa gat tat ttg atg ctg atg tct aga gaa gtg	104
Lys Ser Thr Ile Lys Glu Asp Tyr Leu Met Leu Met Ser Arg Glu Val	
	5 10 15
agt gct ttt gtg ggg act ctt ttc ttc att ggc ttg agt tgc tat gcg	152
Ser Ala Phe Val Gly Thr Leu Phe Phe Ile Gly Leu Ser Cys Tyr Ala	
	20 25 30
atc tat cat ggc aac atg ccc gat tat ttg aga ccg gct ttg ata gac	200
Ile Tyr His Gly Asn Met Pro Asp Tyr Leu Arg Pro Ala Leu Ile Asp	
	35 40 45 50
act att aag gca gcg agt gat tcc atc tat tcc agc tgc gac tac atg	248
Thr Ile Lys Ala Ala Ser Asp Ser Ile Tyr Ser Ser Cys Asp Tyr Met	
	55 60 65
gat tat ttt ttg aag gct aga aag atg tta gag ggg ttt gct tgg tgg	296
Asp Tyr Phe Leu Lys Ala Arg Lys Met Leu Glu Gly Phe Ala Trp Trp	
	70 75 80
agc atg ttc aaa gcg gag agc atg ggc tta aat aag ggg ttt atg gtt	344
Ser Met Phe Lys Ala Glu Ser Met Gly Leu Asn Lys Gly Phe Met Val	
	85 90 95
gcg ggc tgg gta gcg ttt atc atc tat aac gct ctt agc ggg ata gcc	392
Ala Gly Trp Val Ala Phe Ile Ile Tyr Asn Ala Leu Ser Gly Ile Ala	
	100 105 110
atc agc agg ctg agc gct caa atc att tat tgg tta tca aaa tat ttt	440
Ile Ser Arg Leu Ser Ala Gln Ile Ile Tyr Trp Leu Ser Lys Tyr Phe	
	115 120 125 130
agg agt gag tat gga aaa tgatgttaaa gaagatctag agcaagcaag	488
Arg Ser Glu Tyr Gly Lys	

accaaagtta gagccagaaa agc

511

&lt;210&gt; 178

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Helicobacter pylori

&lt;400&gt; 178

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Met Leu Lys Ser Thr Ile Lys Glu Asp Tyr Leu Met Leu Met Ser Arg
 1           5           10           15
Glu Val Ser Ala Phe Val Gly Thr Leu Phe Phe Ile Gly Leu Ser Cys
      20           25           30
Tyr Ala Ile Tyr His Gly Asn Met Pro Asp Tyr Leu Arg Pro Ala Leu
      35           40           45
Ile Asp Thr Ile Lys Ala Ala Ser Asp Ser Ile Tyr Ser Ser Cys Asp
      50           55           60
Tyr Met Asp Tyr Phe Leu Lys Ala Arg Lys Met Leu Glu Gly Phe Ala
65           70           75           80
Trp Trp Ser Met Phe Lys Ala Glu Ser Met Gly Leu Asn Lys Gly Phe
      85           90           95
Met Val Ala Gly Trp Val Ala Phe Ile Ile Tyr Asn Ala Leu Ser Gly
      100          105          110
Ile Ala Ile Ser Arg Leu Ser Ala Gln Ile Ile Tyr Trp Leu Ser Lys
      115          120          125
Tyr Phe Arg Ser Glu Tyr Gly Lys
      130          135

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&lt;210&gt; 179

&lt;211&gt; 2203

&lt;212&gt; DNA

&lt;213&gt; Helicobacter pylori

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (51)...(2150)

&lt;400&gt; 179

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gagttacaca ctctttgaga acaaaacgcc aaaccattta ggaaattacc atg cta 56
                                   Met Leu
                                   1

aga ttc gtt agt aaa acg att tgc ttg tct tta atc ggc ttg ttc aac 104
Arg Phe Val Ser Lys Thr Ile Cys Leu Ser Leu Ile Gly Leu Phe Asn
      5           10           15

cct tta gaa gcc ttt caa aaa cac caa aaa gac ggc ttt ttt ata gaa 152
Pro Leu Glu Ala Phe Gln Lys His Gln Lys Asp Gly Phe Phe Ile Glu
      20           25           30

gct ggg ttt gaa act ggg tta tta gaa gga acg caa act aaa gaa gaa 200
Ala Gly Phe Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Lys Glu Glu
      35           40           45           50

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gtc ata acc acc caa aaa atc tat gaa aac ccc cta acc cac cca caa	248
Val Ile Thr Thr Gln Lys Ile Tyr Glu Asn Pro Leu Thr His Pro Gln	
55 60 65	
act aaa gaa cag cct aaa gaa caa aat aaa agc gat acg gcc acc cca	296
Thr Lys Glu Gln Pro Lys Glu Gln Asn Lys Ser Asp Thr Ala Thr Pro	
70 75 80	
caa agc gct tac gga aaa tac tac ata ccc caa agc acc att tta aaa	344
Gln Ser Ala Tyr Gly Lys Tyr Tyr Ile Pro Gln Ser Thr Ile Leu Lys	
85 90 95	
aat gca acg gct tta ttc acc acg gac aag ata gaa aat ggc tta act	392
Asn Ala Thr Ala Leu Phe Thr Thr Asp Lys Ile Glu Asn Gly Leu Thr	
100 105 110	
ttt tat tct caa aac cct gtg tat gcg aat atg gtt aat ggg agc gta	440
Phe Tyr Ser Gln Asn Pro Val Tyr Ala Asn Met Val Asn Gly Ser Val	
115 120 125 130	
acc ata caa aac ttt ctg cct tat aat tta aac aat gtt gaa ctg agt	488
Thr Ile Gln Asn Phe Leu Pro Tyr Asn Leu Asn Asn Val Glu Leu Ser	
135 140 145	
ttt aaa gac gct caa ggc aag gtg gtc aat tta ggc gtg ata gag acc	536
Phe Lys Asp Ala Gln Gly Lys Val Val Asn Leu Gly Val Ile Glu Thr	
150 155 160	
atc cct aaa caa tct caa att acc ttg cct gca agc ttg ttt aat gat	584
Ile Pro Lys Gln Ser Gln Ile Thr Leu Pro Ala Ser Leu Phe Asn Asp	
165 170 175	
tca gaa ttt gaa caa gct gat agc ttt aat tac caa caa ctt caa gcc	632
Ser Glu Phe Glu Gln Ala Asp Ser Phe Asn Tyr Gln Gln Leu Gln Ala	
180 185 190	
act gcc aca caa ttt tct gac gct aac acg caa agt ttg ttt caa aag	680
Thr Ala Thr Gln Phe Ser Asp Ala Asn Thr Gln Ser Leu Phe Gln Lys	
195 200 205 210	
ctc agc aag atc aca acc aat gta aca atg agt tat gaa aac gcc gat	728
Leu Ser Lys Ile Thr Thr Asn Val Thr Met Ser Tyr Glu Asn Ala Asp	
215 220 225	
acc aac aat ttt aaa ggt aat tgc cat gat tgt gtg tca gat ttc acc	776
Thr Asn Asn Phe Lys Gly Asn Cys His Asp Cys Val Ser Asp Phe Thr	
230 235 240	
cca caa acc gca gaa gaa ttg acc aat tta atg cta gat atg att gcg	824
Pro Gln Thr Ala Glu Glu Leu Thr Asn Leu Met Leu Asp Met Ile Ala	
245 250 255	
gtg ttt gac tct aaa tcg tgg gaa gaa gcc gtt tta aac gct cct ttc	872
Val Phe Asp Ser Lys Ser Trp Glu Glu Ala Val Leu Asn Ala Pro Phe	

260	265	270	
caa ttt tct aac agc tca tca gag tgc ggc tct gac ttt cct aag tgc			920
Gln Phe Ser Asn Ser Ser Ser Glu Cys Gly Ser Asp Phe Pro Lys Cys			
275	280	285	290
gtg aat cct ttc aat aac ggg cgt gtc gct ccc atc tat gaa aaa tac			968
Val Asn Pro Phe Asn Asn Gly Arg Val Ala Pro Ile Tyr Glu Lys Tyr			
	295	300	305
gtg cta acc cca caa tcc gtt ata gat gcg ttt aga aga acg atc aat			1016
Val Leu Thr Pro Gln Ser Val Ile Asp Ala Phe Arg Arg Thr Ile Asn			
	310	315	320
ctt gaa gtg aat atc cta aaa tca ggg ttt gta ggg cta ggg tat gaa			1064
Leu Glu Val Asn Ile Leu Lys Ser Gly Phe Val Gly Leu Gly Tyr Glu			
	325	330	335
ctt gat gat aat gat ggt aat ctg ggg ata gaa gct tct gcc tta aat			1112
Leu Asp Asp Asn Asp Gly Asn Leu Gly Ile Glu Ala Ser Ala Leu Asn			
	340	345	350
cct gaa aaa ttg ttt ggt aaa act ttg aac aaa gtt gat att gtg gaa			1160
Pro Glu Lys Leu Phe Gly Lys Thr Leu Asn Lys Val Asp Ile Val Glu			
	355	360	370
tta aga gac att atc cat gaa ttt agc cac act aaa ggc tat acg cat			1208
Leu Arg Asp Ile Ile His Glu Phe Ser His Thr Lys Gly Tyr Thr His			
	375	380	385
aat ggg aac atg act tat caa aga gtg cgc ttg tgt caa gaa aac ggc			1256
Asn Gly Asn Met Thr Tyr Gln Arg Val Arg Leu Cys Gln Glu Asn Gly			
	390	395	400
gga gcc ata caa gaa tgt gag ggt ggg aaa gaa gag tta gtc aat gga			1304
Gly Ala Ile Gln Glu Cys Glu Gly Gly Lys Glu Glu Leu Val Asn Gly			
	405	410	415
aaa gaa gaa cta aaa ttt aca aat ggg aaa gaa gtg aaa gat cag gat			1352
Lys Glu Glu Leu Lys Phe Thr Asn Gly Lys Glu Val Lys Asp Gln Asp			
	420	425	430
ggt tac acc tat gat gta tgt tct ttt tat aag gac aac cac caa gtc			1400
Gly Tyr Thr Tyr Asp Val Cys Ser Phe Tyr Lys Asp Asn His Gln Val			
	435	440	450
tat aca gcg agc aat tac ccc aat tcc att tat acg aat tgc gct caa			1448
Tyr Thr Ala Ser Asn Tyr Pro Asn Ser Ile Tyr Thr Asn Cys Ala Gln			
	455	460	465
gtc cct gct ggg ctt ata ggg gtt acc acc gct gtc tgg caa cag ctc			1496
Val Pro Ala Gly Leu Ile Gly Val Thr Thr Ala Val Trp Gln Gln Leu			
	470	475	480
atc aat caa aac gct ctg ccc att aat ttc gct aat cta aat agc cca			1544

Ile	Asn	Gln	Asn	Ala	Leu	Pro	Ile	Asn	Phe	Ala	Asn	Leu	Asn	Ser	Pro		
		485						490					495				
acc	aac	cac	tta	aac	gcc	ggg	ttg	aac	gca	caa	aat	ttt	gca	acc	tct	1592	
Thr	Asn	His	Leu	Asn	Ala	Gly	Leu	Asn	Ala	Gln	Asn	Phe	Ala	Thr	Ser		
	500					505					510						
ata	gtc	agc	gcg	atc	gcg	caa	aat	ttt	tcc	acc	act	tcc	acc	acc	act	1640	
Ile	Val	Ser	Ala	Ile	Ala	Gln	Asn	Phe	Ser	Thr	Thr	Ser	Thr	Thr	Thr		
	515				520					525					530		
tac	cgc	tct	tca	agt	aag	aat	ttt	aga	agc	cct	att	tta	ggg	gtt	aat	1688	
Tyr	Arg	Ser	Ser	Ser	Lys	Asn	Phe	Arg	Ser	Pro	Ile	Leu	Gly	Val	Asn		
				535					540					545			
gtt	aaa	ata	ggc	tac	caa	cat	tat	ttc	aat	gac	tac	ata	ggg	tta	gcc	1736	
Val	Lys	Ile	Gly	Tyr	Gln	His	Tyr	Phe	Asn	Asp	Tyr	Ile	Gly	Leu	Ala		
			550					555					560				
tat	tac	ggc	att	atc	aaa	tac	aat	tac	gcc	aaa	act	aac	gat	gaa	aaa	1784	
Tyr	Tyr	Gly	Ile	Ile	Lys	Tyr	Asn	Tyr	Ala	Lys	Thr	Asn	Asp	Glu	Lys		
		565					570					575					
atc	cag	caa	tta	agc	tat	ggg	ggg	gga	atg	gat	gtg	ttg	ttt	gat	ttc	1832	
Ile	Gln	Gln	Leu	Ser	Tyr	Gly	Gly	Gly	Met	Asp	Val	Leu	Phe	Asp	Phe		
	580					585					590						
atc	acc	act	tac	gct	aac	aaa	aag	caa	gac	aac	cca	act	aaa	aaa	gtt	1880	
Ile	Thr	Thr	Tyr	Ala	Asn	Lys	Lys	Gln	Asp	Asn	Pro	Thr	Lys	Lys	Val		
	595				600					605					610		
ttt	gct	tcc	tct	ttt	ggg	gtg	ttt	ggg	ggg	tta	agg	ggc	tta	tac	aat	1928	
Phe	Ala	Ser	Ser	Phe	Gly	Val	Phe	Gly	Gly	Leu	Arg	Gly	Leu	Tyr	Asn		
				615					620					625			
agc	tat	tat	gtc	ttc	aac	caa	gtc	aaa	gga	agc	ggg	aat	tta	gat	ata	1976	
Ser	Tyr	Tyr	Val	Phe	Asn	Gln	Val	Lys	Gly	Ser	Gly	Asn	Leu	Asp	Ile		
			630					635					640				
gtt	act	ggg	ttt	aat	tac	cgc	tac	aag	cat	tct	aaa	tat	tct	gta	ggc	2024	
Val	Thr	Gly	Phe	Asn	Tyr	Arg	Tyr	Lys	His	Ser	Lys	Tyr	Ser	Val	Gly		
		645					650					655					
att	agc	gtt	cct	tta	atc	caa	agc	ggg	att	aaa	atc	gct	tct	aat	aat	2072	
Ile	Ser	Val	Pro	Leu	Ile	Gln	Ser	Gly	Ile	Lys	Ile	Ala	Ser	Asn	Asn		
	660					665					670						
ggc	atc	tat	gcg	aac	tcc	gtt	gtt	ttg	aat	gaa	ggg	ggc	agt	cat	ttt	2120	
Gly	Ile	Tyr	Ala	Asn	Ser	Val	Val	Leu	Asn	Glu	Gly	Gly	Ser	His	Phe		
	675				680					685					690		
aaa	gtg	ttt	ttt	aat	tac	ggg	tgg	att	ttt	taggatttaa	aatccccaat					2170	
Lys	Val	Phe	Phe	Asn	Tyr	Gly	Trp	Ile	Phe								
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2203

<210> 180

<211> 700

<212> PRT

<213> Helicobacter pylori

<400> 180

Met	Leu	Arg	Phe	Val	Ser	Lys	Thr	Ile	Cys	Leu	Ser	Leu	Ile	Gly	Leu
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Phe	Asn	Pro	Leu	Glu	Ala	Phe	Gln	Lys	His	Gln	Lys	Asp	Gly	Phe	Phe
			20					25					30		
Ile	Glu	Ala	Gly	Phe	Glu	Thr	Gly	Leu	Leu	Glu	Gly	Thr	Gln	Thr	Lys
			35				40					45			
Glu	Glu	Val	Ile	Thr	Thr	Gln	Lys	Ile	Tyr	Glu	Asn	Pro	Leu	Thr	His
	50					55					60				
Pro	Gln	Thr	Lys	Glu	Gln	Pro	Lys	Glu	Gln	Asn	Lys	Ser	Asp	Thr	Ala
65					70					75					80
Thr	Pro	Gln	Ser	Ala	Tyr	Gly	Lys	Tyr	Tyr	Ile	Pro	Gln	Ser	Thr	Ile
				85					90					95	
Leu	Lys	Asn	Ala	Thr	Ala	Leu	Phe	Thr	Thr	Asp	Lys	Ile	Glu	Asn	Gly
			100					105					110		
Leu	Thr	Phe	Tyr	Ser	Gln	Asn	Pro	Val	Tyr	Ala	Asn	Met	Val	Asn	Gly
		115					120					125			
Ser	Val	Thr	Ile	Gln	Asn	Phe	Leu	Pro	Tyr	Asn	Leu	Asn	Asn	Val	Glu
	130					135					140				
Leu	Ser	Phe	Lys	Asp	Ala	Gln	Gly	Lys	Val	Val	Asn	Leu	Gly	Val	Ile
145					150					155					160
Glu	Thr	Ile	Pro	Lys	Gln	Ser	Gln	Ile	Thr	Leu	Pro	Ala	Ser	Leu	Phe
				165					170					175	
Asn	Asp	Ser	Glu	Phe	Glu	Gln	Ala	Asp	Ser	Phe	Asn	Tyr	Gln	Gln	Leu
			180					185					190		
Gln	Ala	Thr	Ala	Thr	Gln	Phe	Ser	Asp	Ala	Asn	Thr	Gln	Ser	Leu	Phe
		195					200					205			
Gln	Lys	Leu	Ser	Lys	Ile	Thr	Thr	Asn	Val	Thr	Met	Ser	Tyr	Glu	Asn
	210					215					220				
Ala	Asp	Thr	Asn	Asn	Phe	Lys	Gly	Asn	Cys	His	Asp	Cys	Val	Ser	Asp
225					230					235					240
Phe	Thr	Pro	Gln	Thr	Ala	Glu	Glu	Leu	Thr	Asn	Leu	Met	Leu	Asp	Met
				245					250					255	
Ile	Ala	Val	Phe	Asp	Ser	Lys	Ser	Trp	Glu	Glu	Ala	Val	Leu	Asn	Ala
			260					265					270		
Pro	Phe	Gln	Phe	Ser	Asn	Ser	Ser	Ser	Glu	Cys	Gly	Ser	Asp	Phe	Pro
		275					280					285			
Lys	Cys	Val	Asn	Pro	Phe	Asn	Asn	Gly	Arg	Val	Ala	Pro	Ile	Tyr	Glu
	290					295					300				
Lys	Tyr	Val	Leu	Thr	Pro	Gln	Ser	Val	Ile	Asp	Ala	Phe	Arg	Arg	Thr
305					310					315					320
Ile	Asn	Leu	Glu	Val	Asn	Ile	Leu	Lys	Ser	Gly	Phe	Val	Gly	Leu	Gly
			325						330					335	
Tyr	Glu	Leu	Asp	Asp	Asn	Asp	Gly	Asn	Leu	Gly	Ile	Glu	Ala	Ser	Ala
		340						345					350		
Leu	Asn	Pro	Glu	Lys	Leu	Phe	Gly	Lys	Thr	Leu	Asn	Lys	Val	Asp	Ile
		355					360					365			
Val	Glu	Leu	Arg	Asp	Ile	Ile	His	Glu	Phe	Ser	His	Thr	Lys	Gly	Tyr



370	375	380
Thr His Asn Gly Asn Met Thr Tyr Gln Arg Val Arg Leu Cys Gln Glu		
385	390	395
Asn Gly Gly Ala Ile Gln Glu Cys Glu Gly Gly Lys Glu Glu Leu Val		400
	405	410
Asn Gly Lys Glu Glu Leu Lys Phe Thr Asn Gly Lys Glu Val Lys Asp		415
	420	425
Gln Asp Gly Tyr Thr Tyr Asp Val Cys Ser Phe Tyr Lys Asp Asn His		430
	435	440
Gln Val Tyr Thr Ala Ser Asn Tyr Pro Asn Ser Ile Tyr Thr Asn Cys		445
	450	455
Ala Gln Val Pro Ala Gly Leu Ile Gly Val Thr Thr Ala Val Trp Gln		460
465	470	475
Gln Leu Ile Asn Gln Asn Ala Leu Pro Ile Asn Phe Ala Asn Leu Asn		480
	485	490
Ser Pro Thr Asn His Leu Asn Ala Gly Leu Asn Ala Gln Asn Phe Ala		495
	500	505
Thr Ser Ile Val Ser Ala Ile Ala Gln Asn Phe Ser Thr Thr Ser Thr		510
	515	520
Thr Thr Tyr Arg Ser Ser Ser Lys Asn Phe Arg Ser Pro Ile Leu Gly		525
	530	535
Val Asn Val Lys Ile Gly Tyr Gln His Tyr Phe Asn Asp Tyr Ile Gly		540
545	550	555
Leu Ala Tyr Tyr Gly Ile Ile Lys Tyr Asn Tyr Ala Lys Thr Asn Asp		560
	565	570
Glu Lys Ile Gln Gln Leu Ser Tyr Gly Gly Gly Met Asp Val Leu Phe		575
	580	585
Asp Phe Ile Thr Thr Tyr Ala Asn Lys Lys Gln Asp Asn Pro Thr Lys		590
	595	600
Lys Val Phe Ala Ser Ser Phe Gly Val Phe Gly Gly Leu Arg Gly Leu		605
	610	615
Tyr Asn Ser Tyr Tyr Val Phe Asn Gln Val Lys Gly Ser Gly Asn Leu		620
625	630	635
Asp Ile Val Thr Gly Phe Asn Tyr Arg Tyr Lys His Ser Lys Tyr Ser		640
	645	650
Val Gly Ile Ser Val Pro Leu Ile Gln Ser Gly Ile Lys Ile Ala Ser		655
	660	665
Asn Asn Gly Ile Tyr Ala Asn Ser Val Val Leu Asn Glu Gly Gly Ser		670
	675	680
His Phe Lys Val Phe Phe Asn Tyr Gly Trp Ile Phe		685
690	695	700

<210> 181

<211> 397

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(344)

<400> 181

tcgttttggg aaaagatata gcccatgcgc gtttcaaggg taatgaaagc atg gtc  
Met Val

56

tat gaa gaa aat ttt gtg cat gcc ggg ttt gtg ctt att gcg tgc aat 104  
 Tyr Glu Glu Asn Phe Val His Ala Gly Phe Val Leu Ile Ala Cys Asn  
           5                          10                          15

tat gcg gcc ttg tgc gcg ttg aat aaa aga cac agc gtg gtg gtt tct 152  
 Tyr Ala Ala Leu Cys Ala Leu Asn Lys Arg His Ser Val Val Val Ser  
           20                          25                          30

aat aac atc aat ttt tat gcc ccc cta gaa ttg aat caa gaa gca ctc 200  
 Asn Asn Ile Asn Phe Tyr Ala Pro Leu Glu Leu Asn Gln Glu Ala Leu  
           35                          40                          45                          50

att aaa gcg caa gtg att caa gat ggc gtg aaa aaa gct gaa ata aaa 248  
 Ile Lys Ala Gln Val Ile Gln Asp Gly Val Lys Lys Ala Glu Ile Lys  
                           55                          60                          65

ata gag gcg ttt gtg tta gac att cag gtt tta gag gga atg ata gaa 296  
 Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met Ile Glu  
                           70                          75                          80

att gtg gtg ttt gat aaa aag cct ttt aaa ttc aat ttt aaa gaa gag 344  
 Ile Val Val Phe Asp Lys Lys Pro Phe Lys Phe Asn Phe Lys Glu Glu  
                           85                          90                          95

tagttaaatg gttattgttt tagtcgtgga tagtttttaa gacaccagta atg 397

<210> 182

<211> 98

<212> PRT

<213> *Helicobacter pylori*

<400> 182

Met Val Tyr Glu Glu Asn Phe Val His Ala Gly Phe Val Leu Ile Ala  
   1                          5                          10                          15  
 Cys Asn Tyr Ala Ala Leu Cys Ala Leu Asn Lys Arg His Ser Val Val  
                           20                          25                          30  
 Val Ser Asn Asn Ile Asn Phe Tyr Ala Pro Leu Glu Leu Asn Gln Glu  
                           35                          40                          45  
 Ala Leu Ile Lys Ala Gln Val Ile Gln Asp Gly Val Lys Lys Ala Glu  
   50                          55                          60  
 Ile Lys Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met  
   65                          70                          75                          80  
 Ile Glu Ile Val Val Phe Asp Lys Lys Pro Phe Lys Phe Asn Phe Lys  
                           85                          90                          95  
 Glu Glu

<210> 183

<211> 1261

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (51)...(1208)

<400> 183

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atgatagtaa ggaaataaga gtggaatgca agaatcaccc tattgaaaag atg gca      56
                                     Met Ala
                                     1

gaa aaa tta gag gaa act aat cct gaa tgg ttt gaa aaa tgg agg gaa      104
Glu Lys Leu Glu Glu Thr Asn Pro Glu Trp Phe Glu Lys Trp Arg Glu
      5                      10                      15

aaa caa tac acc caa act ggc gaa tct aag cca tca aaa cga atc aaa      152
Lys Gln Tyr Thr Gln Thr Gly Glu Ser Lys Pro Ser Lys Arg Ile Lys
      20                      25                      30

gtt ttt aaa aac ttt acg gca ttt gat gac aga ttg tat aca att gaa      200
Val Phe Lys Asn Phe Thr Ala Phe Asp Asp Arg Leu Tyr Thr Ile Glu
      35                      40                      45                      50

tgt aat tta aaa aat ctg gat acc cat caa aaa aag ttt gaa att tgt      248
Cys Asn Leu Lys Asn Leu Asp Thr His Gln Lys Lys Phe Glu Ile Cys
      55                      60                      65

ggg gct ctg tat gac att tat gaa caa att ttt gat gaa aca cca agc      296
Gly Ala Leu Tyr Asp Ile Tyr Glu Gln Ile Phe Asp Glu Thr Pro Ser
      70                      75                      80

ttg aaa ggg cgc gat tta gaa aca tac aaa gca caa gat ttg tca aag      344
Leu Lys Gly Arg Asp Leu Glu Thr Tyr Lys Ala Gln Asp Leu Ser Lys
      85                      90                      95

aaa ttc atg cat tta ggt ttt gaa cag atc tca aaa gat tta aac gac      392
Lys Phe Met His Leu Gly Phe Glu Gln Ile Ser Lys Asp Leu Asn Asp
      100                      105                      110

tct aga ttg aac gct tta ttg tgc tat gag gaa aaa gtc atg caa gct      440
Ser Arg Leu Asn Ala Leu Leu Cys Tyr Glu Glu Lys Val Met Gln Ala
      115                      120                      125                      130

ttg gct aaa aaa tac cct agt ttt tta caa gat ttg cat gat ata aaa      488
Leu Ala Lys Lys Tyr Pro Ser Phe Leu Gln Asp Leu His Asp Ile Lys
      135                      140                      145

aaa tac agg aat aaa gat aaa cac ggc gag aaa cca caa gat ggg tct      536
Lys Tyr Arg Asn Lys Asp Lys His Gly Glu Lys Pro Gln Asp Gly Ser
      150                      155                      160

tct tta acg aga gtg gaa tta gaa aga tac aga gat gga att tat ttt      584
Ser Leu Thr Arg Val Glu Leu Glu Arg Tyr Arg Asp Gly Ile Tyr Phe
      165                      170                      175

cta gta gaa aat ctt tta aaa aac ccc ttg att aaa gag aga gaa aat      632
Leu Val Glu Asn Leu Leu Lys Asn Pro Leu Ile Lys Glu Arg Glu Asn
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180	185	190	
gct caa gaa gaa aaa cat tat aag aaa aat gca gag att gac gac cga			680
Ala Gln Glu Glu Lys His Tyr Lys Lys Asn Ala Glu Ile Asp Asp Arg			
195	200	205	210
tcc cag cta tca aac tta aac gca ccc aaa ccc tta ttt gaa tgt ttt			728
Ser Gln Leu Ser Asn Leu Asn Ala Pro Lys Pro Leu Phe Glu Cys Phe			
	215	220	225
gta gga gtt aat ctg gcc aaa gcc aaa tat tat tct aaa aaa gaa gaa			776
Val Gly Val Asn Leu Ala Lys Ala Lys Tyr Tyr Ser Lys Lys Glu Glu			
	230	235	240
aga gaa aaa gaa aag atg atc ttg aat ttt tgt aag ata ttt gaa att			824
Arg Glu Lys Glu Lys Met Ile Leu Asn Phe Cys Lys Ile Phe Glu Ile			
	245	250	255
att ctt ttt gaa gct atc caa aaa caa cca aag cct gat ttt aaa aat			872
Ile Leu Phe Glu Ala Ile Gln Lys Gln Pro Lys Pro Asp Phe Lys Asn			
	260	265	270
aaa gac gag ctt tta ggg gat tat cct aat ctt aaa aat tta gat tct			920
Lys Asp Glu Leu Leu Gly Asp Tyr Pro Asn Leu Lys Asn Leu Asp Ser			
	275	280	285
tta aga gaa gtg agg gaa gac ttt ttg aaa aga gcg ttt aag aat gat			968
Leu Arg Glu Val Arg Glu Asp Phe Leu Lys Arg Ala Phe Lys Asn Asp			
	295	300	305
gaa gcg agt ttg gga gcg tat gtg tta gtg ttg ctt agc tgt aag tat			1016
Glu Ala Ser Leu Gly Ala Tyr Val Leu Val Leu Leu Ser Cys Lys Tyr			
	310	315	320
ttt gag agc gtg ttt gaa aaa gtt caa gaa tgg cta gat ttt atc gct			1064
Phe Glu Ser Val Phe Glu Lys Val Gln Glu Trp Leu Asp Phe Ile Ala			
	325	330	335
agg ctt att gct ttg aga ggc cat gtg cac aag ata act aaa gaa ctt			1112
Arg Leu Ile Ala Leu Arg Gly His Val His Lys Ile Thr Lys Glu Leu			
	340	345	350
gaa aga tta gaa gaa gag gat tta gaa aaa ttg gaa aaa caa gca cta			1160
Glu Arg Leu Glu Glu Glu Asp Leu Glu Lys Leu Glu Lys Gln Ala Leu			
	355	360	365
gaa tat ttt aat aaa ata gca aat aaa ata tat cta aag gag aaa cga			1208
Glu Tyr Phe Asn Lys Ile Ala Asn Lys Ile Tyr Leu Lys Glu Lys Arg			
	375	380	385
tgagcgggaa tgaagaattg gagctaagag ccagagaaac tgagttggat aaa			1261
<210> 184			
<211> 386			
<212> PRT			

<213> Helicobacter pylori

<400> 184

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Met Ala Glu Lys Leu Glu Glu Thr Asn Pro Glu Trp Phe Glu Lys Trp
 1          5          10          15
Arg Glu Lys Gln Tyr Thr Gln Thr Gly Glu Ser Lys Pro Ser Lys Arg
      20          25          30
Ile Lys Val Phe Lys Asn Phe Thr Ala Phe Asp Asp Arg Leu Tyr Thr
      35          40          45
Ile Glu Cys Asn Leu Lys Asn Leu Asp Thr His Gln Lys Lys Phe Glu
      50          55          60
Ile Cys Gly Ala Leu Tyr Asp Ile Tyr Glu Gln Ile Phe Asp Glu Thr
      65          70          75          80
Pro Ser Leu Lys Gly Arg Asp Leu Glu Thr Tyr Lys Ala Gln Asp Leu
      85          90          95
Ser Lys Lys Phe Met His Leu Gly Phe Glu Gln Ile Ser Lys Asp Leu
      100          105          110
Asn Asp Ser Arg Leu Asn Ala Leu Leu Cys Tyr Glu Glu Lys Val Met
      115          120          125
Gln Ala Leu Ala Lys Lys Tyr Pro Ser Phe Leu Gln Asp Leu His Asp
      130          135          140
Ile Lys Lys Tyr Arg Asn Lys Asp Lys His Gly Glu Lys Pro Gln Asp
      145          150          155          160
Gly Ser Ser Leu Thr Arg Val Glu Leu Glu Arg Tyr Arg Asp Gly Ile
      165          170          175
Tyr Phe Leu Val Glu Asn Leu Leu Lys Asn Pro Leu Ile Lys Glu Arg
      180          185          190
Glu Asn Ala Gln Glu Glu Lys His Tyr Lys Lys Asn Ala Glu Ile Asp
      195          200          205
Asp Arg Ser Gln Leu Ser Asn Leu Asn Ala Pro Lys Pro Leu Phe Glu
      210          215          220
Cys Phe Val Gly Val Asn Leu Ala Lys Ala Lys Tyr Tyr Ser Lys Lys
      225          230          235          240
Glu Glu Arg Glu Lys Glu Lys Met Ile Leu Asn Phe Cys Lys Ile Phe
      245          250          255
Glu Ile Ile Leu Phe Glu Ala Ile Gln Lys Gln Pro Lys Pro Asp Phe
      260          265          270
Lys Asn Lys Asp Glu Leu Leu Gly Asp Tyr Pro Asn Leu Lys Asn Leu
      275          280          285
Asp Ser Leu Arg Glu Val Arg Glu Asp Phe Leu Lys Arg Ala Phe Lys
      290          295          300
Asn Asp Glu Ala Ser Leu Gly Ala Tyr Val Leu Val Leu Leu Ser Cys
      305          310          315          320
Lys Tyr Phe Glu Ser Val Phe Glu Lys Val Gln Glu Trp Leu Asp Phe
      325          330          335
Ile Ala Arg Leu Ile Ala Leu Arg Gly His Val His Lys Ile Thr Lys
      340          345          350
Glu Leu Glu Arg Leu Glu Glu Glu Asp Leu Glu Lys Leu Glu Lys Gln
      355          360          365
Ala Leu Glu Tyr Phe Asn Lys Ile Ala Asn Lys Ile Tyr Leu Lys Glu
      370          375          380
Lys Arg
      385
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<210> 185  
 <211> 412  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(359)

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 Met Phe  
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ttg caa gtt gta gca aga act cta aga aag aat gtc aat ata tta gaa 104  
 Leu Gln Val Val Ala Arg Thr Leu Arg Lys Asn Val Asn Ile Leu Glu  
 5 10 15

gag caa ggt ttt att gaa gtc att aaa gga aaa caa aga tac ttg tat 152  
 Glu Gln Gly Phe Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr Leu Tyr  
 20 25 30

gtg tat ctt aaa gat tac aga gaa tta gag ggc tat aac tcc gta gga 200  
 Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser Val Gly  
 35 40 45 50

gct aat caa aag aac aat atc cca tcg cct ttt ttc tta cag att atg 248  
 Ala Asn Gln Lys Asn Asn Ile Pro Ser Pro Phe Phe Leu Gln Ile Met  
 55 60 65

cgt ttc tta gaa aag ttt gcc aaa gaa att gag aga gta aaa ata aca 296  
 Arg Phe Leu Glu Lys Phe Ala Lys Glu Ile Glu Arg Val Lys Ile Thr  
 70 75 80

aca aag aat gtg tta tgc ata ttc cta gcc aag agc tta tgc aaa gag 344  
 Thr Lys Asn Val Leu Cys Ile Phe Leu Ala Lys Ser Leu Cys Lys Glu  
 85 90 95

tta ata atg ttg ttt taaaattcac gcctatttct aatcctaata ccacttacac 399  
 Leu Ile Met Leu Phe  
 100

tttatcctac aag 412

<210> 186  
 <211> 103  
 <212> PRT  
 <213> Helicobacter pylori

<400> 186  
 Met Phe Leu Gln Val Val Ala Arg Thr Leu Arg Lys Asn Val Asn Ile  
 1 5 10 15  
 Leu Glu Glu Gln Gly Phe Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr  
 20 25 30  
 Leu Tyr Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser

<400> 187																	
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											Met	Gln					
											1						
aaa	gcc	tta	tta	cat	tca	tca	ttc	ttt	tta	cct	tta	ttt	tta	tct	ttt	104	
Lys	Ala	Leu	Leu	His	Ser	Ser	Phe	Phe	Leu	Pro	Leu	Phe	Leu	Ser	Phe		
		5					10					15					
tgt	atc	gct	gaa	gaa	aat	ggg	gcg	tat	gcg	agc	gtg	ggg	ttt	gaa	tat	152	
Cys	Ile	Ala	Glu	Glu	Asn	Gly	Ala	Tyr	Ala	Ser	Val	Gly	Phe	Glu	Tyr		
		20				25					30						
tcc	att	agt	cat	gcc	gtt	gaa	cac	aat	aac	ccc	ttt	tta	aat	caa	gaa	200	
Ser	Ile	Ser	His	Ala	Val	Glu	His	Asn	Asn	Pro	Phe	Leu	Asn	Gln	Glu		
		35			40					45					50		
cg	c	atc	caa	atc	att	tct	aac	gct	caa	aat	aaa	atc	tat	aaa	ctc	cat	248
Arg	Ile	Gln	Ile	Ile	Ser	Asn	Ala	Gln	Asn	Lys	Ile	Tyr	Lys	Leu	His		
				55					60					65			
caa	gtt	aaa	aat	gaa	atc	aca	agc	atg	cct	aaa	acc	ttt	gca	tat	atc	296	
Gln	Val	Lys	Asn	Glu	Ile	Thr	Ser	Met	Pro	Lys	Thr	Phe	Ala	Tyr	Ile		
			70					75					80				
aac	aac	gct	tta	aaa	aac	aac	tcc	aaa	tta	acc	ccc	act	gaa	atg	caa	344	
Asn	Asn	Ala	Leu	Lys	Asn	Asn	Ser	Lys	Leu	Thr	Pro	Thr	Glu	Met	Gln		
		85					90					95					
gcc	gaa	caa	tac	tac	ctc	caa	tcc	acc	ttt	caa	aac	att	gaa	aaa	ata	392	
Ala	Glu	Gln	Tyr	Tyr	Leu	Gln	Ser	Thr	Phe	Gln	Asn	Ile	Glu	Lys	Ile		
		100				105					110						
gta	atg	ctt	agc	ggg	ggc	gtt	tca	tct	aac	cca	caa	tta	gtc	caa	gcg	440	
Val	Met	Leu	Ser	Gly	Gly	Val	Ser	Ser	Asn	Pro	Gln	Leu	Val	Gln	Ala		

115	120	125	130	
ttg gaa aaa atg caa gaa ccc att act aac cct tta gaa ttt gaa gaa				488
Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu Glu Phe Glu Glu	135	140	145	
aac tta aga aat tta gaa gtg caa ttt gct caa tct caa aac cgc atg				536
Asn Leu Arg Asn Leu Glu Val Gln Phe Ala Gln Ser Gln Asn Arg Met	150	155	160	
ctt tct tct tta tct tct caa atc gct gcc att tca aat tcc tta aac				584
Leu Ser Ser Leu Ser Ser Gln Ile Ala Ala Ile Ser Asn Ser Leu Asn	165	170	175	
gcg ctt gat cct aac tct tat tct aaa aac att tca agc atg tat ggg				632
Ala Leu Asp Pro Asn Ser Tyr Ser Lys Asn Ile Ser Ser Met Tyr Gly	180	185	190	
gtg agt ttg agc gta ggt tat aag cat ttc ttt acc aag aaa aaa aat				680
Val Ser Leu Ser Val Gly Tyr Lys His Phe Phe Thr Lys Lys Lys Asn	195	200	205	210
caa ggg ttg cgc tat tac ttg ttt tat gac tat ggt tac act aat ttt				728
Gln Gly Leu Arg Tyr Tyr Leu Phe Tyr Asp Tyr Gly Tyr Thr Asn Phe	215	220	225	
ggg ttt gtg ggc aat ggc ttt gat ggt tta ggc aaa atg aat aac cat				776
Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys Met Asn Asn His	230	235	240	
ctc tat ggg ctt ggg ata gac tat ctt tat aat ttc att gat aat gca				824
Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Tyr Asn Phe Ile Asp Asn Ala	245	250	255	
aaa aaa cac tct agc gta ggt ttt tat ctg ggt ttt gct tta gcg ggg				872
Lys Lys His Ser Ser Val Gly Phe Tyr Leu Gly Phe Ala Leu Ala Gly	260	265	270	
agt tcg tgg gta ggg agt ggt ttg agc atg tgg gtg agc caa acg gat				920
Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val Ser Gln Thr Asp	275	280	285	290
ttt atc aac aat tac ttg acg ggc tat caa gct aaa atg cac acg agt				968
Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys Met His Thr Ser	295	300	305	
ttt ttc cag atc cct ttg aat ttt ggg gtt cgt gtg aat gtc aat agg				1016
Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val Asn Val Asn Arg	310	315	320	
cat aat ggc ttt gaa atg ggc ttg aaa atc cct tta gcg atg aat tcc				1064
His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro Leu Ala Met Asn Ser	325	330	335	
ttt tat gaa acg cat ggc aaa ggg cta aac act tcc ctc ttt ttc aaa				1112



Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Thr Ser Leu Phe Phe Lys  
 340 345 350

cgc ctt gtc atg ttt aac gtg agt tac gtt tat agt ttt taggggggta 1161  
 Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr Ser Phe  
 355 360 365

aatgccttca aacgctcttt tgattgaaga aatcactcat tta 1204

<210> 188

<211> 367

<212> PRT

<213> Helicobacter pylori

<400> 188

Met Gln Lys Ala Leu Leu His Ser Ser Phe Phe Leu Pro Leu Phe Leu  
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 Ser Phe Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser Val Gly Phe  
 20 25 30  
 Glu Tyr Ser Ile Ser His Ala Val Glu His Asn Asn Pro Phe Leu Asn  
 35 40 45  
 Gln Glu Arg Ile Gln Ile Ile Ser Asn Ala Gln Asn Lys Ile Tyr Lys  
 50 55 60  
 Leu His Gln Val Lys Asn Glu Ile Thr Ser Met Pro Lys Thr Phe Ala  
 65 70 75 80  
 Tyr Ile Asn Asn Ala Leu Lys Asn Asn Ser Lys Leu Thr Pro Thr Glu  
 85 90 95  
 Met Gln Ala Glu Gln Tyr Tyr Leu Gln Ser Thr Phe Gln Asn Ile Glu  
 100 105 110  
 Lys Ile Val Met Leu Ser Gly Gly Val Ser Ser Asn Pro Gln Leu Val  
 115 120 125  
 Gln Ala Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu Glu Phe  
 130 135 140  
 Glu Glu Asn Leu Arg Asn Leu Glu Val Gln Phe Ala Gln Ser Gln Asn  
 145 150 155 160  
 Arg Met Leu Ser Ser Leu Ser Ser Gln Ile Ala Ala Ile Ser Asn Ser  
 165 170 175  
 Leu Asn Ala Leu Asp Pro Asn Ser Tyr Ser Lys Asn Ile Ser Ser Met  
 180 185 190  
 Tyr Gly Val Ser Leu Ser Val Gly Tyr Lys His Phe Phe Thr Lys Lys  
 195 200 205  
 Lys Asn Gln Gly Leu Arg Tyr Tyr Leu Phe Tyr Asp Tyr Gly Tyr Thr  
 210 215 220  
 Asn Phe Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys Met Asn  
 225 230 235 240  
 Asn His Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Tyr Asn Phe Ile Asp  
 245 250 255  
 Asn Ala Lys Lys His Ser Ser Val Gly Phe Tyr Leu Gly Phe Ala Leu  
 260 265 270  
 Ala Gly Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val Ser Gln  
 275 280 285  
 Thr Asp Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys Met His  
 290 295 300  
 Thr Ser Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val Asn Val  
 305 310 315 320



Trp	Gln	Gln	Ser	Gly	Pro	Gly	Gly	Val	Ile	Asn	Pro	Arg	Gly	Ile	Gly		
				135					140					145			
tgg	gaa	tac	atg	ggt	gag	tgg	aac	ggc	ttg	ttc	cct	aac	tac	tat	ccg	536	
Trp	Glu	Tyr	Met	Gly	Glu	Trp	Asn	Gly	Leu	Phe	Pro	Asn	Tyr	Tyr	Pro		
			150					155					160				
gct	aac	gcc	tac	ttg	cct	ggt	ggc	tca	agg	cgc	tat	caa	gtc	tat	aaa	584	
Ala	Asn	Ala	Tyr	Leu	Pro	Gly	Gly	Ser	Arg	Arg	Tyr	Gln	Val	Tyr	Lys		
		165						170				175					
gca	aat	ttg	acc	tat	gat	agc	gac	agg	gtc	cat	atg	gta	atg	ggg	cgt	632	
Ala	Asn	Leu	Thr	Tyr	Asp	Ser	Asp	Arg	Val	His	Met	Val	Met	Gly	Arg		
	180						185				190						
ttt	gac	att	acc	gag	cag	gag	caa	atg	gat	tgg	att	tac	caa	ttg	ttc	680	
Phe	Asp	Ile	Thr	Glu	Gln	Glu	Gln	Met	Asp	Trp	Ile	Tyr	Gln	Leu	Phe		
195					200					205					210		
caa	ggg	ttt	tat	ggg	act	ttc	aag	ctc	act	aag	aat	atg	aaa	ttc	ttg	728	
Gln	Gly	Phe	Tyr	Gly	Thr	Phe	Lys	Leu	Thr	Lys	Asn	Met	Lys	Phe	Leu		
				215					220					225			
ctc	ttt	agt	ggt	tgg	ggt	cgt	ggt	atc	gct	gat	ggt	cag	tgg	ttg	ttc	776	
Leu	Phe	Ser	Gly	Trp	Gly	Arg	Gly	Ile	Ala	Asp	Gly	Gln	Trp	Leu	Phe		
			230					235					240				
cct	atc	tat	cgt	gaa	aag	cct	tgg	ggg	gtt	cat	aaa	gcg	ggt	att	att	824	
Pro	Ile	Tyr	Arg	Glu	Lys	Pro	Trp	Gly	Val	His	Lys	Ala	Gly	Ile	Ile		
		245					250					255					
tat	cgc	cct	aca	aag	aat	ttg	atg	atc	cac	cct	tat	gtg	tat	ctt	atc	872	
Tyr	Arg	Pro	Thr	Lys	Asn	Leu	Met	Ile	His	Pro	Tyr	Val	Tyr	Leu	Ile		
	260					265					270						
cca	atg	gta	ggc	aca	ttg	cct	ggt	gct	aaa	ata	gaa	tac	gat	acc	aat	920	
Pro	Met	Val	Gly	Thr	Leu	Pro	Gly	Ala	Lys	Ile	Glu	Tyr	Asp	Thr	Asn		
275					280					285					290		
cct	gaa	ttt	agc	ggt	agg	ggc	att	agg	aac	aga	acg	act	ttc	tat	gcg	968	
Pro	Glu	Phe	Ser	Gly	Arg	Gly	Ile	Arg	Asn	Arg	Thr	Thr	Phe	Tyr	Ala		
			295						300					305			
ttg	tat	gac	tat	cgt	tgg	aat	aac	gct	gaa	tac	ggt	cgt	tac	gcg	ccc	1016	
Leu	Tyr	Asp	Tyr	Arg	Trp	Asn	Asn	Ala	Glu	Tyr	Gly	Arg	Tyr	Ala	Pro		
			310					315					320				
gct	cgt	tat	aac	act	tgg	gat	ccg	ttc	ttg	gat	aat	ggt	aag	tgg	cgt	1064	
Ala	Arg	Tyr	Asn	Thr	Trp	Asp	Pro	Phe	Leu	Asp	Asn	Gly	Lys	Trp	Arg		
		325					330					335					
ggc	ttg	caa	ggt	cct	ggt	ggt	gcg	acg	ctc	ctt	tta	cgc	cac	cat	ata	1112	
Gly	Leu	Gln	Gly	Pro	Gly	Gly	Ala	Thr	Leu	Leu	Leu	Arg	His	His	Ile		
	340					345					350						

gat att aac aac tac ttt gtg gtt ggt ggt gct tat ctc aac att ggt	1160
Asp Ile Asn Asn Tyr Phe Val Val Gly Gly Ala Tyr Leu Asn Ile Gly	
355 360 365 370	
aac cct aac atg aac tta ggt act tgg ggt aac cct gtg gct gtt gat	1208
Asn Pro Asn Met Asn Leu Gly Thr Trp Gly Asn Pro Val Ala Val Asp	
375 380 385	
ggg atc gaa caa tgg gtc ggt agt atc tat agc tta ggg ttt gcg ggg	1256
Gly Ile Glu Gln Trp Val Gly Ser Ile Tyr Ser Leu Gly Phe Ala Gly	
390 395 400	
att gac aac att acc gat gct gac gcg ttc acc gag tat gtt aaa ggt	1304
Ile Asp Asn Ile Thr Asp Ala Asp Ala Phe Thr Glu Tyr Val Lys Gly	
405 410 415	
gga ggc aag cat ggt aag ttt agt tgg agc gtt tat cag cgc ttc act	1352
Gly Gly Lys His Gly Lys Phe Ser Trp Ser Val Tyr Gln Arg Phe Thr	
420 425 430	
acc gct cca agg gct ttg gaa tat ggt atc ggt atg tat cta gac tat	1400
Thr Ala Pro Arg Ala Leu Glu Tyr Gly Ile Gly Met Tyr Leu Asp Tyr	
435 440 445 450	
cag ttc agc aag cat gtt aaa gcg ggt ctc aaa ctc gta tgg tta gag	1448
Gln Phe Ser Lys His Val Lys Ala Gly Leu Lys Leu Val Trp Leu Glu	
455 460 465	
ttc caa att cgt gcg ggt tac aac cct gga acc ggt ttc ctt ggg cca	1496
Phe Gln Ile Arg Ala Gly Tyr Asn Pro Gly Thr Gly Phe Leu Gly Pro	
470 475 480	
aac ggt cag ccg ctt aac ttg aat act ggt ttg ttt gag tct tca gcg	1544
Asn Gly Gln Pro Leu Asn Leu Asn Thr Gly Leu Phe Glu Ser Ser Ala	
485 490 495	
ttc gct caa ggc cct caa aac atg ggc ggt atc gca aaa agc atc act	1592
Phe Ala Gln Gly Pro Gln Asn Met Gly Gly Ile Ala Lys Ser Ile Thr	
500 505 510	
caa gac aga agc cat ttg atg aca cac att agt tat agt ttc	1634
Gln Asp Arg Ser His Leu Met Thr His Ile Ser Tyr Ser Phe	
515 520 525	
taagagagtt ctccccctat ctcttagata tgcctttttg tattttttatt tta	1687

<210> 190

<211> 528

<212> PRT

<213> Helicobacter pylori

<400> 190

Met Lys Leu Lys Lys Arg Lys Val Ala Ala Ala Leu Leu Lys Arg Phe
1 5 10 15
Thr Leu Pro Leu Leu Phe Thr Thr Gly Ser Leu Gly Ala Val Thr Tyr

-249-

Leu Glu Phe Gln Ile Arg Ala Gly Tyr Asn Pro Gly Thr Gly Phe Leu  
 465 470 475 480  
 Gly Pro Asn Gly Gln Pro Leu Asn Leu Asn Thr Gly Leu Phe Glu Ser  
 485 490 495  
 Ser Ala Phe Ala Gln Gly Pro Gln Asn Met Gly Gly Ile Ala Lys Ser  
 500 505 510  
 Ile Thr Gln Asp Arg Ser His Leu Met Thr His Ile Ser Tyr Ser Phe  
 515 520 525

<210> 191  
 <211> 412  
 <212> DNA  
 <213> *Helicobacter pylori*

<220>  
 <221> CDS  
 <222> (51)...(359)

<400> 191  
 ttttgtctga tttgttgcta ccaaaaccat taccaaccaa agcagatccc atg ttt 56  
 Met Phe  
 1  
  
 ttg ata cta tcg aat cca ttc ttc aac act tct gcc ata aaa ttc ttg 104  
 Leu Ile Leu Ser Asn Pro Phe Phe Asn Thr Ser Ala Ile Lys Phe Leu  
 5 10 15  
  
 ata ttg tcc ata ggc aag ttg aat ttt ttc cct aat att tca tta agt 152  
 Ile Leu Ser Ile Gly Lys Leu Asn Phe Phe Pro Asn Ile Ser Leu Ser  
 20 25 30  
  
 ccc atc att aac atc agg aag aac aaa aaa ttt aat atc ata gaa aac 200  
 Pro Ile Ile Asn Ile Arg Lys Asn Lys Lys Phe Asn Ile Ile Glu Asn  
 35 40 45 50  
  
 aaa tca ctg gat aaa cct gta aaa aga ttt gtt ccg cca ccc aac aaa 248  
 Lys Ser Leu Asp Lys Pro Val Lys Arg Phe Val Pro Pro Pro Asn Lys  
 55 60 65  
  
 gaa gct aaa att ttt ccc atg atc agt cct ttt att ttt ggt tgt gta 296  
 Glu Ala Lys Ile Phe Pro Met Ile Ser Pro Phe Ile Phe Gly Cys Val  
 70 75 80  
  
 agt tct tgc ttg ttc gga tct cta atg cgt gtt tta gta gga agc att 344  
 Ser Ser Cys Leu Phe Gly Ser Leu Met Arg Val Leu Val Gly Ser Ile  
 85 90 95  
  
 tca caa tgg cat acc taaagctact aagaaaattc ttgaatctat tggttaagatt 399  
 Ser Gln Trp His Thr  
 100  
  
 actcatgaaa tca 412

<210> 192

<211> 103  
 <212> PRT  
 <213> Helicobacter pylori

<400> 192  
 Met Phe Leu Ile Leu Ser Asn Pro Phe Phe Asn Thr Ser Ala Ile Lys  
 1 5 10 15  
 Phe Leu Ile Leu Ser Ile Gly Lys Leu Asn Phe Phe Pro Asn Ile Ser  
 20 25 30  
 Leu Ser Pro Ile Ile Asn Ile Arg Lys Asn Lys Lys Phe Asn Ile Ile  
 35 40 45  
 Glu Asn Lys Ser Leu Asp Lys Pro Val Lys Arg Phe Val Pro Pro Pro  
 50 55 60  
 Asn Lys Glu Ala Lys Ile Phe Pro Met Ile Ser Pro Phe Ile Phe Gly  
 65 70 75 80  
 Cys Val Ser Ser Cys Leu Phe Gly Ser Leu Met Arg Val Leu Val Gly  
 85 90 95  
 Ser Ile Ser Gln Trp His Thr  
 100

<210> 193  
 <211> 447  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (67)...(405)

<400> 193  
 tccaatccgt ctaatatctc tttattttcg ctcaattcct taaccataac gggtttttta 60  
 ggcgctt gtg ggg gtt act ggg cta aag ttt gga gcg ttt tgc act tct 108  
 Val Gly Val Thr Gly Leu Lys Phe Gly Ala Phe Cys Thr Ser  
 1 5 10  
 ttt tct tct ttt ttt aga ttt tcc ttt atc att tct tct atc ctt cct 156  
 Phe Ser Ser Phe Phe Arg Phe Ser Phe Ile Ile Ser Ser Ile Leu Pro  
 15 20 25 30  
 tct atc att tct tct tgc gtg ttt tct tgt ggg ttt tct tct ttt tta 204  
 Ser Ile Ile Ser Ser Cys Val Phe Ser Cys Gly Phe Ser Ser Phe Leu  
 35 40 45  
 ggg tgg ttg ggg gtt ttt tgg ttt tct gtt ttg ttg tca ttt tct att 252  
 Gly Trp Leu Gly Val Phe Trp Phe Ser Val Leu Leu Ser Phe Ser Ile  
 50 55 60  
 atg ggt gca agt gtg ggc atg ata ggt ttg ggc gtg gtg ggc gta aga 300  
 Met Gly Ala Ser Val Gly Met Ile Gly Leu Gly Val Val Gly Val Arg  
 65 70 75  
 gtt tct ttt gta ggc gtg ggt tct ctt tct tta gtt tct tgt tta att 348  
 Val Ser Phe Val Gly Val Gly Ser Leu Ser Leu Val Ser Cys Leu Ile  
 80 85 90

tct ttt aaa ggg ggg tta gtg ggg tta gtc aaa tca tca aat cgg ttt	396
Ser Phe Lys Gly Gly Leu Val Gly Leu Val Lys Ser Ser Asn Arg Phe	
95 100 105 110	

ctt tta ggg taaatggtgt aatgggtagg ggggtgggag gaaatttgga	445
Leu Leu Gly	

ct	447
----	-----

<210> 194  
 <211> 113  
 <212> PRT  
 <213> Helicobacter pylori

<400> 194

Val Gly Val Thr Gly Leu Lys Phe Gly Ala Phe Cys Thr Ser Phe Ser	
1 5 10 15	
Ser Phe Phe Arg Phe Ser Phe Ile Ile Ser Ser Ile Leu Pro Ser Ile	
20 25 30	
Ile Ser Ser Cys Val Phe Ser Cys Gly Phe Ser Ser Phe Leu Gly Trp	
35 40 45	
Leu Gly Val Phe Trp Phe Ser Val Leu Leu Ser Phe Ser Ile Met Gly	
50 55 60	
Ala Ser Val Gly Met Ile Gly Leu Gly Val Val Gly Val Arg Val Ser	
65 70 75 80	
Phe Val Gly Val Gly Ser Leu Ser Leu Val Ser Cys Leu Ile Ser Phe	
85 90 95	
Lys Gly Gly Leu Val Gly Leu Val Lys Ser Ser Asn Arg Phe Leu Leu	
100 105 110	
Gly	

<210> 195  
 <211> 1180  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1127)

<400> 195

ccaagaaaga gtataatagc gcataagaat ttaactgatg aagaggttta atg cta	56
Met Leu	
1	
gaa aat aga gtt aag acc aag caa att ttt atc ggt ggc gtg gcc ata	104
Glu Asn Arg Val Lys Thr Lys Gln Ile Phe Ile Gly Gly Val Ala Ile	
5 10 15	
ggg ggt gat gct ccc ata agc acg caa agc atg acc ttt agc aaa acc	152
Gly Gly Asp Ala Pro Ile Ser Thr Gln Ser Met Thr Phe Ser Lys Thr	



20	25	30	
gct gat att gaa agc act aaa aat caa att gac aga ctc aaa ctc gcc			200
Ala Asp Ile Glu Ser Thr Lys Asn Gln Ile Asp Arg Leu Lys Leu Ala			
35	40	45	50
ggg gcc gat tta gtg agg gtg gcg gtg agt aat gaa aag gac gct cta			248
Gly Ala Asp Leu Val Arg Val Ala Val Ser Asn Glu Lys Asp Ala Leu			
	55	60	65
gcc tta aaa gaa ttg aaa aaa gtg tcc cct ttg cct tta atc gct gat			296
Ala Leu Lys Glu Leu Lys Lys Val Ser Pro Leu Pro Leu Ile Ala Asp			
	70	75	80
att cat ttc cat tat aaa ttc gct ctc att gcc gct caa agc gtg gat			344
Ile His Phe His Tyr Lys Phe Ala Leu Ile Ala Ala Gln Ser Val Asp			
	85	90	95
gcg atc agg att aac ccc gga aac atc ggc tct aaa gag aag atc aaa			392
Ala Ile Arg Ile Asn Pro Gly Asn Ile Gly Ser Lys Glu Lys Ile Lys			
	100	105	110
gcg gtg gtt gat gct tgt aaa gaa aaa aac att cct ata aga att ggc			440
Ala Val Val Asp Ala Cys Lys Glu Lys Asn Ile Pro Ile Arg Ile Gly			
115	120	125	130
gtg aat gct ggg agt tta gaa aag cag ttt gat caa aaa tac gga ccc			488
Val Asn Ala Gly Ser Leu Glu Lys Gln Phe Asp Gln Lys Tyr Gly Pro			
	135	140	145
acc cca aaa ggc atg gta gaa agc gct ttg tat aac gcc aaa ctt tta			536
Thr Pro Lys Gly Met Val Glu Ser Ala Leu Tyr Asn Ala Lys Leu Leu			
	150	155	160
gaa gat ttg gat ttt acc aat ttt aag att tct tta aaa gcg agc gat			584
Glu Asp Leu Asp Phe Thr Asn Phe Lys Ile Ser Leu Lys Ala Ser Asp			
	165	170	175
gtg att cgc acc ata gaa gct tac agg atg ctt cgc cct ctt gtg atc			632
Val Ile Arg Thr Ile Glu Ala Tyr Arg Met Leu Arg Pro Leu Val Ile			
	180	185	190
tat cct ttc cat ttg ggg gtt acg gag gcg ggg aat ctt ttt agc tcc			680
Tyr Pro Phe His Leu Gly Val Thr Glu Ala Gly Asn Leu Phe Ser Ser			
195	200	205	210
agt atc aaa tcc gct atg gct tta ggg ggg ctt tta atg gag ggc att			728
Ser Ile Lys Ser Ala Met Ala Leu Gly Gly Leu Leu Met Glu Gly Ile			
	215	220	225
ggg gat acg atg cgc gta tcc atc aca ggg gaa tta gaa aat gaa atc			776
Gly Asp Thr Met Arg Val Ser Ile Thr Gly Glu Leu Glu Asn Glu Ile			
	230	235	240
aaa gtg gcc aga gca att tta cgc cat agc ggg cgg ttg aaa gaa ggg			824

Lys Val Ala Arg Ala Ile Leu Arg His Ser Gly Arg Leu Lys Glu Gly  
 245 250 255

att aat tgg att tct tgc ccc act tgc ggg cgc att gaa gcc aat tta 872  
 Ile Asn Trp Ile Ser Cys Pro Thr Cys Gly Arg Ile Glu Ala Asn Leu  
 260 265 270

gtg gat atg gcg atc aag gta gaa aaa cgc tta agc cac atc aaa acc 920  
 Val Asp Met Ala Ile Lys Val Glu Lys Arg Leu Ser His Ile Lys Thr  
 275 280 285 290

cct tta gac att agc gtg atg ggt tgc gtg gtg aat gct ttg ggt gaa 968  
 Pro Leu Asp Ile Ser Val Met Gly Cys Val Val Asn Ala Leu Gly Glu  
 295 300 305

gcc aag cat gca gac atg gcg atc gct ttt ggg aat cgc agc ggt ttg 1016  
 Ala Lys His Ala Asp Met Ala Ile Ala Phe Gly Asn Arg Ser Gly Leu  
 310 315 320

atc att aaa gag ggt aaa gtc att cac aaa ctg gct gaa aag gat tta 1064  
 Ile Ile Lys Glu Gly Lys Val Ile His Lys Leu Ala Glu Lys Asp Leu  
 325 330 335

ttt gaa act ttt gtg ata gaa gtg gaa aat tta gct aaa gaa aga gaa 1112  
 Phe Glu Thr Phe Val Ile Glu Val Glu Asn Leu Ala Lys Glu Arg Glu  
 340 345 350

aaa agt tta aag gat taggcatgat caataagttt aaaaattttg tgagcaacta 1167  
 Lys Ser Leu Lys Asp  
 355

ccagcaatct aac 1180

<210> 196  
 <211> 359  
 <212> PRT  
 <213> Helicobacter pylori

<400> 196  
 Met Leu Glu Asn Arg Val Lys Thr Lys Gln Ile Phe Ile Gly Gly Val  
 1 5 10 15  
 Ala Ile Gly Gly Asp Ala Pro Ile Ser Thr Gln Ser Met Thr Phe Ser  
 20 25 30  
 Lys Thr Ala Asp Ile Glu Ser Thr Lys Asn Gln Ile Asp Arg Leu Lys  
 35 40 45  
 Leu Ala Gly Ala Asp Leu Val Arg Val Ala Val Ser Asn Glu Lys Asp  
 50 55 60  
 Ala Leu Ala Leu Lys Glu Leu Lys Lys Val Ser Pro Leu Pro Leu Ile  
 65 70 75 80  
 Ala Asp Ile His Phe His Tyr Lys Phe Ala Leu Ile Ala Ala Gln Ser  
 85 90 95  
 Val Asp Ala Ile Arg Ile Asn Pro Gly Asn Ile Gly Ser Lys Glu Lys  
 100 105 110  
 Ile Lys Ala Val Val Asp Ala Cys Lys Glu Lys Asn Ile Pro Ile Arg  
 115 120 125

Ile Gly Val Asn Ala Gly Ser Leu Glu Lys Gln Phe Asp Gln Lys Tyr  
 130 135 140  
 Gly Pro Thr Pro Lys Gly Met Val Glu Ser Ala Leu Tyr Asn Ala Lys  
 145 150 155 160  
 Leu Leu Glu Asp Leu Asp Phe Thr Asn Phe Lys Ile Ser Leu Lys Ala  
 165 170 175  
 Ser Asp Val Ile Arg Thr Ile Glu Ala Tyr Arg Met Leu Arg Pro Leu  
 180 185 190  
 Val Ile Tyr Pro Phe His Leu Gly Val Thr Glu Ala Gly Asn Leu Phe  
 195 200 205  
 Ser Ser Ser Ile Lys Ser Ala Met Ala Leu Gly Gly Leu Leu Met Glu  
 210 215 220  
 Gly Ile Gly Asp Thr Met Arg Val Ser Ile Thr Gly Glu Leu Glu Asn  
 225 230 235 240  
 Glu Ile Lys Val Ala Arg Ala Ile Leu Arg His Ser Gly Arg Leu Lys  
 245 250 255  
 Glu Gly Ile Asn Trp Ile Ser Cys Pro Thr Cys Gly Arg Ile Glu Ala  
 260 265 270  
 Asn Leu Val Asp Met Ala Ile Lys Val Glu Lys Arg Leu Ser His Ile  
 275 280 285  
 Lys Thr Pro Leu Asp Ile Ser Val Met Gly Cys Val Val Asn Ala Leu  
 290 295 300  
 Gly Glu Ala Lys His Ala Asp Met Ala Ile Ala Phe Gly Asn Arg Ser  
 305 310 315 320  
 Gly Leu Ile Ile Lys Glu Gly Lys Val Ile His Lys Leu Ala Glu Lys  
 325 330 335  
 Asp Leu Phe Glu Thr Phe Val Ile Glu Val Glu Asn Leu Ala Lys Glu  
 340 345 350  
 Arg Glu Lys Ser Leu Lys Asp  
 355

<210> 197  
 <211> 1399  
 <212> DNA  
 <213> *Helicobacter pylori*

<220>  
 <221> CDS  
 <222> (51)...(1346)

<400> 197  
 gcctatgaaa tcttaaagcg ttatccggct aaagcaaagg tataaataac atg aaa 56  
 Met Lys  
 1  
  
 aaa ttt tta atc act tta tta tta gga gtt ttt atg ggg tta caa gcg 104  
 Lys Phe Leu Ile Thr Leu Leu Leu Gly Val Phe Met Gly Leu Gln Ala  
 5 10 15  
  
 agc gct ttg aca cac caa gaa atc aat caa gct aaa gtc cct gtg att 152  
 Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala Lys Val Pro Val Ile  
 20 25 30  
  
 tat gaa gaa aac cat ttg ttg cct atg ggg ttt atc cat tta gcc ttt 200

Tyr	Glu	Glu	Asn	His	Leu	Leu	Pro	Met	Gly	Phe	Ile	His	Leu	Ala	Phe		
35					40					45					50		
agg	ggg	ggt	ggg	agc	tta	agc	gat	aaa	aac	cag	ttg	ggt	ttg	gcg	aaa	248	
Arg	Gly	Gly	Gly	Ser	Leu	Ser	Asp	Lys	Asn	Gln	Leu	Gly	Leu	Ala	Lys		
				55				60						65			
tta	ttc	gcg	caa	ggt	tta	aac	gaa	ggc	act	aaa	gag	ctt	ggt	gcg	gtg	296	
Leu	Phe	Ala	Gln	Val	Leu	Asn	Glu	Gly	Thr	Lys	Glu	Leu	Gly	Ala	Val		
			70					75					80				
ggg	ttt	gcg	caa	ctt	tta	gag	caa	aaa	gcg	atc	agt	ttg	aat	gtg	gat	344	
Gly	Phe	Ala	Gln	Leu	Leu	Glu	Gln	Lys	Ala	Ile	Ser	Leu	Asn	Val	Asp		
		85					90					95					
acc	agc	aca	gaa	gat	ttg	caa	atc	act	tta	gaa	ttt	tta	aaa	gaa	tac	392	
Thr	Ser	Thr	Glu	Asp	Leu	Gln	Ile	Thr	Leu	Glu	Phe	Leu	Lys	Glu	Tyr		
	100					105					110						
gaa	gat	gaa	gcc	att	acg	cgc	tta	aaa	gag	ctt	tta	aaa	tcc	cct	aat	440	
Glu	Asp	Glu	Ala	Ile	Thr	Arg	Leu	Lys	Glu	Leu	Leu	Lys	Ser	Pro	Asn		
115					120				125						130		
ttc	acg	caa	aac	gct	tta	gaa	aaa	gtc	aaa	acc	caa	atg	tta	gcc	gca	488	
Phe	Thr	Gln	Asn	Ala	Leu	Glu	Lys	Val	Lys	Thr	Gln	Met	Leu	Ala	Ala		
			135					140						145			
ctt	tta	caa	aaa	gaa	agc	gat	ttt	gac	tat	ttg	gct	aaa	ttg	act	tta	536	
Leu	Leu	Gln	Lys	Glu	Ser	Asp	Phe	Asp	Tyr	Leu	Ala	Lys	Leu	Thr	Leu		
		150						155					160				
aag	caa	gag	ctt	ttt	gct	aac	acc	cct	tta	gct	aac	gca	gcc	tta	ggc	584	
Lys	Gln	Glu	Leu	Phe	Ala	Asn	Thr	Pro	Leu	Ala	Asn	Ala	Ala	Leu	Gly		
	165					170						175					
act	aaa	gag	agc	att	caa	aaa	atc	aag	cta	gac	gat	ttg	aaa	cag	caa	632	
Thr	Lys	Glu	Ser	Ile	Gln	Lys	Ile	Lys	Leu	Asp	Asp	Leu	Lys	Gln	Gln		
	180					185				190							
ttt	gct	aag	gtc	ttt	gaa	ctc	aat	aag	ctc	gtg	gtg	gtg	ctt	ggg	ggc	680	
Phe	Ala	Lys	Val	Phe	Glu	Leu	Asn	Lys	Leu	Val	Val	Val	Leu	Gly	Gly		
195					200				205					210			
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Val	Thr	Pro	Gly	Leu	Val	Glu	Ser	Asn	Thr	Glu	Ser	Asn	Glu	Ala	Leu	
			295					300					305			
gcg	caa	aaa	ata	gac	ggg	gtt	ttt	gat	gtc	gct	atc	atc	aca	ggg	gag	1016
Ala	Gln	Lys	Ile	Asp	Gly	Val	Phe	Asp	Val	Ala	Ile	Ile	Thr	Gly	Glu	
		310					315					320				
ttg	aat	tcc	aaa	acg	att	gct	tca	caa	ttg	aaa	acc	ccc	caa	aaa	atc	1064
Leu	Asn	Ser	Lys	Thr	Ile	Ala	Ser	Gln	Leu	Lys	Thr	Pro	Gln	Lys	Ile	
		325				330					335					
tta	ctc	aag	gat	aag	gcg	caa	ttg	gaa	aat	atc	tta	caa	gcc	acc	acg	1112
Leu	Leu	Lys	Asp	Lys	Ala	Gln	Leu	Glu	Asn	Ile	Leu	Gln	Ala	Thr	Thr	
	340				345					350						
att	caa	ggc	gat	ttg	att	tta	ttc	gct	aat	gac	gcc	cct	aat	tac	att	1160
Ile	Gln	Gly	Asp	Leu	Ile	Leu	Phe	Ala	Asn	Asp	Ala	Pro	Asn	Tyr	Ile	
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1213

<210> 204

<211> 370

<212> PRT

<213> Helicobacter pylori

<220>

<221> VARIANT

<222> 4

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<400> 204

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			20					25					30		
Gln	Thr	Ala	Lys	Asp	Lys	Ile	Thr	Ser	Leu	Lys	Asn	Leu	Lys	Val	Ile
		35					40					45			
Ala	Ile	Thr	Gly	Ser	Phe	Gly	Lys	Thr	Ser	Thr	Lys	Asn	Phe	Leu	Leu
	50					55					60				
Gln	Ile	Leu	Gln	Thr	Thr	Phe	Asn	Ala	His	Ala	Ser	Pro	Lys	Ser	Val
65				70					75					80	
Asn	Thr	Leu	Leu	Gly	Leu	Ala	Asn	Asp	Ile	Asn	Gln	Asn	Leu	Asp	Asp
			85					90					95		
Arg	Ser	Glu	Ile	Tyr	Ile	Ala	Glu	Ala	Gly	Ala	Arg	Asn	Lys	Gly	Asp
		100					105					110			
Ile	Lys	Glu	Ile	Thr	Cys	Leu	Ile	Glu	Pro	His	Leu	Val	Val	Val	Ala
	115					120					125				
Glu	Val	Gly	Glu	Gln	His	Leu	Glu	Tyr	Phe	Lys	Thr	Leu	Glu	Asn	Ile
	130					135				140					
Cys	Glu	Thr	Lys	Ala	Glu	Leu	Leu	Asp	Ser	Lys	Arg	Leu	Glu	Lys	Ala
145				150					155					160	
Phe	Cys	Tyr	Ser	Val	Glu	Lys	Ile	Lys	Pro	Tyr	Ala	Pro	Lys	Asp	Ser
			165					170					175		
Pro	Leu	Ile	Asp	Tyr	Ser	Ser	Leu	Val	Lys	Asn	Ile	Gln	Ser	Thr	Leu
		180					185					190			
Lys	Gly	Thr	Ser	Phe	Glu	Met	Leu	Ile	Gly	Ser	Val	Trp	Glu	Arg	Phe
	195					200					205				
Glu	Thr	Lys	Val	Leu	Gly	Glu	Phe	Ser	Ala	Tyr	Asn	Ile	Ala	Ser	Ala
	210				215				220						
Ile	Leu	Ile	Ala	Lys	His	Leu	Gly	Leu	Glu	Thr	Glu	Arg	Ile	Lys	Arg
225				230					235					240	
Leu	Val	Leu	Glu	Leu	Asn	Pro	Ile	Ala	His	Arg	Leu	Gln	Leu	Leu	Glu
			245					250					255		
Val	Asn	Gln	Lys	Ile	Ile	Ile	Asp	Asp	Ser	Phe	Asn	Gly	Asn	Leu	Lys
		260					265					270			
Gly	Met	Leu	Glu	Gly	Ile	Arg	Leu	Ala	Ser	Leu	His	Lys	Gly	Arg	Lys
	275					280					285				
Val	Ile	Val	Thr	Pro	Gly	Leu	Val	Glu	Ser	Asn	Thr	Glu	Ser	Asn	Glu
	290				295						300				
Ala	Leu	Ala	Gln	Lys	Ile	Asp	Gly	Val	Phe	Asp	Val	Ala	Ile	Ile	Thr
305				310					315					320	
Gly	Glu	Leu	Asn	Ser	Lys	Thr	Ile	Ala	Ser	Gln	Leu	Lys	Thr	Pro	Gln
			325					330					335		



Ala	Ser	Ser	Asn	Asp	Val	Val	Leu	Gln	Val	Ala	Phe	Glu	Asn	Leu	His	
				135					140						145	
caa	agc	act	ctg	tct	aaa	atg	tcg	caa	ctg	agc	caa	gaa	gaa	aag	gaa	536
Gln	Ser	Thr	Leu	Ser	Lys	Met	Ser	Gln	Leu	Ser	Gln	Glu	Glu	Lys	Glu	
			150					155					160			
ctc	aat	acg	caa	gct	tta	aaa	gtc	aaa	aac	agc	att	caa	aaa	atc	tca	584
Leu	Asn	Thr	Gln	Ala	Leu	Lys	Val	Lys	Asn	Ser	Ile	Gln	Lys	Ile	Ser	
			165				170						175			
tcc	atc	ata	gat	gag	caa	aaa	act	cgt	gaa	gta	acc	tta	aaa	tcc	ttg	632
Ser	Ile	Ile	Asp	Glu	Gln	Lys	Thr	Arg	Glu	Val	Thr	Leu	Lys	Ser	Leu	
	180						185				190					
aaa	acc	gaa	caa	gat	aag	ctc	att	ttg	agc	atg	caa	aaa	gat	tat	gcg	680
Lys	Thr	Glu	Gln	Asp	Lys	Leu	Ile	Leu	Ser	Met	Gln	Lys	Asp	Tyr	Ala	
195					200					205					210	
atc	tac	aac	caa	cgc	cta	acc	ctt	tta	gaa	aaa	gag	cgc	cag	aat	tta	728
Ile	Tyr	Asn	Gln	Arg	Leu	Thr	Leu	Leu	Glu	Lys	Glu	Arg	Gln	Asn	Leu	
				215					220					225		
aac	gct	ctt	tta	aaa	cgc	ttg	aat	atc	atc	aaa	caa	aac	aga	gaa	aat	776
Asn	Ala	Leu	Leu	Lys	Arg	Leu	Asn	Ile	Ile	Lys	Gln	Asn	Arg	Glu	Asn	
			230					235					240			
gaa	gaa	aaa	gtc	agt	ttg	aaa	aaa	tct	tct	caa	gcc	tta	gaa	gtc	aaa	824
Glu	Glu	Lys	Val	Ser	Leu	Lys	Lys	Ser	Ser	Gln	Ala	Leu	Glu	Val	Lys	
		245					250					255				
caa	gtg	gct	agc	tct	tat	caa	aat	atc	aac	acc	acg	agc	tat	aac	gga	872
Gln	Val	Ala	Ser	Ser	Tyr	Gln	Asn	Ile	Asn	Thr	Thr	Ser	Tyr	Asn	Gly	
	260					265					270					
cca	aaa	acg	atc	gct	ccc	ttg	aac	gat	tat	gaa	gtg	gtg	caa	aaa	ttt	920
Pro	Lys	Thr	Ile	Ala	Pro	Leu	Asn	Asp	Tyr	Glu	Val	Val	Gln	Lys	Phe	
275					280					285					290	
ggc	ccc	tat	att	gac	ccg	gtt	tat	aat	tta	aaa	att	ttt	agc	gag	tct	968
Gly	Pro	Tyr	Ile	Asp	Pro	Val	Tyr	Asn	Leu	Lys	Ile	Phe	Ser	Glu	Ser	
				295					300					305		
att	acg	ctc	gtg	tca	aaa	acc	cca	aac	gct	ttg	gtg	cgt	aat	ggt	tta	1016
Ile	Thr	Leu	Val	Ser	Lys	Thr	Pro	Asn	Ala	Leu	Val	Arg	Asn	Val	Leu	
			310					315					320			
gac	ggg	aaa	atc	gtg	ttc	gct	aaa	gaa	atc	aac	atg	ctt	aaa	aaa	gtc	1064
Asp	Gly	Lys	Ile	Val	Phe	Ala	Lys	Glu	Ile	Asn	Met	Leu	Lys	Lys	Val	
		325					330					335				
gtt	atc	att	gag	cat	aaa	aat	ggg	atc	cgc	acg	att	tat	tct	caa	ttg	1112
Val	Ile	Ile	Glu	His	Lys	Asn	Gly	Ile	Arg	Thr	Ile	Tyr	Ser	Gln	Leu	
	340					345					350					

gat aaa atc gct ccc acc att aaa agc ggc atg cgg atc caa aaa ggc 1160  
 Asp Lys Ile Ala Pro Thr Ile Lys Ser Gly Met Arg Ile Gln Lys Gly  
 355 360 365 370

tat gtt tta ggg cgc att gat caa cgc ttg ggc ttt gaa gtt acc atg 1208  
 Tyr Val Leu Gly Arg Ile Asp Gln Arg Leu Gly Phe Glu Val Thr Met  
 375 380 385

aga gaa aaa cac atc aac ccc tta gaa ctc atc gca cgc aat 1250  
 Arg Glu Lys His Ile Asn Pro Leu Glu Leu Ile Ala Arg Asn  
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<212> PRT

<213> Helicobacter pylori

<400> 206

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 Leu Leu Lys Lys Thr His Glu Glu Lys Asn Gln Leu Asn Ser Arg Leu  
 35 40 45  
 Ser Ser Leu Gly Glu Ala Ile Arg Ser Lys Glu Leu Gln Lys Ala Glu  
 50 55 60  
 Met Glu Arg Gln Met Ile Ala Leu Lys Lys Ser Leu Glu Lys Asn Arg  
 65 70 75 80  
 Asn Glu Ser Leu Ala Gln Glu Lys Val Leu Thr Asn Tyr Arg Lys Ser  
 85 90 95  
 Leu Asp His Leu Gln Lys Lys Arg Ser Phe Leu Gln Lys Arg Val Phe  
 100 105 110  
 Asp Thr Leu Leu Gln Asp Phe Leu Phe Ser Gln Ala Leu Lys Gly Gln  
 115 120 125  
 Asn Leu Ala Ser Ser Asn Asp Val Val Leu Gln Val Ala Phe Glu Asn  
 130 135 140  
 Leu His Gln Ser Thr Leu Ser Lys Met Ser Gln Leu Ser Gln Glu Glu  
 145 150 155 160  
 Lys Glu Leu Asn Thr Gln Ala Leu Lys Val Lys Asn Ser Ile Gln Lys  
 165 170 175  
 Ile Ser Ser Ile Ile Asp Glu Gln Lys Thr Arg Glu Val Thr Leu Lys  
 180 185 190  
 Ser Leu Lys Thr Glu Gln Asp Lys Leu Ile Leu Ser Met Gln Lys Asp  
 195 200 205  
 Tyr Ala Ile Tyr Asn Gln Arg Leu Thr Leu Leu Glu Lys Glu Arg Gln  
 210 215 220  
 Asn Leu Asn Ala Leu Leu Lys Arg Leu Asn Ile Ile Lys Gln Asn Arg  
 225 230 235 240  
 Glu Asn Glu Glu Lys Val Ser Leu Lys Lys Ser Ser Gln Ala Leu Glu  
 245 250 255  
 Val Lys Gln Val Ala Ser Ser Tyr Gln Asn Ile Asn Thr Thr Ser Tyr  
 260 265 270  
 Asn Gly Pro Lys Thr Ile Ala Pro Leu Asn Asp Tyr Glu Val Val Gln





ttccactcta ggc

361

<210> 208

<211> 86

<212> PRT

<213> Helicobacter pylori

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Val	Thr	Met	Pro	Val	Ser	Gly	Asn	Asp	Ala	Gln	Tyr	Ser	Lys	Glu	Gly
			20					25					30		
Arg	Ala	Ser	Cys	Trp	Ser	Val	Phe	Ser	Leu	Val	Ala	Ala	Gly	Asn	Cys
		35					40					45			
Ser	Val	Glu	Lys	Ala	Ala	Lys	Ser	Gly	Gly	Val	Thr	Lys	Ile	Lys	Met
	50					55					60				
Val	Ser	Arg	Glu	Thr	Asn	Asn	Phe	Leu	Gly	Ile	Val	Gly	Lys	Tyr	Thr
65					70					75					80
Thr	Ile	Val	Gln	Gly	Asp										
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<211> 1564

<212> DNA

<213> Helicobacter pylori

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<400> 209

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					1		
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Glu	Trp	Met	Gln	Asn	His	Arg	Lys
		5					10
							15
agc	acg	atc	gct	ttt	att	gcc	gct
Ser	Thr	Ile	Ala	Phe	Ile	Ala	Ala
	20					25	
							30
agc	ttt	tct	tta	gat	agc	gat	agc
Ser	Phe	Ser	Leu	Asp	Ser	Asp	Ser
	35				40		45
							50
att	tct	caa	gaa	gaa	tta	gcc	caa
Ile	Ser	Gln	Glu	Glu	Leu	Ala	Gln
			55				60
							65
tat	gct	gag	tct	atc	cct	gat	ttt
Tyr	Ala	Glu	Ser	Ile	Pro	Asp	Phe
			70				75
							80

aaa gcc atg cat tta gaa aaa agc gct tta gat tcg ctc atc aat caa	344
Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln	
85 90 95	
gcc tta ttg aga aat ctc gct tta gat tta ggg ctt ggc gct aca aag	392
Ala Leu Leu Arg Asn Leu Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys	
100 105 110	
caa gaa gtg gcg aaa gag atc aga aaa acg agc gtt ttc caa aaa gat	440
Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Ser Val Phe Gln Lys Asp	
115 120 125 130	
ggc gtt ttt gat gaa gaa ttg tat aaa aat atc tta aag caa agc cat	488
Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His	
135 140 145	
tac cgc ccc aaa cat ttt gaa gaa agc gtt gaa agg ctt tta atc ctt	536
Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu	
150 155 160	
caa aaa atc agc act cta ttc ccc aaa acc act acc cct ttg gag caa	584
Gln Lys Ile Ser Thr Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln	
165 170 175	
tcc agc cta tcg ctt tgg gca aaa ttg caa gac aaa tta gac att ctt	632
Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu	
180 185 190	
atc cta aac cct agt gat gtt aaa atc tct ctt aat gaa gaa gag atg	680
Ile Leu Asn Pro Ser Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met	
195 200 205 210	
aaa aaa tat tac gag tcc cat aaa aag gat ttt aaa aag ccc acg agc	728
Lys Lys Tyr Tyr Glu Ser His Lys Lys Asp Phe Lys Lys Pro Thr Ser	
215 220 225	
ttt aaa aca cgc tct tta tat ttt gac gct agt ttg gaa aaa cct gat	776
Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Pro Asp	
230 235 240	
ttg aag gag ttg gag gaa tac tac cat aaa aac aag gtg tct tat ttg	824
Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu	
245 250 255	
gac aaa gag ggg aaa ttg cag gat ttt aaa agc gtt caa gag caa gtc	872
Asp Lys Glu Gly Lys Leu Gln Asp Phe Lys Ser Val Gln Glu Gln Val	
260 265 270	
aag cat gat tta agc atg caa aaa gcg aat gaa aaa gcc tta agg agc	920
Lys His Asp Leu Ser Met Gln Lys Ala Asn Glu Lys Ala Leu Arg Ser	
275 280 285 290	
tat atc gct cta aaa aaa gcg aac gcg caa aac tac acc aca caa gat	968
Tyr Ile Ala Leu Lys Lys Ala Asn Ala Gln Asn Tyr Thr Thr Gln Asp	

295	300	305	
ttt gaa gag aac aac tcc ccc tat act gct gaa atc acg caa aaa ctc			1016
Phe Glu Glu Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln Lys Leu			
310	315	320	
acc gct ctc aaa ccc ctt gaa atc cta aag cca gag cct ttt aaa gat			1064
Thr Ala Leu Lys Pro Leu Glu Ile Leu Lys Pro Glu Pro Phe Lys Asp			
325	330	335	
ggg ttt att gtg gtg caa ctc atc tct caa att aaa gac gaa ttg caa			1112
Gly Phe Ile Val Val Gln Leu Ile Ser Gln Ile Lys Asp Glu Leu Gln			
340	345	350	
aat ttt aat gaa gct aaa agc gct ctt aaa acc cgc cta act caa gaa			1160
Asn Phe Asn Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr Gln Glu			
355	360	365	370
aaa acc ctt atg gcg ttg caa act tta gcc aaa gaa aag ctt aag gat			1208
Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu Lys Asp			
375	380	385	
ttt aag ggc aaa agc gtg ggc tat gta agc cct aat ttt gga ggc act			1256
Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly Gly Thr			
390	395	400	
att agt gag ctt aac caa gaa gaa agt gct aag ttt atc aac gct ctt			1304
Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn Ala Leu			
405	410	415	
ttt aac cgc cag gaa aaa aag ggg ttt atc gct att aat aat aaa gtg			1352
Phe Asn Arg Gln Glu Lys Lys Gly Phe Ile Ala Ile Asn Asn Lys Val			
420	425	430	
gtg ctc tat caa atc aca gaa caa aat ttc aac cac tca ttt agt gca			1400
Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Ser Phe Ser Ala			
435	440	445	450
gaa gaa agc cag tat atg cag cgt tta gtc aat aac act aaa acg gat			1448
Glu Glu Ser Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys Thr Asp			
455	460	465	
ttt ttt gat aaa gcg ttg ata gaa gaa ttg aaa aaa cgc tat aag ata			1496
Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr Lys Ile			
470	475	480	
gtc aaa tac att caa taaatgcaag gggaaatcat ggaacataaaa gaaatcgтта			1551
Val Lys Tyr Ile Gln			
485			
taggggttga tct			1564
<210> 210			
<211> 487			
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<213> Helicobacter pylori

<400> 210

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			20					25					30		
Gln	Tyr	Ser	Phe	Ser	Leu	Asp	Ser	Asp	Ser	Ala	Ala	Lys	Val	Gly	Gln
		35					40					45			
Ile	Lys	Ile	Ser	Gln	Glu	Glu	Leu	Ala	Gln	Glu	Tyr	Arg	Arg	Leu	Lys
	50					55					60				
Asp	Ala	Tyr	Ala	Glu	Ser	Ile	Pro	Asp	Phe	Lys	Glu	Leu	Thr	Lys	Asp
65					70					75					80
Gln	Ile	Lys	Ala	Met	His	Leu	Glu	Lys	Ser	Ala	Leu	Asp	Ser	Leu	Ile
				85					90					95	
Asn	Gln	Ala	Leu	Leu	Arg	Asn	Leu	Ala	Leu	Asp	Leu	Gly	Leu	Gly	Ala
			100					105					110		
Thr	Lys	Gln	Glu	Val	Ala	Lys	Glu	Ile	Arg	Lys	Thr	Ser	Val	Phe	Gln
		115					120					125			
Lys	Asp	Gly	Val	Phe	Asp	Glu	Glu	Leu	Tyr	Lys	Asn	Ile	Leu	Lys	Gln
	130					135					140				
Ser	His	Tyr	Arg	Pro	Lys	His	Phe	Glu	Glu	Ser	Val	Glu	Arg	Leu	Leu
145					150					155					160
Ile	Leu	Gln	Lys	Ile	Ser	Thr	Leu	Phe	Pro	Lys	Thr	Thr	Thr	Pro	Leu
			165						170					175	
Glu	Gln	Ser	Ser	Leu	Ser	Leu	Trp	Ala	Lys	Leu	Gln	Asp	Lys	Leu	Asp
			180					185				190			
Ile	Leu	Ile	Leu	Asn	Pro	Ser	Asp	Val	Lys	Ile	Ser	Leu	Asn	Glu	Glu
	195						200					205			
Glu	Met	Lys	Lys	Tyr	Tyr	Glu	Ser	His	Lys	Lys	Asp	Phe	Lys	Lys	Pro
	210					215					220				
Thr	Ser	Phe	Lys	Thr	Arg	Ser	Leu	Tyr	Phe	Asp	Ala	Ser	Leu	Glu	Lys
225					230					235					240
Pro	Asp	Leu	Lys	Glu	Leu	Glu	Glu	Tyr	Tyr	His	Lys	Asn	Lys	Val	Ser
			245						250					255	
Tyr	Leu	Asp	Lys	Glu	Gly	Lys	Leu	Gln	Asp	Phe	Lys	Ser	Val	Gln	Glu
			260					265					270		
Gln	Val	Lys	His	Asp	Leu	Ser	Met	Gln	Lys	Ala	Asn	Glu	Lys	Ala	Leu
		275					280					285			
Arg	Ser	Tyr	Ile	Ala	Leu	Lys	Lys	Ala	Asn	Ala	Gln	Asn	Tyr	Thr	Thr
	290					295					300				
Gln	Asp	Phe	Glu	Glu	Asn	Asn	Ser	Pro	Tyr	Thr	Ala	Glu	Ile	Thr	Gln
305					310					315					320
Lys	Leu	Thr	Ala	Leu	Lys	Pro	Leu	Glu	Ile	Leu	Lys	Pro	Glu	Pro	Phe
			325						330					335	
Lys	Asp	Gly	Phe	Ile	Val	Val	Gln	Leu	Ile	Ser	Gln	Ile	Lys	Asp	Glu
		340						345					350		
Leu	Gln	Asn	Phe	Asn	Glu	Ala	Lys	Ser	Ala	Leu	Lys	Thr	Arg	Leu	Thr
		355					360					365			
Gln	Glu	Lys	Thr	Leu	Met	Ala	Leu	Gln	Thr	Leu	Ala	Lys	Glu	Lys	Leu
	370					375					380				
Lys	Asp	Phe	Lys	Gly	Lys	Ser	Val	Gly	Tyr	Val	Ser	Pro	Asn	Phe	Gly
385					390					395					400
Gly	Thr	Ile	Ser	Glu	Leu	Asn	Gln	Glu	Glu	Ser	Ala	Lys	Phe	Ile	Asn
				405					410					415	

Ala	Leu	Phe	Asn	Arg	Gln	Glu	Lys	Lys	Gly	Phe	Ile	Ala	Ile	Asn	Asn		
			420					425					430				
Lys	Val	Val	Leu	Tyr	Gln	Ile	Thr	Glu	Gln	Asn	Phe	Asn	His	Ser	Phe		
		435					440				445						
Ser	Ala	Glu	Glu	Ser	Gln	Tyr	Met	Gln	Arg	Leu	Val	Asn	Asn	Thr	Lys		
	450				455					460							
Thr	Asp	Phe	Phe	Asp	Lys	Ala	Leu	Ile	Glu	Glu	Leu	Lys	Lys	Arg	Tyr		
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Lys	Ile	Val	Lys	Tyr	Ile	Gln											
				485													

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 <213> Helicobacter pylori

<220>  
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 <222> (51)...(1382)

<400> 211																
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His	Phe	Ser	Val	Lys	Arg	Leu	Leu	Gly	Leu	Ser	Ser	Val	Leu	Leu	Val	
		5					10					15				
act	tta	gga	gcg	agc	atg	cac	gca	caa	tct	tac	tta	ccc	aaa	cat	gag	152
Thr	Leu	Gly	Ala	Ser	Met	His	Ala	Gln	Ser	Tyr	Leu	Pro	Lys	His	Glu	
	20					25				30						
agc	gtt	acc	tta	aaa	aac	ggg	ttg	caa	gtc	gtg	agc	gtc	ccc	cta	gaa	200
Ser	Val	Thr	Leu	Lys	Asn	Gly	Leu	Gln	Val	Val	Ser	Val	Pro	Leu	Glu	
	35				40				45					50		
aat	aaa	acc	ggg	gtt	ata	gaa	gtg	gat	gtg	ctt	tat	aaa	gtc	ggc	tct	248
Asn	Lys	Thr	Gly	Val	Ile	Glu	Val	Asp	Val	Leu	Tyr	Lys	Val	Gly	Ser	
			55					60						65		
aga	aac	gaa	acc	atg	gga	aag	agc	ggg	atc	gct	cac	atg	tta	gag	cat	296
Arg	Asn	Glu	Thr	Met	Gly	Lys	Ser	Gly	Ile	Ala	His	Met	Leu	Glu	His	
			70					75					80			
ttg	aat	ttt	aaa	agc	acc	aaa	aac	ctt	aaa	gcc	ggc	gaa	ttt	gat	aaa	344
Leu	Asn	Phe	Lys	Ser	Thr	Lys	Asn	Leu	Lys	Ala	Gly	Glu	Phe	Asp	Lys	
		85				90					95					
atc	gtt	aag	cgt	ttt	ggg	ggc	gtg	agt	aac	gct	tct	acg	agt	ttt	gat	392
Ile	Val	Lys	Arg	Phe	Gly	Gly	Val	Ser	Asn	Ala	Ser	Thr	Ser	Phe	Asp	
	100				105					110						
att	acg	cgc	tac	ttc	att	aaa	acc	agt	cag	gct	aac	ttg	gat	aag	tct	440

Ile Thr Arg Tyr Phe Ile Lys Thr Ser Gln Ala Asn Leu Asp Lys Ser	
115 120 125 130	
tta gaa ttg ttc gct gaa acc atg ggt tca ttg aat tta aaa gaa gat	488
Leu Glu Leu Phe Ala Glu Thr Met Gly Ser Leu Asn Leu Lys Glu Asp	
135 140 145	
gag ttt ttg cct gag cgt caa gtg gtc gct gaa gaa agg cga tgg cgc	536
Glu Phe Leu Pro Glu Arg Gln Val Val Ala Glu Glu Arg Arg Trp Arg	
150 155 160	
act gat aat tcc cct atc ggc atg ctt tat ttc cgc ttt ttt aac acc	584
Thr Asp Asn Ser Pro Ile Gly Met Leu Tyr Phe Arg Phe Phe Asn Thr	
165 170 175	
gct tat gtc tat cac ccc tac cat tgg acg ccc att ggt ttt atg gat	632
Ala Tyr Val Tyr His Pro Tyr His Trp Thr Pro Ile Gly Phe Met Asp	
180 185 190	
gat att caa aat tgg act tta aaa gac att aaa aaa ttc cat tcg ctc	680
Asp Ile Gln Asn Trp Thr Leu Lys Asp Ile Lys Lys Phe His Ser Leu	
195 200 205 210	
tat tat cag cct aaa aac gct atc gtt ttg gtg gta ggc gat gtc aat	728
Tyr Tyr Gln Pro Lys Asn Ala Ile Val Leu Val Val Gly Asp Val Asn	
215 220 225	
tcc caa aag gtt ttt gaa ttg agt aaa aag cat ttt gaa tcc tta aaa	776
Ser Gln Lys Val Phe Glu Leu Ser Lys Lys His Phe Glu Ser Leu Lys	
230 235 240	
aac ctt gat gaa aaa gct atc ccc acc cct tac atg aaa gag cct aag	824
Asn Leu Asp Glu Lys Ala Ile Pro Thr Pro Tyr Met Lys Glu Pro Lys	
245 250 255	
caa gat gga gcc aga acg gca gtc gtg cat aaa gat ggg gtc cat tta	872
Gln Asp Gly Ala Arg Thr Ala Val Val His Lys Asp Gly Val His Leu	
260 265 270	
gaa tgg gtg gcc ctt ggg tat aaa gtg cct gct ttc aag cat aaa gat	920
Glu Trp Val Ala Leu Gly Tyr Lys Val Pro Ala Phe Lys His Lys Asp	
275 280 285 290	
caa gtc gcc tta gac gca cta agt agg ctt tta ggc gaa ggc aaa agc	968
Gln Val Ala Leu Asp Ala Leu Ser Arg Leu Leu Gly Glu Gly Lys Ser	
295 300 305	
tcg tgg ttg caa agc gaa tta gtg gat aaa aaa cgc ttg gct tct caa	1016
Ser Trp Leu Gln Ser Glu Leu Val Asp Lys Lys Arg Leu Ala Ser Gln	
310 315 320	
gct ttc tcg cac aac atg caa tta caa gat gaa agc gtg ttt tta ttc	1064
Ala Phe Ser His Asn Met Gln Leu Gln Asp Glu Ser Val Phe Leu Phe	
325 330 335	

att gcg ggg ggt aat cct aat gtc aaa gcc gaa gcc tta caa aaa gaa 1112  
 Ile Ala Gly Gly Asn Pro Asn Val Lys Ala Glu Ala Leu Gln Lys Glu  
 340 345 350

atc gta gcg ctt tta gaa aag ctg aaa aaa ggc gaa atc act caa gcg 1160  
 Ile Val Ala Leu Leu Glu Lys Leu Lys Lys Gly Glu Ile Thr Gln Ala  
 355 360 365 370

gaa tta gac aag ctc aaa atc aat caa aaa gct gac ttt att tct aat 1208  
 Glu Leu Asp Lys Leu Lys Ile Asn Gln Lys Ala Asp Phe Ile Ser Asn  
 375 380 385

tta gaa agt tct agc gat gtt gcg ggg ctt ttt gcg gac tat tta gtg 1256  
 Leu Glu Ser Ser Ser Asp Val Ala Gly Leu Phe Ala Asp Tyr Leu Val  
 390 395 400

caa aac gat att caa ggc ttg acg gat tac cag cga caa ttt ttg gat 1304  
 Gln Asn Asp Ile Gln Gly Leu Thr Asp Tyr Gln Arg Gln Phe Leu Asp  
 405 410 415

tta aaa gtg agc gat ttg gtg cgt gtg gcc aat gaa tat ttt aaa gac 1352  
 Leu Lys Val Ser Asp Leu Val Arg Val Ala Asn Glu Tyr Phe Lys Asp  
 420 425 430

acc caa tca acc acc gtg ttt ttg aaa cct taaaagagcc ttataacatg 1402  
 Thr Gln Ser Thr Thr Val Phe Leu Lys Pro  
 435 440

caatttcatt catctagcgc gttgattacg cct 1435

<210> 212

<211> 444

<212> PRT

<213> *Helicobacter pylori*

<400> 212

Met Lys His Phe Ser Val Lys Arg Leu Leu Gly Leu Ser Ser Val Leu  
 1 5 10 15  
 Leu Val Thr Leu Gly Ala Ser Met His Ala Gln Ser Tyr Leu Pro Lys  
 20 25 30  
 His Glu Ser Val Thr Leu Lys Asn Gly Leu Gln Val Val Ser Val Pro  
 35 40 45  
 Leu Glu Asn Lys Thr Gly Val Ile Glu Val Asp Val Leu Tyr Lys Val  
 50 55 60  
 Gly Ser Arg Asn Glu Thr Met Gly Lys Ser Gly Ile Ala His Met Leu  
 65 70 75 80  
 Glu His Leu Asn Phe Lys Ser Thr Lys Asn Leu Lys Ala Gly Glu Phe  
 85 90 95  
 Asp Lys Ile Val Lys Arg Phe Gly Gly Val Ser Asn Ala Ser Thr Ser  
 100 105 110  
 Phe Asp Ile Thr Arg Tyr Phe Ile Lys Thr Ser Gln Ala Asn Leu Asp  
 115 120 125  
 Lys Ser Leu Glu Leu Phe Ala Glu Thr Met Gly Ser Leu Asn Leu Lys  
 130 135 140  
 Glu Asp Glu Phe Leu Pro Glu Arg Gln Val Val Ala Glu Glu Arg Arg



145		150		155		160									
Trp	Arg	Thr	Asp	Asn	Ser	Pro	Ile	Gly	Met	Leu	Tyr	Phe	Arg	Phe	Phe
			165						170					175	
Asn	Thr	Ala	Tyr	Val	Tyr	His	Pro	Tyr	His	Trp	Thr	Pro	Ile	Gly	Phe
			180						185				190		
Met	Asp	Asp	Ile	Gln	Asn	Trp	Thr	Leu	Lys	Asp	Ile	Lys	Lys	Phe	His
		195					200					205			
Ser	Leu	Tyr	Tyr	Gln	Pro	Lys	Asn	Ala	Ile	Val	Leu	Val	Val	Gly	Asp
	210					215					220				
Val	Asn	Ser	Gln	Lys	Val	Phe	Glu	Leu	Ser	Lys	Lys	His	Phe	Glu	Ser
225					230					235					240
Leu	Lys	Asn	Leu	Asp	Glu	Lys	Ala	Ile	Pro	Thr	Pro	Tyr	Met	Lys	Glu
			245						250					255	
Pro	Lys	Gln	Asp	Gly	Ala	Arg	Thr	Ala	Val	Val	His	Lys	Asp	Gly	Val
		260						265					270		
His	Leu	Glu	Trp	Val	Ala	Leu	Gly	Tyr	Lys	Val	Pro	Ala	Phe	Lys	His
	275						280					285			
Lys	Asp	Gln	Val	Ala	Leu	Asp	Ala	Leu	Ser	Arg	Leu	Leu	Gly	Glu	Gly
	290					295					300				
Lys	Ser	Ser	Trp	Leu	Gln	Ser	Glu	Leu	Val	Asp	Lys	Lys	Arg	Leu	Ala
305					310					315					320
Ser	Gln	Ala	Phe	Ser	His	Asn	Met	Gln	Leu	Gln	Asp	Glu	Ser	Val	Phe
			325					330						335	
Leu	Phe	Ile	Ala	Gly	Gly	Asn	Pro	Asn	Val	Lys	Ala	Glu	Ala	Leu	Gln
		340						345					350		
Lys	Glu	Ile	Val	Ala	Leu	Leu	Glu	Lys	Leu	Lys	Lys	Gly	Glu	Ile	Thr
	355						360					365			
Gln	Ala	Glu	Leu	Asp	Lys	Leu	Lys	Ile	Asn	Gln	Lys	Ala	Asp	Phe	Ile
	370					375					380				
Ser	Asn	Leu	Glu	Ser	Ser	Ser	Asp	Val	Ala	Gly	Leu	Phe	Ala	Asp	Tyr
385					390					395					400
Leu	Val	Gln	Asn	Asp	Ile	Gln	Gly	Leu	Thr	Asp	Tyr	Gln	Arg	Gln	Phe
			405					410						415	
Leu	Asp	Leu	Lys	Val	Ser	Asp	Leu	Val	Arg	Val	Ala	Asn	Glu	Tyr	Phe
		420						425					430		
Lys	Asp	Thr	Gln	Ser	Thr	Thr	Val	Phe	Leu	Lys	Pro				
	435						440								

<210> 213  
 <211> 250  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(197)

<400> 213  
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 Met Met  
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aaa aaa acc ctt ttt atc tct ttg gct tta gcg tta agc ttg aat gcg 104  
 Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu Asn Ala

5	10	15	
ggc aat atc caa atc cag agc atg ccc aaa gtt aaa gag cga gtg agt			152
Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg Val Ser			
20	25	30	
gtc ccc tct aaa gac gat acg gat cta ttc tta cca cga ttc tat			197
Val Pro Ser Lys Asp Asp Thr Asp Leu Phe Leu Pro Arg Phe Tyr			
35	40	45	
taaggactct attaaggcgg tggatgaatat ctccactgaa aagaagatta aaa			250
<210> 214			
<211> 49			
<212> PRT			
<213> Helicobacter pylori			
<400> 214			
Met Met Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu			
1	5	10	15
Asn Ala Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg			
20	25	30	
Val Ser Val Pro Ser Lys Asp Asp Thr Asp Leu Phe Leu Pro Arg Phe			
35	40	45	
Tyr			
<210> 215			
<211> 328			
<212> DNA			
<213> Helicobacter pylori			
<220>			
<221> CDS			
<222> (51)...(275)			
<400> 215			
ttaagattgc gggtatactg aaaaaaaciaa tatgaaatca aggagcttgt atg caa			56
		Met Gln	
		1	
cag cgt cat tta ggc cct tta aaa gtg ggt gca tta gct cta ggg tgc			104
Gln Arg His Leu Gly Pro Leu Lys Val Gly Ala Leu Ala Leu Gly Cys			
5	10	15	
atg ggc atg act tat ggg tat ggg gaa gtc cat gat aaa aag cag atg			152
Met Gly Met Thr Tyr Gly Tyr Gly Glu Val His Asp Lys Lys Gln Met			
20	25	30	
gtt aaa ctt atc cat aag gct ttg gaa ttg ggt att aac ttt ttt gac			200
Val Lys Leu Ile His Lys Ala Leu Glu Leu Gly Ile Asn Phe Phe Asp			
35	40	45	50
act gca gag gct tat ggg gaa gat aat gaa aag ctt tta ggc gaa cga			248

-279-

55										60										65										
aat	att	gat	gtg	aaa	agc	gtc	aat	act	agg	gat	aga	aaa	aga	gat	aac	296														
Asn	Ile	Asp	Val	Lys	Ser	Val	Asn	Thr	Arg	Asp	Arg	Lys	Arg	Asp	Asn															
70					75					80																				
cac	ttg	aaa	aca	gcg	gac	ttt	ttt	gat	gtg	gta	aaa	tac	ccc	aaa	ggg	344														
His	Leu	Lys	Thr	Ala	Asp	Phe	Phe	Asp	Val	Val	Lys	Tyr	Pro	Lys	Gly															
85				90				95																						
agc	ttt	aaa	atg	acc	aaa	tac	gaa	gat	ggg	aaa	atc	tat	ggg	gat	ttg	392														
Ser	Phe	Lys	Met	Thr	Lys	Tyr	Glu	Asp	Gly	Lys	Ile	Tyr	Gly	Asp	Leu															
100			105			110																								
act	ctt	cgt	ggc	gta	acc	aag	cct	gtc	gta	ttg	gaa	gcc	aaa	atc	caa	440														
Thr	Leu	Arg	Gly	Val	Thr	Lys	Pro	Val	Val	Leu	Glu	Ala	Lys	Ile	Gln															
115		120		125		130																								
gcc	ccc	tta	caa	aac	ccc	atg	aat	aaa	aaa	gaa	ttc	atg	gtg	tta	caa	488														
Ala	Pro	Leu	Gln	Asn	Pro	Met	Asn	Lys	Lys	Glu	Phe	Met	Val	Leu	Gln															
135				140				145																						
gct	gaa	ggc	aaa	atc	aac	cgc	aag	gat	ttt	ggg	atc	ggg	aaa	acc	ttt	536														
Ala	Glu	Gly	Lys	Ile	Asn	Arg	Lys	Asp	Phe	Gly	Ile	Gly	Lys	Thr	Phe															
150			155			160																								
agc	gat	gct	gtc	gtt	gga	gat	gag	gta	aag	att	gag	ctc	aaa	cta	gaa	584														
Ser	Asp	Ala	Val	Val	Gly	Asp	Glu	Val	Lys	Ile	Glu	Leu	Lys	Leu	Glu															
165			170			175																								
gct tac gcc caa taatcgtttt gcaagagata gatatcttct tctcttgcgt																636														
Ala Tyr Ala Gln																														
180																														
ttttctaaca gca																649														
<210> 218																														
<211> 182																														
<212> PRT																														
<213> Helicobacter pylori																														
<400> 218																														
Met	Lys	Lys	Ala	Leu	Ile	Ser	Thr	Leu	Phe	Gly	Val	Ser	Leu	Ala	Phe															
1	5			10			15																							
Ala	Lys	Pro	Tyr	Thr	Ile	Asp	Lys	Ala	Asn	Ser	Ser	Val	Trp	Phe	Glu															
20			25			30																								
Val	Lys	His	Phe	Thr	Phe	Asn	Glu	Thr	Arg	Gly	Ala	Phe	Asp	Asn	Phe															
35		40		45																										
Asp	Gly	Lys	Ile	Asp	Leu	Glu	Pro	Asn	Thr	Lys	Met	Leu	Ser	Val	Phe															
50		55		60																										
Glu	Gly	Asn	Ile	Asp	Val	Lys	Ser	Val	Asn	Thr	Arg	Asp	Arg	Lys	Arg															
65	70			75			80																							
Asp	Asn	His	Leu	Lys	Thr	Ala	Asp	Phe	Phe	Asp	Val	Val	Lys	Tyr	Pro															
85			90			95																								
Lys	Gly	Ser	Phe	Lys	Met	Thr	Lys	Tyr	Glu	Asp	Gly	Lys	Ile	Tyr	Gly															

	100		105		110										
Asp	Leu	Thr	Leu	Arg	Gly	Val	Thr	Lys	Pro	Val	Val	Leu	Glu	Ala	Lys
	115		120		125										
Ile	Gln	Ala	Pro	Leu	Gln	Asn	Pro	Met	Asn	Lys	Lys	Glu	Phe	Met	Val
	130		135		140										
Leu	Gln	Ala	Glu	Gly	Lys	Ile	Asn	Arg	Lys	Asp	Phe	Gly	Ile	Gly	Lys
145			150		155				160						
Thr	Phe	Ser	Asp	Ala	Val	Val	Gly	Asp	Glu	Val	Lys	Ile	Glu	Leu	Lys
			165		170				175						
Leu	Glu	Ala	Tyr	Ala	Gln										
	180														

<210> 219  
 <211> 478  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(425)

<400> 219	
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	Met Lys
	1
aag tta gcc gct tta ttt tta gta agc gtg ttg ggg gtt atg ggt tta	104
Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met Gly Leu	
	5 10 15
aac gca tgg gag caa acc cta aaa gct aat gac ttg gaa gtg aaa atc	152
Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val Lys Ile	
	20 25 30
aaa tcc gtg ggt aac ccc att aaa ggc gat aac act ttc att ctc agc	200
Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile Leu Ser	
	35 40 45 50
ccc act tta aaa ggt aag gct tta gaa aaa gct atc gtt agg gtg cag	248
Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg Val Gln	
	55 60 65
ttt atg atg cct gaa atg ccc ggc atg cca gcg atg aaa gaa atg gcg	296
Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu Met Ala	
	70 75 80
caa gtg agt gaa aaa aac ggc ctt tat gaa gct aaa acc aat ctt tct	344
Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn Leu Ser	
	85 90 95
atg aac ggg aca tgg cag gtt agg gtg gat att aaa tct aaa gag ggt	392
Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys Glu Gly	
	100 105 110

cag gtt tat cgc gct aaa aca agc ctg gat tta taagagcatg ctatctttta 445  
 Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu  
 115 120 125

taagcgcggtt tgataaaagg ggcgtttcaa tac 478

<210> 220  
 <211> 125  
 <212> PRT  
 <213> Helicobacter pylori

<400> 220  
 Met Lys Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met  
 1 5 10 15  
 Gly Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val  
 20 25 30  
 Lys Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile  
 35 40 45  
 Leu Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg  
 50 55 60  
 Val Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu  
 65 70 75 80  
 Met Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn  
 85 90 95  
 Leu Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys  
 100 105 110  
 Glu Gly Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu  
 115 120 125

<210> 221  
 <211> 1117  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1064)

<400> 221  
 agcgcttttaa atagcactta tttgtcttta caaaacctta aaggattaga atg aaa 56  
 Met Lys  
 1  
 cgg att tta tgg tta gcc ttg att tta ttt ttt agc ccc tta ttc gct 104  
 Arg Ile Leu Trp Leu Ala Leu Ile Leu Phe Phe Ser Pro Leu Phe Ala  
 5 10 15  
 aac gct caa aaa act caa gaa att aaa aaa act aaa gaa gct aaa agc 152  
 Asn Ala Gln Lys Thr Gln Glu Ile Lys Lys Thr Lys Glu Ala Lys Ser  
 20 25 30  
 caa acc cgt ttt aat att tcc acc act aag gtc ata gaa aaa gaa ttt 200  
 Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val Ile Glu Lys Glu Phe  
 35 40 45 50

tct caa agc cgg cgc tat tac gcg ctt tta gag ccc aat gaa gcg ctg	248
Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Leu Glu Pro Asn Glu Ala Leu	
55 60 65	
att ttt tct caa acc ctg cgt ttt gat ggc tat gtg gaa aag ctt tat	296
Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr Val Glu Lys Leu Tyr	
70 75 80	
gcg aat aaa acc tat acc ccc att aaa aag ggc gac agg tta ttg agc	344
Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys Gly Asp Arg Leu Leu Ser	
85 90 95	
gtg tat tcc cct gaa tta gtg agc gct caa agc gaa ttg cta tca tca	392
Val Tyr Ser Pro Glu Leu Val Ser Ala Gln Ser Glu Leu Leu Ser Ser	
100 105 110	
ttg aaa ttc aac caa caa gtg gga gcg att aaa gaa aaa tta aaa cta	440
Leu Lys Phe Asn Gln Gln Val Gly Ala Ile Lys Glu Lys Leu Lys Leu	
115 120 125 130	
tta ggg tta gaa aac tct agc att gaa aaa atc att agc agc cat aaa	488
Leu Gly Leu Glu Asn Ser Ser Ile Glu Lys Ile Ile Ser Ser His Lys	
135 140 145	
gtc caa aat gaa atg act att tac tct cac ttc aac ggc att att ttt	536
Val Gln Asn Glu Met Thr Ile Tyr Ser His Phe Asn Gly Ile Ile Phe	
150 155 160	
aaa aaa agc ccg gat ctc aat gag ggg agc ttc att aaa aaa ggg caa	584
Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser Phe Ile Lys Lys Gly Gln	
165 170 175	
gag ttg ttt caa atc ata gat tta agc caa ttg tgg gcg ctg gtt aaa	632
Glu Leu Phe Gln Ile Ile Asp Leu Ser Gln Leu Trp Ala Leu Val Lys	
180 185 190	
gtc aat caa gag gat tta gaa ttt tta aaa aac acg cat aaa gcg atc	680
Val Asn Gln Glu Asp Leu Glu Phe Leu Lys Asn Thr His Lys Ala Ile	
195 200 205 210	
ttg ttt gta gaa ggg att aaa ggc gag caa gaa atc acg ctt gaa aat	728
Leu Phe Val Glu Gly Ile Lys Gly Glu Gln Glu Ile Thr Leu Glu Asn	
215 220 225	
atc aac ccc atc atc aac aaa gaa gat aaa atg cta gaa gcg cgc ttc	776
Ile Asn Pro Ile Ile Asn Lys Glu Asp Lys Met Leu Glu Ala Arg Phe	
230 235 240	
aat gtg cct aat gtt aaa cag att tat tac cct aac atg ttc gct caa	824
Asn Val Pro Asn Val Lys Gln Ile Tyr Tyr Pro Asn Met Phe Ala Gln	
245 250 255	
gta gaa atc ttt caa aaa cca caa aaa atg aag att ttg cct aaa gaa	872
Val Glu Ile Phe Gln Lys Pro Gln Lys Met Lys Ile Leu Pro Lys Glu	

260	265	270	
gcg gtt ttg att aaa ggg ggg aaa gct atc gtg ttt aaa aaa gac gat			920
Ala Val Leu Ile Lys Gly Gly Lys Ala Ile Val Phe Lys Lys Asp Asp			
275	280	285	290
ttt ggc tta agc ccg tta gaa att aaa gcc gtc cgc ttg agc gat ggg			968
Phe Gly Leu Ser Pro Leu Glu Ile Lys Ala Val Arg Leu Ser Asp Gly			
	295	300	305
agt tat gag att tta gag ggt tta aag gcg ggc gaa gaa gtc gct aat			1016
Ser Tyr Glu Ile Leu Glu Gly Leu Lys Ala Gly Glu Glu Val Ala Asn			
	310	315	320
aac gct tta ttc gtg cta gac gct gac gct caa aac aat ggg gat tat			1064
Asn Ala Leu Phe Val Leu Asp Ala Asp Ala Gln Asn Asn Gly Asp Tyr			
	325	330	335
tgaatgatag aaaagatcat tgatttaagc gttaaaaaca aactccttac cac			1117
<210> 222			
<211> 338			
<212> PRT			
<213> Helicobacter pylori			
<400> 222			
Met Lys Arg Ile Leu Trp Leu Ala Leu Ile Leu Phe Phe Ser Pro Leu			
1	5	10	15
Phe Ala Asn Ala Gln Lys Thr Gln Glu Ile Lys Lys Thr Lys Glu Ala			
	20	25	30
Lys Ser Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val Ile Glu Lys			
	35	40	45
Glu Phe Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Leu Glu Pro Asn Glu			
	50	55	60
Ala Leu Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr Val Glu Lys			
	65	70	75
Leu Tyr Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys Gly Asp Arg Leu			
	85	90	95
Leu Ser Val Tyr Ser Pro Glu Leu Val Ser Ala Gln Ser Glu Leu Leu			
	100	105	110
Ser Ser Leu Lys Phe Asn Gln Gln Val Gly Ala Ile Lys Glu Lys Leu			
	115	120	125
Lys Leu Leu Gly Leu Glu Asn Ser Ser Ile Glu Lys Ile Ile Ser Ser			
	130	135	140
His Lys Val Gln Asn Glu Met Thr Ile Tyr Ser His Phe Asn Gly Ile			
	145	150	155
Ile Phe Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser Phe Ile Lys Lys			
	165	170	175
Gly Gln Glu Leu Phe Gln Ile Ile Asp Leu Ser Gln Leu Trp Ala Leu			
	180	185	190
Val Lys Val Asn Gln Glu Asp Leu Glu Phe Leu Lys Asn Thr His Lys			
	195	200	205
Ala Ile Leu Phe Val Glu Gly Ile Lys Gly Glu Gln Glu Ile Thr Leu			
	210	215	220
Glu Asn Ile Asn Pro Ile Ile Asn Lys Glu Asp Lys Met Leu Glu Ala			



225		230		235		240
Arg	Phe	Asn	Val	Pro	Asn	Val
		245		250		255
Ala	Gln	Val	Glu	Ile	Phe	Gln
		260		265		270
Lys	Glu	Ala	Val	Leu	Ile	Lys
		275		280		285
Asp	Asp	Phe	Gly	Leu	Ser	Pro
		290		295		300
Asp	Gly	Ser	Tyr	Glu	Ile	Leu
		305		310		315
Ala	Asn	Asn	Ala	Leu	Phe	Val
		325		330		335
Asp	Tyr					

<210> 223  
 <211> 1249  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(1196)

<400> 223  
 aaaacttaga taaaataaca cgataaaacc atagtaataa agataacccc atg aga 56  
 Met Arg  
 1

ttt ttt tgc ttt ttc tta ttt ttt cta acc ttt tca aac gca cag ata 104  
 Phe Phe Cys Phe Phe Leu Phe Phe Leu Thr Phe Ser Asn Ala Gln Ile  
 5 10 15

atg atg act ttt gat tct caa act aac gcc aaa ctc tcg cgc tct aac 152  
 Met Met Thr Phe Asp Ser Gln Thr Asn Ala Lys Leu Ser Arg Ser Asn  
 20 25 30

gaa ca'g ctt tca gac atg ctc tat aaa ctc aat gaa agt tta aga atc 200  
 Glu Gln Leu Ser Asp Met Leu Tyr Lys Leu Asn Glu Ser Leu Arg Ile  
 35 40 45 50

tat caa agc gtg ctt tcc aat aac caa gat caa ctc aaa gaa atc aaa 248  
 Tyr Gln Ser Val Leu Ser Asn Asn Gln Asp Gln Leu Lys Glu Ile Lys  
 55 60 65

aaa gct aac agc acc cta aat agc caa agg cgt ttt ttt aac gcc agc 296  
 Lys Ala Asn Ser Thr Leu Asn Ser Gln Arg Arg Phe Phe Asn Ala Ser  
 70 75 80

cag atc cgc ctt atg gac act gat gca cta ttg aaa caa agc gct ttg 344  
 Gln Ile Arg Leu Met Asp Thr Asp Ala Leu Leu Lys Gln Ser Ala Leu  
 85 90 95

gaa tta gaa aaa tta caa gct tta gaa aaa cac ata aaa aag ggc atg	392
Glu Leu Glu Lys Leu Gln Ala Leu Glu Lys His Ile Lys Lys Gly Met	
100 105 110	
gaa caa gaa cgc tta ata gaa gaa tcc caa acg ctt ttt tta caa gag	440
Glu Gln Glu Arg Leu Ile Glu Glu Ser Gln Thr Leu Phe Leu Gln Glu	
115 120 125 130	
cat tgc cct tat ttg agc ggc gtt aag aat tta gaa gag gct tca aac	488
His Cys Pro Tyr Leu Ser Gly Val Lys Asn Leu Glu Glu Ala Ser Asn	
135 140 145	
gct tta gaa gtc caa gag caa aac aac gcc ctt ttc tta ctc aaa gag	536
Ala Leu Glu Val Gln Glu Gln Asn Asn Ala Leu Phe Leu Leu Lys Glu	
150 155 160	
cct aaa ctc gcc cgt ttg ctc tca cga ttg gat ttg atg agc gct tta	584
Pro Lys Leu Ala Arg Leu Leu Ser Arg Leu Asp Leu Met Ser Ala Leu	
165 170 175	
aac gcc ttg tgc gat cag gtt tta gaa aac caa gcc cat aac caa caa	632
Asn Ala Leu Cys Asp Gln Val Leu Glu Asn Gln Ala His Asn Gln Gln	
180 185 190	
tcc cat aac aaa att tta gaa tac aac gct ctt aaa aac cat gat ttt	680
Ser His Asn Lys Ile Leu Glu Tyr Asn Ala Leu Lys Asn His Asp Phe	
195 200 205 210	
caa gcc tat aaa gcc atg cgt ttg aaa aaa ttt aaa aac aag ctt caa	728
Gln Ala Tyr Lys Ala Met Arg Leu Lys Phe Lys Asn Lys Leu Gln	
215 220 225	
agt caa atc caa gcc caa gaa gac gct cta aaa acc ttt tta ccc tta	776
Ser Gln Ile Gln Ala Gln Glu Asp Ala Leu Lys Thr Phe Leu Pro Leu	
230 235 240	
gaa aaa cgc ttg gaa act tta aaa acg cat ttt tta tgc gat aaa gaa	824
Glu Lys Arg Leu Glu Thr Leu Lys Thr His Phe Leu Cys Asp Lys Glu	
245 250 255	
aac cta aaa tca tgc gct aaa gaa ttg cac caa cgc tac caa aac gcc	872
Asn Leu Lys Ser Cys Ala Lys Glu Leu His Gln Arg Tyr Gln Asn Ala	
260 265 270	
ctt ata gag cga gat aaa gaa tta aaa aac gct aaa aat aat aaa gaa	920
Leu Ile Glu Arg Asp Lys Glu Leu Lys Asn Ala Lys Asn Asn Lys Glu	
275 280 285 290	
aag cat gct cta atc tta gcc aat tac gag cat act tta aaa acc ttg	968
Lys His Ala Leu Ile Leu Ala Asn Tyr Glu His Thr Leu Lys Thr Leu	
295 300 305	
aat ata gaa ttt tta agc gaa tta aat aag caa atg gcg ttt ttg aat	1016
Asn Ile Glu Phe Leu Ser Glu Leu Asn Lys Gln Met Ala Phe Leu Asn	
310 315 320	

gaa acc atg gcg tta aac gcc cga gtt tta gcc ctt tta gcc aaa cag 1064  
 Glu Thr Met Ala Leu Asn Ala Arg Val Leu Ala Leu Leu Ala Lys Gln  
 325 330 335

cat gcc aaa acg cca aag cct ttc aat ttg agc ggt ggt tta agc ggt 1112  
 His Ala Lys Thr Pro Lys Pro Phe Asn Leu Ser Gly Gly Leu Ser Gly  
 340 345 350

gat ttg agc ggt ggg aaa gct ctt att aaa aat atc cgc tta gat ccg 1160  
 Asp Leu Ser Gly Gly Lys Ala Leu Ile Lys Asn Ile Arg Leu Asp Pro  
 355 360 365 370

cat gga ttc cct agc ttt aaa aat ttt aag caa gag taggacaata 1206  
 His Gly Phe Pro Ser Phe Lys Asn Phe Lys Gln Glu  
 375 380

tttgacaagc aaaaacaatt atagtaaaat aagagcataa ctt 1249

<210> 224  
 <211> 382  
 <212> PRT  
 <213> Helicobacter pylori

<400> 224  
 Met Arg Phe Phe Cys Phe Phe Leu Phe Phe Leu Thr Phe Ser Asn Ala  
 1 5 10 15  
 Gln Ile Met Met Thr Phe Asp Ser Gln Thr Asn Ala Lys Leu Ser Arg  
 20 25 30  
 Ser Asn Glu Gln Leu Ser Asp Met Leu Tyr Lys Leu Asn Glu Ser Leu  
 35 40 45  
 Arg Ile Tyr Gln Ser Val Leu Ser Asn Asn Gln Asp Gln Leu Lys Glu  
 50 55 60  
 Ile Lys Lys Ala Asn Ser Thr Leu Asn Ser Gln Arg Arg Phe Phe Asn  
 65 70 75 80  
 Ala Ser Gln Ile Arg Leu Met Asp Thr Asp Ala Leu Leu Lys Gln Ser  
 85 90 95  
 Ala Leu Glu Leu Glu Lys Leu Gln Ala Leu Glu Lys His Ile Lys Lys  
 100 105 110  
 Gly Met Glu Gln Glu Arg Leu Ile Glu Glu Ser Gln Thr Leu Phe Leu  
 115 120 125  
 Gln Glu His Cys Pro Tyr Leu Ser Gly Val Lys Asn Leu Glu Glu Ala  
 130 135 140  
 Ser Asn Ala Leu Glu Val Gln Glu Gln Asn Asn Ala Leu Phe Leu Leu  
 145 150 155 160  
 Lys Glu Pro Lys Leu Ala Arg Leu Leu Ser Arg Leu Asp Leu Met Ser  
 165 170 175  
 Ala Leu Asn Ala Leu Cys Asp Gln Val Leu Glu Asn Gln Ala His Asn  
 180 185 190  
 Gln Gln Ser His Asn Lys Ile Leu Glu Tyr Asn Ala Leu Lys Asn His  
 195 200 205  
 Asp Phe Gln Ala Tyr Lys Ala Met Arg Leu Lys Lys Phe Lys Asn Lys  
 210 215 220  
 Leu Gln Ser Gln Ile Gln Ala Gln Glu Asp Ala Leu Lys Thr Phe Leu  
 225 230 235 240



Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu Lys Ser	
85 90 95	
gac aaa agc tct cgt ttt gaa act ttt atc agc att atg gat att tta	392
Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp Ile Leu	
100 105 110	
aaa gag cat aat cat gaa aat ttc tcc atc tcc acg caa gct cag	437
Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala Gln	
115 120 125	
taaagttttca acgagtggtta gcttttttaaat ctctttttgcc ctatacgcta tag	490

<210> 226  
 <211> 129  
 <212> PRT  
 <213> Helicobacter pylori

<400> 226	
Met Lys Ser Ile Arg Arg Gly Asp Gly Leu Asn Val Val Pro Phe Ile	
1 5 10 15	
Asp Ile Met Leu Val Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe	
20 25 30	
Ile Ala Gln Gly Lys Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala	
35 40 45	
Glu Lys Ser Gln Pro Asn Asp Gln Lys Val Val Val Ile Ser Val Asp	
50 55 60	
Glu His Asp Asn Ile Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala	
65 70 75 80	
Leu Ser Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu	
85 90 95	
Lys Ser Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp	
100 105 110	
Ile Leu Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala	
115 120 125	
Gln	

<210> 227  
 <211> 958  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(905)

<400> 227	
tcgtttttgaa actttttatca gcattatgga tatttttaaaa gagcataatc atg aaa	56
Met Lys	
1	
att tct cca tct cca cgc aag ctc agt aaa gtt tca acg agt gtt agc	104
Ile Ser Pro Ser Pro Arg Lys Leu Ser Lys Val Ser Thr Ser Val Ser	

5					10					15					
ttt tta atc tct ttt gcc cta tac gct ata ggg ttt ggc tat ttt tta	152														
Phe Leu Ile Ser Phe Ala Leu Tyr Ala Ile Gly Phe Gly Tyr Phe Leu															
20 25 30															
ctg cgc gaa gac gcc cca gag cct tta gcg caa gcc ggg acc act aag	200														
Leu Arg Glu Asp Ala Pro Glu Pro Leu Ala Gln Ala Gly Thr Thr Lys															
35 40 45 50															
gtt acc atg agt tta gcc agc atc aac act aat tcc aat aca aag act	248														
Val Thr Met Ser Leu Ala Ser Ile Asn Thr Asn Ser Asn Thr Lys Thr															
55 60 65															
aat gct gag tcg gct aaa ccc aaa gaa gag cct aaa gaa aaa ccc aag	296														
Asn Ala Glu Ser Ala Lys Pro Lys Glu Glu Pro Lys Glu Lys Pro Lys															
70 75 80															
aaa gaa gag cca aaa aaa gaa gaa ccc aaa aag gag gtt aca aag cct	344														
Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Val Thr Lys Pro															
85 90 95															
aaa cct aag cct aaa ccc aag cca aag cca aaa cca aaa cct aag cct	392														
Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro															
100 105 110															
gaa ccc aaa cct gaa cca aaa ccc gag cct aag cct gag cct aaa gtt	440														
Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Val															
115 120 125 130															
gaa gag gtt aaa aaa gaa gag cct aaa gaa gag ccc aaa aaa gaa gaa	488														
Glu Glu Val Lys Lys Glu Glu Pro Lys Glu Glu Pro Lys Lys Glu Glu															
135 140 145															
gct aaa gag gaa gct aaa gaa aaa agc gct cct aaa caa gta aca act	536														
Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val Thr Thr															
150 155 160															
aag gat ata gtc aaa gaa aaa gac aag caa gaa gaa tcc aac aaa acc	584														
Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn Lys Thr															
165 170 175															
tct gag ggg gcc act tct gaa gct caa gct tat aac cca ggg gtg agc	632														
Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly Val Ser															
180 185 190															
aac gaa ttt tta atg aag atc caa acc gct att tct tct aaa aac cgc	680														
Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys Asn Arg															
195 200 205 210															
tac cct aaa atg gcg cag att agg ggt att gag ggc gaa gtg ttg gtg	728														
Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val Leu Val															
215 220 225															
agc ttt acg atc aat gct gat ggg agc gtt acg gac att aaa gtg gtc	776														

Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys Val Val  
 230 235 240

aaa agc aac acc aca gat att tta aac cat gcg gct tta gaa gcc att 824  
 Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu Ala Ile  
 245 250 255

aaa agc gcg gca cat cta ttc cct aaa cca gaa gaa acc gtg cat cta 872  
 Lys Ser Ala Ala His Leu Phe Pro Lys Pro Glu Glu Thr Val His Leu  
 260 265 270

aaa atc cct atc gct tat agc ttg aaa gaa gac tgattagtct ttcttttagg 925  
 Lys Ile Pro Ile Ala Tyr Ser Leu Lys Glu Asp  
 275 280 285

ggcgattcaa gccttaaaag ccgggtcaaa atc 958

<210> 228  
 <211> 285  
 <212> PRT  
 <213> Helicobacter pylori

<400> 228

Met Lys Ile Ser Pro Ser Pro Arg Lys Leu Ser Lys Val Ser Thr Ser  
 1 5 10 15  
 Val Ser Phe Leu Ile Ser Phe Ala Leu Tyr Ala Ile Gly Phe Gly Tyr  
 20 25 30  
 Phe Leu Leu Arg Glu Asp Ala Pro Glu Pro Leu Ala Gln Ala Gly Thr  
 35 40 45  
 Thr Lys Val Thr Met Ser Leu Ala Ser Ile Asn Thr Asn Ser Asn Thr  
 50 55 60  
 Lys Thr Asn Ala Glu Ser Ala Lys Pro Lys Glu Glu Pro Lys Glu Lys  
 65 70 75 80  
 Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Val Thr  
 85 90 95  
 Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro  
 100 105 110  
 Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro  
 115 120 125  
 Lys Val Glu Glu Val Lys Lys Glu Glu Pro Lys Glu Glu Pro Lys Lys  
 130 135 140  
 Glu Glu Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val  
 145 150 155 160  
 Thr Thr Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn  
 165 170 175  
 Lys Thr Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly  
 180 185 190  
 Val Ser Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys  
 195 200 205  
 Asn Arg Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val  
 210 215 220  
 Leu Val Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys  
 225 230 235 240  
 Val Val Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu  
 245 250 255

Ala	Ile	Lys	Ser	Ala	Ala	His	Leu	Phe	Pro	Lys	Pro	Glu	Glu	Thr	Val
			260					265					270		
His	Leu	Lys	Ile	Pro	Ile	Ala	Tyr	Ser	Leu	Lys	Glu	Asp			
		275					280					285			

<210> 229  
 <211> 757  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(704)

<400> 229 ttgatgaaaa aaataacgct cctcttttta aaactctttt agaggatgcc atg aga															56	
														Met Arg		
														1		
gtg tct tct aaa gag att tta ctc att gtg ggg ggg agc agt ttt tac															104	
Val	Ser	Ser	Lys	Glu	Ile	Leu	Leu	Ile	Val	Gly	Gly	Ser	Ser	Phe	Tyr	
		5					10					15				
ctc aaa tcc att tta gaa ggt ttg agc cgc atg cca aaa ctg agc ggt															152	
Leu	Lys	Ser	Ile	Leu	Glu	Gly	Leu	Ser	Arg	Met	Pro	Lys	Leu	Ser	Gly	
	20					25					30					
gag gag gtt gta aaa ata gag cga gaa att gcc act ctt tct aac cct															200	
Glu	Glu	Val	Val	Lys	Ile	Glu	Arg	Glu	Ile	Ala	Thr	Leu	Ser	Asn	Pro	
	35				40				45					50		
tat ata ttt tta aaa tcc att gac cct aac atg gct ttt aaa atc cat															248	
Tyr	Ile	Phe	Leu	Lys	Ser	Ile	Asp	Pro	Asn	Met	Ala	Phe	Lys	Ile	His	
			55					60						65		
cca aac gac act tac cgc acc cat aag gct tta gaa atc ttt tat gcc															296	
Pro	Asn	Asp	Thr	Tyr	Arg	Thr	His	Lys	Ala	Leu	Glu	Ile	Phe	Tyr	Ala	
			70					75					80			
acc tgc acg ccc cca agc gag tat ttt aag gcc aac cct aaa aaa ccc															344	
Thr	Cys	Thr	Pro	Pro	Ser	Glu	Tyr	Phe	Lys	Ala	Asn	Pro	Lys	Lys	Pro	
		85				90					95					
ttt gag cat gct atc tcc tta ttc gct ctg tct att gaa aaa agc gcg															392	
Phe	Glu	His	Ala	Ile	Ser	Leu	Phe	Ala	Leu	Ser	Ile	Glu	Lys	Ser	Ala	
	100					105					110					
ctc cat aac aat atc aaa cgg cgc acc aaa aac atg ctc cat tca ggg															440	
Leu	His	Asn	Asn	Ile	Lys	Arg	Arg	Thr	Lys	Asn	Met	Leu	His	Ser	Gly	
115				120					125					130		
ctt gtt gaa gaa atc aaa gcc ctc tat act caa tac cct aaa gat tcg															488	
Leu	Val	Glu	Glu	Ile	Lys	Ala	Leu	Tyr	Thr	Gln	Tyr	Pro	Lys	Asp	Ser	
				135				140						145		



cag cct ttt aaa gcc ata ggc gtt aaa gag agc gtt ctt ttt tta gaa 536  
Gln Pro Phe Lys Ala Ile Gly Val Lys Glu Ser Val Leu Phe Leu Glu  
150 155 160

aaa cga ctc act tta aag gag cta gaa gaa gcg att acc tct aac acc 584  
Lys Arg Leu Thr Leu Lys Glu Leu Glu Glu Ala Ile Thr Ser Asn Thr  
165 170 175

atg aaa tta gcc aag cgc caa aac act ttc aat aaa acc caa ttc aat 632  
Met Lys Leu Ala Lys Arg Gln Asn Thr Phe Asn Lys Thr Gln Phe Asn  
180 185 190

aac ctt tat gtg ggg agc gct gaa gaa gtt agg cat gcg att tta aaa 680  
Asn Leu Tyr Val Gly Ser Ala Glu Glu Val Arg His Ala Ile Leu Lys  
195 200 205 210

cac tca aaa agc ggc att aaa gga taatctaattg gatacacaaa acttaccgga 734  
His Ser Lys Ser Gly Ile Lys Gly  
215

tcaaattatc cctattttta tga 757

<210> 230  
<211> 218  
<212> PRT  
<213> Helicobacter pylori

<400> 230  
Met Arg Val Ser Ser Lys Glu Ile Leu Leu Ile Val Gly Gly Ser Ser  
1 5 10 15  
Phe Tyr Leu Lys Ser Ile Leu Glu Gly Leu Ser Arg Met Pro Lys Leu  
20 25 30  
Ser Gly Glu Glu Val Val Lys Ile Glu Arg Glu Ile Ala Thr Leu Ser  
35 40 45  
Asn Pro Tyr Ile Phe Leu Lys Ser Ile Asp Pro Asn Met Ala Phe Lys  
50 55 60  
Ile His Pro Asn Asp Thr Tyr Arg Thr His Lys Ala Leu Glu Ile Phe  
65 70 75 80  
Tyr Ala Thr Cys Thr Pro Pro Ser Glu Tyr Phe Lys Ala Asn Pro Lys  
85 90 95  
Lys Pro Phe Glu His Ala Ile Ser Leu Phe Ala Leu Ser Ile Glu Lys  
100 105 110  
Ser Ala Leu His Asn Asn Ile Lys Arg Arg Thr Lys Asn Met Leu His  
115 120 125  
Ser Gly Leu Val Glu Glu Ile Lys Ala Leu Tyr Thr Gln Tyr Pro Lys  
130 135 140  
Asp Ser Gln Pro Phe Lys Ala Ile Gly Val Lys Glu Ser Val Leu Phe  
145 150 155 160  
Leu Glu Lys Arg Leu Thr Leu Lys Glu Leu Glu Glu Ala Ile Thr Ser  
165 170 175  
Asn Thr Met Lys Leu Ala Lys Arg Gln Asn Thr Phe Asn Lys Thr Gln  
180 185 190  
Phe Asn Asn Leu Tyr Val Gly Ser Ala Glu Glu Val Arg His Ala Ile  
195 200 205

Leu Lys His Ser Lys Ser Gly Ile Lys Gly  
 210 215

<210> 231  
 <211> 454  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(401)

<400> 231  
 ctatatgaac aaagccttaa aagacttgaa aaaaggaata actcatacct atg cga 56  
 Met Arg  
 1  
 aac aat aaa acg cct ttt ttg agc gcg att ttt acg gca tca att agg 104  
 Asn Asn Lys Thr Pro Phe Leu Ser Ala Ile Phe Thr Ala Ser Ile Arg  
 5 10 15  
 ggt tac caa cgc ttt ttt tcg gct ttc acc cct tca agc tgc cgg ttt 152  
 Gly Tyr Gln Arg Phe Phe Ser Ala Phe Thr Pro Ser Ser Cys Arg Phe  
 20 25 30  
 tac ccc act tgt tcc aac tac gct ctg tgg ttg ctc tgt ttt gaa agc 200  
 Tyr Pro Thr Cys Ser Asn Tyr Ala Leu Trp Leu Leu Cys Phe Glu Ser  
 35 40 45 50  
 cct ttg agc gct atg ggt aag atc gct ata agg ata ctc tca tgc aac 248  
 Pro Leu Ser Ala Met Gly Lys Ile Ala Ile Arg Ile Leu Ser Cys Asn  
 55 60 65  
 cct ttt tgc tct ggg ggc att gct tac cct act act cgc ttg aaa cgc 296  
 Pro Phe Cys Ser Gly Gly Ile Ala Tyr Pro Thr Thr Arg Leu Lys Arg  
 70 75 80  
 cca agc ctg atc caa tct cat aaa gat tct aat cgc aat ttt aaa acc 344  
 Pro Ser Leu Ile Gln Ser His Lys Asp Ser Asn Arg Asn Phe Lys Thr  
 85 90 95  
 atc act ttt tgg ctc gtt ccc aca aaa agc cac gca act tac tac atc 392  
 Ile Thr Phe Trp Leu Val Pro Thr Lys Ser His Ala Thr Tyr Tyr Ile  
 100 105 110  
 att aag gtt taatcacaat ggataaaaac aacaataatc tccgcttgat 441  
 Ile Lys Val  
 115  
 ttttagcgatc gct 454

<210> 232  
 <211> 117  
 <212> PRT

<213> Helicobacter pylori

<400> 232

Met	Arg	Asn	Asn	Lys	Thr	Pro	Phe	Leu	Ser	Ala	Ile	Phe	Thr	Ala	Ser
1				5				10						15	
Ile	Arg	Gly	Tyr	Gln	Arg	Phe	Phe	Ser	Ala	Phe	Thr	Pro	Ser	Ser	Cys
		20						25					30		
Arg	Phe	Tyr	Pro	Thr	Cys	Ser	Asn	Tyr	Ala	Leu	Trp	Leu	Leu	Cys	Phe
		35					40					45			
Glu	Ser	Pro	Leu	Ser	Ala	Met	Gly	Lys	Ile	Ala	Ile	Arg	Ile	Leu	Ser
	50					55					60				
Cys	Asn	Pro	Phe	Cys	Ser	Gly	Gly	Ile	Ala	Tyr	Pro	Thr	Thr	Arg	Leu
65					70					75					80
Lys	Arg	Pro	Ser	Leu	Ile	Gln	Ser	His	Lys	Asp	Ser	Asn	Arg	Asn	Phe
				85					90					95	
Lys	Thr	Ile	Thr	Phe	Trp	Leu	Val	Pro	Thr	Lys	Ser	His	Ala	Thr	Tyr
			100					105						110	
Tyr	Ile	Ile	Lys	Val											
			115												

<210> 233

<211> 1153

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (51)...(1100)

<400> 233

ttataataag aaagttttta ttatttttaa tgctatttta ggagttcatc atg aaa	56
Met Lys	
1	
aaa tcc att tta ttg ggc gtt tgc ttg gct ttt tct tgc gct cat gcc	104
Lys Ser Ile Leu Leu Gly Val Cys Leu Ala Phe Ser Cys Ala His Ala	
5 10 15	
cta aac gat tta gaa ttg atc aaa aaa gcg agg gaa agc cag cta gaa	152
Leu Asn Asp Leu Glu Leu Ile Lys Lys Ala Arg Glu Ser Gln Leu Glu	
20 25 30	
ccc atg cct atg ggc aaa gcg ctc aaa gaa tac cag att aaa aag acc	200
Pro Met Pro Met Gly Lys Ala Leu Lys Glu Tyr Gln Ile Lys Lys Thr	
35 40 45 50	
aga gat gtg ggt att ggc acc aaa aac agc gaa atc atg acc tcc gct	248
Arg Asp Val Gly Ile Gly Thr Lys Asn Ser Glu Ile Met Thr Ser Ala	
55 60 65	
caa gtg gaa tta ggc aaa atg ctc tat ttt gac cct agg att tcc act	296
Gln Val Glu Leu Gly Lys Met Leu Tyr Phe Asp Pro Arg Ile Ser Thr	
70 75 80	

tcc tac ctc gtg tct tgc aac aca tgc cat aat ctg ggc tta ggc ggg	344
Ser Tyr Leu Val Ser Cys Asn Thr Cys His Asn Leu Gly Leu Gly Gly	
85 90 95	
gtg gat tta gtc cca agc gcc ata ggc tct caa tgg aag aaa aac ccc	392
Val Asp Leu Val Pro Ser Ala Ile Gly Ser Gln Trp Lys Lys Asn Pro	
100 105 110	
cac ctt tta agc tcc cca acg gtg tat aac tct gtg ttt aac gat gtg	440
His Leu Leu Ser Ser Pro Thr Val Tyr Asn Ser Val Phe Asn Asp Val	
115 120 125 130	
cag ttt tgg gat ggc agg gtt acg cat tta aac gaa cag gcg caa ggg	488
Gln Phe Trp Asp Gly Arg Val Thr His Leu Asn Glu Gln Ala Gln Gly	
135 140 145	
ccc atc cag tct tct ttt gaa atg ggg gct gat ccc aaa gtg gtg gta	536
Pro Ile Gln Ser Ser Phe Glu Met Gly Ala Asp Pro Lys Val Val Val	
150 155 160	
gaa aaa atc aat tcc atg cca ggc tat gtc aag ctc ttt aga aaa gcc	584
Glu Lys Ile Asn Ser Met Pro Gly Tyr Val Lys Leu Phe Arg Lys Ala	
165 170 175	
tat ggc tct aaa gtc aaa att gat ttt aaa ttg atc gct gat agt atc	632
Tyr Gly Ser Lys Val Lys Ile Asp Phe Lys Leu Ile Ala Asp Ser Ile	
180 185 190	
gct atg ttt gaa gcc acg ctt att acc cca agc cgt tac gac gat ttt	680
Ala Met Phe Glu Ala Thr Leu Ile Thr Pro Ser Arg Tyr Asp Asp Phe	
195 200 205 210	
tta aga ggc aat cct aaa gcg ctc agc aaa gcc gaa aaa gag ggg ctg	728
Leu Arg Gly Asn Pro Lys Ala Leu Ser Lys Ala Glu Lys Glu Gly Leu	
215 220 225	
aat tta ttc att tct aaa ggc tgt gtg gct tgc cat aac ggc att aat	776
Asn Leu Phe Ile Ser Lys Gly Cys Val Ala Cys His Asn Gly Ile Asn	
230 235 240	
ctt ggg gga acg atg cag cct ttt ggg gtg gtc aaa cct tat aaa ttc	824
Leu Gly Gly Thr Met Gln Pro Phe Gly Val Val Lys Pro Tyr Lys Phe	
245 250 255	
gct aat gtg ggc gat ttc aaa ggc gat aaa aac ggg ctt gtg aaa gtg	872
Ala Asn Val Gly Asp Phe Lys Gly Asp Lys Asn Gly Leu Val Lys Val	
260 265 270	
cct act tta agg aat atc acc gaa acg atg ccc tat ttc cat aac ggg	920
Pro Thr Leu Arg Asn Ile Thr Glu Thr Met Pro Tyr Phe His Asn Gly	
275 280 285 290	
caa ttc tgg gat gtt aag gat gcg att aaa gaa atg ggc tct atc cag	968
Gln Phe Trp Asp Val Lys Asp Ala Ile Lys Glu Met Gly Ser Ile Gln	
295 300 305	

tta ggc att gaa atc agc gat gaa gaa gcg aaa aaa att gaa act ttc 1016  
 Leu Gly Ile Glu Ile Ser Asp Glu Glu Ala Lys Lys Ile Glu Thr Phe  
                   310                                  315                                  320

ttt gga gcc tta agg ggt aaa aaa cct aaa ata atc tac cca gaa ctc 1064  
 Phe Gly Ala Leu Arg Gly Lys Lys Pro Lys Ile Ile Tyr Pro Glu Leu  
                   325                                  330                                  335

ccc ata atg aca gac aaa acc cct aaa ccc tct ttt tgatttaaaaa 1110  
 Pro Ile Met Thr Asp Lys Thr Pro Lys Pro Ser Phe  
                   340                                  345                                  350

aagtcctttt aggggtcttt ggcgctaaat ctaaaaaata ctc 1153

<210> 234

<211> 350

<212> PRT

<213> Helicobacter pylori

<400> 234

Met Lys Lys Ser Ile Leu Leu Gly Val Cys Leu Ala Phe Ser Cys Ala  
   1                  5                                  10                                  15  
 His Ala Leu Asn Asp Leu Glu Leu Ile Lys Lys Ala Arg Glu Ser Gln  
                   20                                  25                                  30  
 Leu Glu Pro Met Pro Met Gly Lys Ala Leu Lys Glu Tyr Gln Ile Lys  
                   35                                  40                                  45  
 Lys Thr Arg Asp Val Gly Ile Gly Thr Lys Asn Ser Glu Ile Met Thr  
                   50                                  55                                  60  
 Ser Ala Gln Val Glu Leu Gly Lys Met Leu Tyr Phe Asp Pro Arg Ile  
  65                                  70                                  75                                  80  
 Ser Thr Ser Tyr Leu Val Ser Cys Asn Thr Cys His Asn Leu Gly Leu  
                   85                                  90                                  95  
 Gly Gly Val Asp Leu Val Pro Ser Ala Ile Gly Ser Gln Trp Lys Lys  
                   100                                  105                                  110  
 Asn Pro His Leu Leu Ser Ser Pro Thr Val Tyr Asn Ser Val Phe Asn  
                   115                                  120                                  125  
 Asp Val Gln Phe Trp Asp Gly Arg Val Thr His Leu Asn Glu Gln Ala  
                   130                                  135                                  140  
 Gln Gly Pro Ile Gln Ser Ser Phe Glu Met Gly Ala Asp Pro Lys Val  
  145                                  150                                  155                                  160  
 Val Val Glu Lys Ile Asn Ser Met Pro Gly Tyr Val Lys Leu Phe Arg  
                   165                                  170                                  175  
 Lys Ala Tyr Gly Ser Lys Val Lys Ile Asp Phe Lys Leu Ile Ala Asp  
                   180                                  185                                  190  
 Ser Ile Ala Met Phe Glu Ala Thr Leu Ile Thr Pro Ser Arg Tyr Asp  
                   195                                  200                                  205  
 Asp Phe Leu Arg Gly Asn Pro Lys Ala Leu Ser Lys Ala Glu Lys Glu  
                   210                                  215                                  220  
 Gly Leu Asn Leu Phe Ile Ser Lys Gly Cys Val Ala Cys His Asn Gly  
  225                                  230                                  235                                  240  
 Ile Asn Leu Gly Gly Thr Met Gln Pro Phe Gly Val Val Lys Pro Tyr  
                   245                                  250                                  255  
 Lys Phe Ala Asn Val Gly Asp Phe Lys Gly Asp Lys Asn Gly Leu Val  
                   260                                  265                                  270

Lys	Val	Pro	Thr	Leu	Arg	Asn	Ile	Thr	Glu	Thr	Met	Pro	Tyr	Phe	His
	275						280					285			
Asn	Gly	Gln	Phe	Trp	Asp	Val	Lys	Asp	Ala	Ile	Lys	Glu	Met	Gly	Ser
	290					295					300				
Ile	Gln	Leu	Gly	Ile	Glu	Ile	Ser	Asp	Glu	Glu	Ala	Lys	Lys	Ile	Glu
305					310					315					320
Thr	Phe	Phe	Gly	Ala	Leu	Arg	Gly	Lys	Lys	Pro	Lys	Ile	Ile	Tyr	Pro
			325					330						335	
Glu	Leu	Pro	Ile	Met	Thr	Asp	Lys	Thr	Pro	Lys	Pro	Ser	Phe		
		340						345					350		

<210> 235  
 <211> 426  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(374)

<400> 235	
gttagagatt tctcccaatt ctcaagtggg agcgagcgtg aaaatccgct atg aaa	56
	Met Lys
	1
 gca atc ttt agc ctc ttt ttc ctt ctt att gtt tta aaa gca aac ccc	104
Ala Ile Phe Ser Leu Phe Phe Leu Leu Ile Val Leu Lys Ala Asn Pro	
5 10 15	
 ata aac cct tta tta gag ccg tta tat ttc ccc agt tac gcg caa ttt	152
Ile Asn Pro Leu Leu Glu Pro Leu Tyr Phe Pro Ser Tyr Ala Gln Phe	
20 25 30	
 tta aac tta gca cct cac ttt gtc att aaa aaa aag cgc gct tat aga	200
Leu Asn Leu Ala Pro His Phe Val Ile Lys Lys Lys Arg Ala Tyr Arg	
35 40 45 50	
 ccc ttt caa tgg ggg aat acc att atc atc aaa cgc cat gat tta gaa	248
Pro Phe Gln Trp Gly Asn Thr Ile Ile Ile Lys Arg His Asp Leu Glu	
55 60 65	
 gaa cgc caa agc aac cag cca agc gat att ttc cgc caa aac gct gaa	296
Glu Arg Gln Ser Asn Gln Pro Ser Asp Ile Phe Arg Gln Asn Ala Glu	
70 75 80	
 atc aat gtg tct tct caa act ttt tta aaa gga atg agc aac gct tct	344
Ile Asn Val Ser Ser Gln Thr Phe Leu Lys Gly Met Ser Asn Ala Ser	
85 90 95	
 tca cga aca gtg ctt gat tca gcc gct cag taaaatgcta aaactttttt	394
Ser Arg Thr Val Leu Asp Ser Ala Ala Gln	
100 105	
 taatcacatt tttcttggtta ttttcttaat cc	426

<210> 236  
 <211> 108  
 <212> PRT  
 <213> Helicobacter pylori

<400> 236  
 Met Lys Ala Ile Phe Ser Leu Phe Phe Leu Leu Ile Val Leu Lys Ala  
 1 5 10 15  
 Asn Pro Ile Asn Pro Leu Leu Glu Pro Leu Tyr Phe Pro Ser Tyr Ala  
 20 25 30  
 Gln Phe Leu Asn Leu Ala Pro His Phe Val Ile Lys Lys Lys Arg Ala  
 35 40 45  
 Tyr Arg Pro Phe Gln Trp Gly Asn Thr Ile Ile Ile Lys Arg His Asp  
 50 55 60  
 Leu Glu Glu Arg Gln Ser Asn Gln Pro Ser Asp Ile Phe Arg Gln Asn  
 65 70 75 80  
 Ala Glu Ile Asn Val Ser Ser Gln Thr Phe Leu Lys Gly Met Ser Asn  
 85 90 95  
 Ala Ser Ser Arg Thr Val Leu Asp Ser Ala Ala Gln  
 100 105

<210> 237  
 <211> 799  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(746)

<400> 237  
 agcgtgagcc caattacgcc acgcctatgt ctagataggg gaggttggaa atg ttt 56  
 Met Phe  
 1  
 agt ttt tta gaa aaa aac ccg ttc ttt ttc act ctt gcg ttt att ttt 104  
 Ser Phe Leu Glu Lys Asn Pro Phe Phe Phe Thr Leu Ala Phe Ile Phe  
 5 10 15  
 gtg ttt gcg atc gcg ggc ttg gtg gag att ttg ccc aac ttc ttc aaa 152  
 Val Phe Ala Ile Ala Gly Leu Val Glu Ile Leu Pro Asn Phe Phe Lys  
 20 25 30  
 tcc gct cgc ccg att gaa ggc tta cgg cct tat acg gtt tta gag aca 200  
 Ser Ala Arg Pro Ile Glu Gly Leu Arg Pro Tyr Thr Val Leu Glu Thr  
 35 40 45 50  
 gcg ggg agg caa att tat atc caa gaa ggt tgc tat cat tgc cat tcc 248  
 Ala Gly Arg Gln Ile Tyr Ile Gln Glu Gly Cys Tyr His Cys His Ser  
 55 60 65  
 cag ctt att cgc cct ttc caa gct gag gtg gat cga tat ggc gcg tat 296  
 Gln Leu Ile Arg Pro Phe Gln Ala Glu Val Asp Arg Tyr Gly Ala Tyr  
 70 75 80

agt ttg agt ggg gaa tac gcg tat gac agg cca ttt ttg tgg ggt tct 344  
 Ser Leu Ser Gly Glu Tyr Ala Tyr Asp Arg Pro Phe Leu Trp Gly Ser  
 85 90 95

aaa agg att ggc cct gat ttg cac agg gta ggg gat tat cgc aca acc 392  
 Lys Arg Ile Gly Pro Asp Leu His Arg Val Gly Asp Tyr Arg Thr Thr  
 100 105 110

gat tgg cat gaa aag cac atg ttt gat cct aaa agc gtt gtg ccg cac 440  
 Asp Trp His Glu Lys His Met Phe Asp Pro Lys Ser Val Val Pro His  
 115 120 125 130

agc atc atg ccc gcc tat aag cat tta ttt aca aaa aag agc gat ttt 488  
 Ser Ile Met Pro Ala Tyr Lys His Leu Phe Thr Lys Lys Ser Asp Phe  
 135 140 145

gac acc gct tat gca gaa gct ttg acg caa aaa aag gtt ttt ggc gtg 536  
 Asp Thr Ala Tyr Ala Glu Ala Leu Thr Gln Lys Lys Val Phe Gly Val  
 150 155 160

cct tat gac aca gaa aac ggc gtg aaa tta ggg agc gta gaa gaa gcg 584  
 Pro Tyr Asp Thr Glu Asn Gly Val Lys Leu Gly Ser Val Glu Glu Ala  
 165 170 175

aaa aaa gcc tat tta gaa gaa gct aaa aaa atc aca gcc gat atg aaa 632  
 Lys Lys Ala Tyr Leu Glu Glu Ala Lys Lys Ile Thr Ala Asp Met Lys  
 180 185 190

gac aag agg gtg cta gaa gcg att gag aga ggt gaa gtg tta gaa att 680  
 Asp Lys Arg Val Leu Glu Ala Ile Glu Arg Gly Glu Val Leu Glu Ile  
 195 200 205 210

gtg gct ttg atc gct tat ttg aat agc ttg ggt aat tcc agg atc aac 728  
 Val Ala Leu Ile Ala Tyr Leu Asn Ser Leu Gly Asn Ser Arg Ile Asn  
 215 220 225

gcc aat caa aac gct aaa taaggggtga atgatggatt tagaaagttt 776  
 Ala Asn Gln Asn Ala Lys  
 230

gagaggtttt gcgtatgcgt ttt 799

<210> 238  
 <211> 232  
 <212> PRT  
 <213> *Helicobacter pylori*

<400> 238  
 Met Phe Ser Phe Leu Glu Lys Asn Pro Phe Phe Phe Thr Leu Ala Phe  
 1 5 10 15  
 Ile Phe Val Phe Ala Ile Ala Gly Leu Val Glu Ile Leu Pro Asn Phe  
 20 25 30  
 Phe Lys Ser Ala Arg Pro Ile Glu Gly Leu Arg Pro Tyr Thr Val Leu  
 35 40 45



Glu	Thr	Ala	Gly	Arg	Gln	Ile	Tyr	Ile	Gln	Glu	Gly	Cys	Tyr	His	Cys	
50						55					60					
His	Ser	Gln	Leu	Ile	Arg	Pro	Phe	Gln	Ala	Glu	Val	Asp	Arg	Tyr	Gly	
65					70					75					80	
Ala	Tyr	Ser	Leu	Ser	Gly	Glu	Tyr	Ala	Tyr	Asp	Arg	Pro	Phe	Leu	Trp	
			85						90					95		
Gly	Ser	Lys	Arg	Ile	Gly	Pro	Asp	Leu	His	Arg	Val	Gly	Asp	Tyr	Arg	
			100					105					110			
Thr	Thr	Asp	Trp	His	Glu	Lys	His	Met	Phe	Asp	Pro	Lys	Ser	Val	Val	
		115					120					125				
Pro	His	Ser	Ile	Met	Pro	Ala	Tyr	Lys	His	Leu	Phe	Thr	Lys	Lys	Ser	
	130					135					140					
Asp	Phe	Asp	Thr	Ala	Tyr	Ala	Glu	Ala	Leu	Thr	Gln	Lys	Lys	Val	Phe	
145					150				155						160	
Gly	Val	Pro	Tyr	Asp	Thr	Glu	Asn	Gly	Val	Lys	Leu	Gly	Ser	Val	Glu	
				165					170					175		
Glu	Ala	Lys	Lys	Ala	Tyr	Leu	Glu	Glu	Ala	Lys	Lys	Ile	Thr	Ala	Asp	
			180					185					190			
Met	Lys	Asp	Lys	Arg	Val	Leu	Glu	Ala	Ile	Glu	Arg	Gly	Glu	Val	Leu	
		195					200					205				
Glu	Ile	Val	Ala	Leu	Ile	Ala	Tyr	Leu	Asn	Ser	Leu	Gly	Asn	Ser	Arg	
	210					215					220					
Ile	Asn	Ala	Asn	Gln	Asn	Ala	Lys									
225						230										

<210> 239  
 <211> 322  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(269)

<400> 239 cttgggtaat tccaggatca acgccaatca aaacgctaaa taaggggtga atg atg <div style="text-align: right;">Met Met</div> <div style="text-align: right;">1</div>															56
gat tta gaa agt ttg aga ggt ttt gcg tat gcg ttt ttt acc att ctt Asp Leu Glu Ser Leu Arg Gly Phe Ala Tyr Ala Phe Phe Thr Ile Leu <div style="text-align: center;">5                      10                      15</div>															104
ttt acg ctc ttt ttg tat gcc tat att ttt agc atg tat aga aag caa Phe Thr Leu Phe Leu Tyr Ala Tyr Ile Phe Ser Met Tyr Arg Lys Gln <div style="text-align: center;">20                      25                      30</div>															152
aaa aaa ggc att atg gat tat gag cga tac gga tac tta gcg tta aat Lys Lys Gly Ile Met Asp Tyr Glu Arg Tyr Gly Tyr Leu Ala Leu Asn <div style="text-align: center;">35                      40                      45                      50</div>															200
gat gct tta gaa gac gag ttg att gaa cca cgc cat aaa aaa gtt cat Asp Ala Leu Glu Asp Glu Leu Ile Glu Pro Arg His Lys Lys Val His <div style="text-align: center;">55                      60                      65</div>															248

gat aat ggc ata aag gaa agt tgaaatggat tttttaaacg accatataaa 299  
 Asp Asn Gly Ile Lys Glu Ser  
 70

tgtttttggc ttgattgcag cgc 322

<210> 240  
 <211> 73  
 <212> PRT  
 <213> Helicobacter pylori

<400> 240  
 Met Met Asp Leu Glu Ser Leu Arg Gly Phe Ala Tyr Ala Phe Phe Thr  
 1 5 10 15  
 Ile Leu Phe Thr Leu Phe Leu Tyr Ala Tyr Ile Phe Ser Met Tyr Arg  
 20 25 30  
 Lys Gln Lys Lys Gly Ile Met Asp Tyr Glu Arg Tyr Gly Tyr Leu Ala  
 35 40 45  
 Leu Asn Asp Ala Leu Glu Asp Glu Leu Ile Glu Pro Arg His Lys Lys  
 50 55 60  
 Val His Asp Asn Gly Ile Lys Glu Ser  
 65 70

<210> 241  
 <211> 1021  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (51)...(968)

<400> 241  
 ttactgattt ttctttgtgt gagctttggc ttagttttgt aaggaatgag atg ata 56  
 Met Ile  
 1

aag agt tgg act aaa aag tgg ttt ttg att tta ttt tta atg gca agt 104  
 Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met Ala Ser  
 5 10 15

tgt tcc agt tat ttg gtg gct aca acc ggt gag aaa tat ttt aaa atg 152  
 Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe Lys Met  
 20 25 30

gct act caa gcc ttt aag aga ggg gac tac cat aaa gcg gtg gct ttt 200  
 Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val Ala Phe  
 35 40 45 50

tat aag agg agc tgt aat tta agg gtg ggg gtt ggt tgc acg agt tta 248  
 Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr Ser Leu  
 55 60 65

ggc tct atg tat gaa gat ggc gat ggc gtg gat cag aat att aca aaa	296
Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile Thr Lys	
70 75 80	
gcc gtt ttt tat tac aga aga ggg tgt aat tta agg aat cat ctc gct	344
Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His Leu Ala	
85 90 95	
tgc gcg agt cta ggc tct atg tat gaa gat ggc gat ggt gtg caa aaa	392
Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Gln Lys	
100 105 110	
aac ctt cca aag gct atc tat tat tac agg aga ggg tgc cac tta aag	440
Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His Leu Lys	
115 120 125 130	
ggg ggt ggt ggc agc tgt ggg agt tta ggt ttt atg tat ttt aat ggc acg	488
Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn Gly Thr	
135 140 145	
ggc gtt aag caa aat tat gcc aaa gcc ctt ttt ctt tct aaa tac gct	536
Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys Tyr Ala	
150 155 160	
tgc agt ttg aat tac ggc att agt tgt aac ttt gta ggg tat atg tat	584
Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr Met Tyr	
165 170 175	
agg aac gcc aaa ggc gta cag aag gat ttg aaa aaa gcc ctt gcg aat	632
Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu Ala Asn	
180 185 190	
ttt aaa aga ggg tgc cat ttg aaa gac gga gcg agt tgt gtg agc ttg	680
Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val Ser Leu	
195 200 205 210	
gga tac atg tat gaa gtc ggt atg gat gtc aaa caa aat gga gag caa	728
Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly Glu Gln	
215 220 225	
gcc ttg aat ctt tat aaa aag ggt tgt tat tta aaa agg ggg agc ggt	776
Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly Ser Gly	
230 235 240	
tgt cat aat gtg gcg gtg atg tat tac acc ggt aag ggc gtt cca aag	824
Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val Pro Lys	
245 250 255	
gat tta gat aaa gcc att tcg tat tat aag aaa ggt tgc act cta ggc	872
Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr Leu Gly	
260 265 270	
ttt agt ggt agc tgt aaa gtg tta gaa gaa gtg att ggc aag aag tct	920
Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys Lys Ser	
275 280 285 290	

gat gat ttg caa gat gac gcg caa aac gac acg caa gat gat atg caa 968  
 Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp Met Gln  
 295 300 305

taagttaaag cttatggact aatgattaaa actcatctta tagaaatctt tct 1021

<210> 242

<211> 306

<212> PRT

<213> Helicobacter pylori

<400> 242

Met Ile Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met  
 1 5 10 15  
 Ala Ser Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe  
 20 25 30  
 Lys Met Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val  
 35 40 45  
 Ala Phe Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr  
 50 55 60  
 Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile  
 65 70 75 80  
 Thr Lys Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His  
 85 90 95  
 Leu Ala Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val  
 100 105 110  
 Gln Lys Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His  
 115 120 125  
 Leu Lys Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn  
 130 135 140  
 Gly Thr Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys  
 145 150 155 160  
 Tyr Ala Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr  
 165 170 175  
 Met Tyr Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu  
 180 185 190  
 Ala Asn Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val  
 195 200 205  
 Ser Leu Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly  
 210 215 220  
 Glu Gln Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly  
 225 230 235 240  
 Ser Gly Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val  
 245 250 255  
 Pro Lys Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr  
 260 265 270  
 Leu Gly Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys  
 275 280 285  
 Lys Ser Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp  
 290 295 300  
 Met Gln  
 305

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<220>
<221> CDS
<222> (51) ... (947)
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-305-

Leu Val Lys Thr Glu Asp Glu Ala Lys Arg Ile Ile Ser Glu Ile Asp  
 165 170 175

aaa cag cca aag gct aaa aaa gaa gct aaa ttc att gag tta gcc aat 632  
 Lys Gln Pro Lys Ala Lys Lys Glu Ala Lys Phe Ile Glu Leu Ala Asn  
 180 185 190

cgg gat acg att gat cct aac agc aag aac gcg caa aat ggc ggt gat 680  
 Arg Asp Thr Ile Asp Pro Asn Ser Lys Asn Ala Gln Asn Gly Gly Asp  
 195 200 205 210

ttg ggg aaa ttc caa aag aac caa atg gct ccg gat ttt tct aaa gcc 728  
 Leu Gly Lys Phe Gln Lys Asn Gln Met Ala Pro Asp Phe Ser Lys Ala  
 215 220 225

gct ttc gct tta act cct ggg gat tac act aaa acc cct gtt aaa aca 776  
 Ala Phe Ala Leu Thr Pro Gly Asp Tyr Thr Lys Thr Pro Val Lys Thr  
 230 235 240

gag ttt ggt tat cat att atc tat ttg att tct aaa gat agc cct gta 824  
 Glu Phe Gly Tyr His Ile Ile Tyr Leu Ile Ser Lys Asp Ser Pro Val  
 245 250 255

act tat act tat gaa cag gct aaa cct acc att aag ggg atg tta caa 872  
 Thr Tyr Thr Tyr Glu Gln Ala Lys Pro Thr Ile Lys Gly Met Leu Gln  
 260 265 270

gaa aag ctt ttc caa gaa cgc atg aat caa cgc att gag gaa cta aga 920  
 Glu Lys Leu Phe Gln Glu Arg Met Asn Gln Arg Ile Glu Glu Leu Arg  
 275 280 285 290

aag cac gct aaa att gtt atc aac aag taattgatga ggtggtatca 967  
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 <213> Helicobacter pylori

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 Asp Gly Arg Pro Ile Thr Lys Ser Asp Phe Asp Met Ile Lys Gln Arg  
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 65 70 75 80  
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Ile	Asp	Lys	Gln	Pro	Lys	Ala	Lys	Lys	Glu	Ala	Lys	Phe	Ile	Glu	Leu		
		180						185					190				
Ala	Asn	Arg	Asp	Thr	Ile	Asp	Pro	Asn	Ser	Lys	Asn	Ala	Gln	Asn	Gly		
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Gly	Asp	Leu	Gly	Lys	Phe	Gln	Lys	Asn	Gln	Met	Ala	Pro	Asp	Phe	Ser		
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Lys	Ala	Ala	Phe	Ala	Leu	Thr	Pro	Gly	Asp	Tyr	Thr	Lys	Thr	Pro	Val		
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Lys	Thr	Glu	Phe	Gly	Tyr	His	Ile	Ile	Tyr	Leu	Ile	Ser	Lys	Asp	Ser		
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Pro	Val	Thr	Tyr	Thr	Tyr	Glu	Gln	Ala	Lys	Pro	Thr	Ile	Lys	Gly	Met		
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Leu	Gln	Glu	Lys	Leu	Phe	Gln	Glu	Arg	Met	Asn	Gln	Arg	Ile	Glu	Glu		
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<211> 376

<212> DNA

<213> *Helicobacter pylori*

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Lys	Val	Val	Phe	Leu	Leu	Leu	Val	Ile	Leu	Gly	Gly	Leu	Glu	Ala	Gln	
		5					10					15				

agt	act	tat	tgc	agt	gat	cat	tgc	gaa	ggc	acg	cca	gat	agc	cgt	atc	152
Ser	Thr	Tyr	Cys	Ser	Asp	His	Cys	Glu	Gly	Thr	Pro	Asp	Ser	Arg	Ile	
		20				25					30					

cct	cct	atg	ggg	ttt	cat	ttc	agt	ttt	gtg	cat	tca	gtg	aaa	tat	tac	200
Pro	Pro	Met	Gly	Phe	His	Phe	Ser	Phe	Val	His	Ser	Val	Lys	Tyr	Tyr	
		35			40				45					50		

ttg	caa	gat	ccg	caa	gag	cgc	gat	cac	aag	ctt	gaa	aaa	tgc	cat	caa	248
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Tyr Met Glu Arg Ile Tyr Gly Val Ile Asp Ala Ser Ser Gly Tyr Ala	
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70 75 80	
cat gct gaa agc gtg aaa gtc att tat gat cct aaa aaa atc agt ttg	344
His Ala Glu Ser Val Lys Val Ile Tyr Asp Pro Lys Lys Ile Ser Leu	
85 90 95	
gac aaa ttg ttg cgt tac tat ttt aag gtg gtt gat ccg gtg agc gtg	392
Asp Lys Leu Leu Arg Tyr Tyr Phe Lys Val Val Asp Pro Val Ser Val	
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Asn Lys Gln Gly Asn Asp Val Gly Arg Gln Tyr Arg Thr Gly Ile Tyr	
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Leu Gln Lys Glu Val Lys Gly Lys Ile Ala Ile Glu Val Glu Pro Leu	
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aaa aat tat gtg agg gct gaa gag tat cat cag gat tat ttg aag aaa	584
Lys Asn Tyr Val Arg Ala Glu Glu Tyr His Gln Asp Tyr Leu Lys Lys	
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His Pro Ser Gly Tyr Cys His Ile Asp Leu Lys Lys Ala Asp Glu Val	
180 185 190	
att gtg gat gac gat aaa tac acc aaa cct agc gat gaa gtt tta aag	680
Ile Val Asp Asp Asp Lys Tyr Thr Lys Pro Ser Asp Glu Val Leu Lys	
195 200 205 210	
aaa aaa ctc acc aaa ctc cag tat gag gtt acg caa aac aaa cac act	728
Lys Lys Leu Thr Lys Leu Gln Tyr Glu Val Thr Gln Asn Lys His Thr	
215 220 225	
gag aaa ccc ttt gaa aac gag tat tac aac aaa gaa gaa gag ggc att	776
Glu Lys Pro Phe Glu Asn Glu Tyr Tyr Asn Lys Glu Glu Glu Gly Ile	
230 235 240	
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Tyr Val Asp Ile Thr Thr Gly Glu Pro Leu Phe Ser Ser Ala Asp Lys	
245 250 255	

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Tyr Asp Ser Gly Cys Gly Trp Pro Ser Phe Ser Lys Pro Ile Asn Lys	
260 265 270	
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275 280 285 290	
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Glu Val Leu Ser Arg Ile Gly Lys Ala His Leu Gly His Val Phe Asn	
295 300 305	
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Asp Gly Pro Lys Glu Leu Gly Gly Leu Arg Tyr Cys Ile Asn Ser Ala	
310 315 320	
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Ala Leu Arg Phe Ile Pro Leu Lys Asp Met Glu Lys Glu Gly Tyr Gly	
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Glu Phe Ile Pro Tyr Ile Lys Lys Gly Glu Leu Lys Lys Tyr Ile Asn	
340 345 350	
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Ser Leu Asp Lys Leu Leu Arg Tyr Tyr Phe Lys Val Val Asp Pro Val	
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 Pro Leu Lys Asn Tyr Val Arg Ala Glu Glu Tyr His Gln Asp Tyr Leu  
 165 170 175  
 Lys Lys His Pro Ser Gly Tyr Cys His Ile Asp Leu Lys Lys Ala Asp  
 180 185 190  
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 195 200 205  
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 210 215 220  
 His Thr Glu Lys Pro Phe Glu Asn Glu Tyr Tyr Asn Lys Glu Glu Glu  
 225 230 235 240  
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 245 250 255  
 Asp Lys Tyr Asp Ser Gly Cys Gly Trp Pro Ser Phe Ser Lys Pro Ile  
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 Phe Asn Asp Gly Pro Lys Glu Leu Gly Gly Leu Arg Tyr Cys Ile Asn  
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 Ser Ala Ala Leu Arg Phe Ile Pro Leu Lys Asp Met Glu Lys Glu Gly  
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 35 40 45 50

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55 60 65	
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70 75 80	
ggg aat tta atc ata ggg ctt agc aac ata ttc ttt agc aat aaa agc	344
Gly Asn Leu Ile Ile Gly Leu Ser Asn Ile Phe Phe Ser Asn Lys Ser	
85 90 95	
gat gat gtg caa tta gtt gca gaa acc aat caa aaa gtt caa gct ctt	392
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Asn Ala Thr Gln Gln Asn Ser Ala Lys Leu Asn Ala Ile Phe Asn Glu	
115 120 125 130	
ata ccg gct gat tat gcg ata gag ttg ccc tct act aac gct gca aat	488
Ile Pro Ala Asp Tyr Ala Ile Glu Leu Pro Ser Thr Asn Ala Ala Asn	
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Lys Asp Lys Ile Leu Tyr Ile Val Ser Asp Pro Met Cys Pro His Cys	
150 155 160	
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Gln Lys Glu Leu Thr Lys Leu Arg Asp His Leu Lys Glu Asn Thr Val	
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Arg Met Val Val Val Gly Trp Leu Gly Val Asn Ser Ala Lys Lys Ala	
180 185 190	
gct tta atc caa gaa gaa atg gcg aaa gct agg gct agg gga gcg agc	680
Ala Leu Ile Gln Glu Glu Met Ala Lys Ala Arg Ala Arg Gly Ala Ser	
195 200 205 210	
gtg gaa gat aag atc tct att ctt gaa aag att tat tcc acc caa tac	728
Val Glu Asp Lys Ile Ser Ile Leu Glu Lys Ile Tyr Ser Thr Gln Tyr	
215 220 225	
gat att aac gct caa aaa gag cct gaa gat tta cgc act aaa gtg gaa	776
Asp Ile Asn Ala Gln Lys Glu Pro Glu Asp Leu Arg Thr Lys Val Glu	
230 235 240	
aat acc act aaa aag att ttt gaa tct ggc gtg att aag ggt gtg cct	824
Asn Thr Thr Lys Lys Ile Phe Glu Ser Gly Val Ile Lys Gly Val Pro	
245 250 255	
ttc tta tac cat tat aag gca tgatataagg ttgctctcat gaaaaaaccc	875
Phe Leu Tyr His Tyr Lys Ala	

260

265

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898

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&lt;211&gt; 265

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&lt;400&gt; 250

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Asp Asn Leu Val Ser Val Ile Glu Lys Gln Thr Asn Lys Lys Val Arg
      35           40           45
Ile Leu Glu Ile Lys Pro Leu Lys Ser Ser Gln Asp Leu Lys Met Val
      50           55           60
Val Ile Glu Asp Pro Asp Thr Lys Tyr Asn Ile Pro Leu Val Val Ser
      65           70           75           80
Lys Asp Gly Asn Leu Ile Ile Gly Leu Ser Asn Ile Phe Phe Ser Asn
      85           90           95
Lys Ser Asp Asp Val Gln Leu Val Ala Glu Thr Asn Gln Lys Val Gln
      100          105          110
Ala Leu Asn Ala Thr Gln Gln Asn Ser Ala Lys Leu Asn Ala Ile Phe
      115          120          125
Asn Glu Ile Pro Ala Asp Tyr Ala Ile Glu Leu Pro Ser Thr Asn Ala
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      145          150          155          160
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Thr Val Arg Met Val Val Val Gly Trp Leu Gly Val Asn Ser Ala Lys
      180          185          190
Lys Ala Ala Leu Ile Gln Glu Glu Met Ala Lys Ala Arg Ala Arg Gly
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Ala Ser Val Glu Asp Lys Ile Ser Ile Leu Glu Lys Ile Tyr Ser Thr
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Gln Tyr Asp Ile Asn Ala Gln Lys Glu Pro Glu Asp Leu Arg Thr Lys
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Val Glu Asn Thr Thr Lys Lys Ile Phe Glu Ser Gly Val Ile Lys Gly
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Val Pro Phe Leu Tyr His Tyr Lys Ala
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&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Helicobacter pylori

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (51)...(707)

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Ala Glu Leu Lys Asp Asp Leu Arg Arg Leu Ser Glu Lys Glu Gln Ser			
35 40 45 50			
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55 60 65			
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Asp Leu Leu Asn Gln Lys Glu Lys Glu Val Glu Glu Lys Leu Lys Asn			
70 75 80			
tta gcc gct aaa gaa gaa gcc ttt aaa acc tta caa acg gaa gaa aaa	344		
Leu Ala Ala Lys Glu Glu Ala Phe Lys Thr Leu Gln Thr Glu Glu Lys			
85 90 95			
aaa cgc ctt aaa aat ttg ata gaa gaa aac gaa ggc att tta aga gaa	392		
Lys Arg Leu Lys Asn Leu Ile Glu Glu Asn Glu Gly Ile Leu Arg Glu			
100 105 110			
atc aag cag gct aaa gac agc aag att ggc gag act tat tct aaa atg	440		
Ile Lys Gln Ala Lys Asp Ser Lys Ile Gly Glu Thr Tyr Ser Lys Met			
115 120 125 130			
aaa gat tct aaa tcg gct ctg att tta gaa aat tta ccc act caa aac	488		
Lys Asp Ser Lys Ser Ala Leu Ile Leu Glu Asn Leu Pro Thr Gln Asn			
135 140 145			
gca tta gaa att tta atg gcg cta aaa ccc caa gaa ctc ggt aaa att	536		
Ala Leu Glu Ile Leu Met Ala Leu Lys Pro Gln Glu Leu Gly Lys Ile			
150 155 160			
tta gcc aaa atg gat cct aaa aaa gcg gcg gct ttg aca gag ttg tgg	584		
Leu Ala Lys Met Asp Pro Lys Lys Ala Ala Ala Leu Thr Glu Leu Trp			
165 170 175			
caa aaa ccc cca aaa gaa aat aaa gaa atc cca aaa acc aca gca ccc	632		
Gln Lys Pro Pro Lys Glu Asn Lys Glu Ile Pro Lys Thr Thr Ala Pro			
180 185 190			
acg ccc cct ata gca ccc acg cct tta aaa gag ccg atg ata aaa gat	680		
Thr Pro Pro Ile Ala Pro Thr Pro Leu Lys Glu Pro Met Ile Lys Asp			



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Ile	Gln	Ile	Lys	Lys	Arg	Phe	Leu	Ala	Asn	Leu	Leu	Leu	Phe	Ser	Leu	
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Phe	Cys	Leu	Lys	Ala	Glu	Thr	Leu	Ser	Glu	Asp	His	Gln	Ile	Leu	Leu	
		20				25				30						
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Ser	Ser	Asp	Ala	Phe	His	Arg	Gly	Asp	Phe	Ala	Ala	Ala	Gln	Lys	Gly	
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Tyr	Met	Asn	Leu	Tyr	Lys	Gln	Thr	Asn	Lys	Val	Val	Tyr	Ala	Lys	Glu	
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Ala	Ala	Ile	Ser	Ala	Ala	Ser	Leu	Gly	Asp	Ile	Lys	Thr	Ala	Met	His	
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Leu	Ala	Met	Leu	Tyr	Gln	Lys	Ile	Thr	Asn	Asn	Arg	Asn	Asp	Val	Ser	
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Ile	Asn	Lys	Ile	Leu	Val	Asp	Gly	Tyr	Ala	Gln	Met	Gly	Gln	Ile	Asp	
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Lys	Lys	Glu	Gly	Leu	Asp	Leu	Leu	Gln	Ser	His	Ile	Asp	Arg	Tyr	Gly	
180			185			190										
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Cys	Ser	Glu	Gln	Leu	Cys	Gln	Lys	Ala	Leu	Asn	Thr	Phe	Thr	Gln	Phe	
195			200			205			210							



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230 235 240	
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Leu Lys Glu Phe Asp Lys Ala Gln Lys Ile Ala Glu Leu Phe Pro Phe	
245 250 255	
gac agg cgt ttg ttg tta gac tta tac acc gca caa aaa aaa ttc gat	872
Asp Arg Arg Leu Leu Leu Asp Leu Tyr Thr Ala Gln Lys Lys Phe Asp	
260 265 270	
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Gln Ala Ser Lys Gln Ala Ser Leu Ile Tyr Gln Glu Lys Lys Asp Pro	
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Lys Phe Leu Gly Leu Glu Ala Ile Tyr His Tyr Glu Ser Leu Ser Ala	
295 300 305	
aat aag aaa aag ctc acc aaa gaa gag atg ttg cct atc att caa aaa	1016
Asn Lys Lys Lys Leu Thr Lys Glu Glu Met Leu Pro Ile Ile Gln Lys	
310 315 320	
tta gag caa gcc acc aaa gag cgc caa gca tgg ctc gct aaa acc aaa	1064
Leu Glu Gln Ala Thr Lys Glu Arg Gln Ala Trp Leu Ala Lys Thr Lys	
325 330 335	
gat aaa gaa gac gcg caa gac gct ttc ttt tat aat ttt tta ggg tat	1112
Asp Lys Glu Asp Ala Gln Asp Ala Phe Phe Tyr Asn Phe Leu Gly Tyr	
340 345 350	
tcc tta ata gat tat gac atg gat att aaa agg ggc atg gat ttt gtg	1160
Ser Leu Ile Asp Tyr Asp Met Asp Ile Lys Arg Gly Met Asp Phe Val	
355 360 365 370	
agg aaa gcc tta gcg ttg gat tct gga tca gtg ctt tat ttg gat tct	1208
Arg Lys Ala Leu Ala Leu Asp Ser Gly Ser Val Leu Tyr Leu Asp Ser	
375 380 385	
tta gca tgg ggt tat tac aaa tta ggg aat tgt ttg gaa gct aaa aaa	1256
Leu Ala Trp Gly Tyr Tyr Lys Leu Gly Asn Cys Leu Glu Ala Lys Lys	
390 395 400	
atc ttt tct agc atc gct aaa gag tct atc caa gcc gaa cct gaa ttg	1304
Ile Phe Ser Ser Ile Ala Lys Glu Ser Ile Gln Ala Glu Pro Glu Leu	
405 410 415	
aaa gaa cac aat aaa atc att caa gaa tgc aag aaa tagggatttt	1350
Lys Glu His Asn Lys Ile Ile Gln Glu Cys Lys Lys	
420 425 430	

agaaaattta caaaaaagct tagccttaaa agagggcatg ctt

1393

<210> 254

<211> 430

<212> PRT

<213> Helicobacter pylori

<400> 254

Met	Asn	Ile	Gln	Ile	Lys	Lys	Arg	Phe	Leu	Ala	Asn	Leu	Leu	Leu	Phe
1				5					10					15	
Ser	Leu	Phe	Cys	Leu	Lys	Ala	Glu	Thr	Leu	Ser	Glu	Asp	His	Gln	Ile
			20					25					30		
Leu	Leu	Ser	Ser	Asp	Ala	Phe	His	Arg	Gly	Asp	Phe	Ala	Ala	Ala	Gln
			35					40				45			
Lys	Gly	Tyr	Met	Asn	Leu	Tyr	Lys	Gln	Thr	Asn	Lys	Val	Val	Tyr	Ala
	50					55					60				
Lys	Glu	Ala	Ala	Ile	Ser	Ala	Ala	Ser	Leu	Gly	Asp	Ile	Lys	Thr	Ala
65					70					75					80
Met	His	Leu	Ala	Met	Leu	Tyr	Gln	Lys	Ile	Thr	Asn	Asn	Arg	Asn	Asp
				85					90					95	
Val	Ser	Ile	Asn	Lys	Ile	Leu	Val	Asp	Gly	Tyr	Ala	Gln	Met	Gly	Gln
			100					105					110		
Ile	Asp	Lys	Ala	Ile	Glu	Leu	Leu	His	Lys	Ile	Arg	Lys	Glu	Glu	Lys
		115				120						125			
Thr	Ile	Ala	Thr	Asp	Asn	Val	Leu	Gly	Thr	Leu	Tyr	Leu	Thr	Gln	Lys
	130					135					140				
Arg	Leu	Asp	Lys	Ala	Phe	Pro	Leu	Leu	Asn	Lys	Phe	Tyr	Asn	Gln	Val
145					150					155					160
His	Asp	Glu	Asp	Ser	Leu	Glu	Lys	Leu	Ile	Thr	Ile	Tyr	Phe	Leu	Gln
				165					170					175	
Asn	Arg	Lys	Lys	Glu	Gly	Leu	Asp	Leu	Leu	Gln	Ser	His	Ile	Asp	Arg
			180					185					190		
Tyr	Gly	Cys	Ser	Glu	Gln	Leu	Cys	Gln	Lys	Ala	Leu	Asn	Thr	Phe	Thr
		195				200						205			
Gln	Phe	Asn	Glu	Leu	Asp	Leu	Ala	Lys	Thr	Thr	Phe	Ala	Arg	Leu	Tyr
	210					215					220				
Glu	Lys	Asn	Pro	Ile	Val	Gln	Asn	Ala	Gln	Phe	Tyr	Ile	Gly	Val	Leu
225					230					235					240
Ile	Leu	Leu	Lys	Glu	Phe	Asp	Lys	Ala	Gln	Lys	Ile	Ala	Glu	Leu	Phe
			245						250					255	
Pro	Phe	Asp	Arg	Arg	Leu	Leu	Leu	Asp	Leu	Tyr	Thr	Ala	Gln	Lys	Lys
			260					265					270		
Phe	Asp	Gln	Ala	Ser	Lys	Gln	Ala	Ser	Leu	Ile	Tyr	Gln	Glu	Lys	Lys
	275					280						285			
Asp	Pro	Lys	Phe	Leu	Gly	Leu	Glu	Ala	Ile	Tyr	His	Tyr	Glu	Ser	Leu
	290					295					300				
Ser	Ala	Asn	Lys	Lys	Lys	Leu	Thr	Lys	Glu	Glu	Met	Leu	Pro	Ile	Ile
305					310					315					320
Gln	Lys	Leu	Glu	Gln	Ala	Thr	Lys	Glu	Arg	Gln	Ala	Trp	Leu	Ala	Lys
			325						330					335	
Thr	Lys	Asp	Lys	Glu	Asp	Ala	Gln	Asp	Ala	Phe	Phe	Tyr	Asn	Phe	Leu
			340					345					350		
Gly	Tyr	Ser	Leu	Ile	Asp	Tyr	Asp	Met	Asp	Ile	Lys	Arg	Gly	Met	Asp
		355					360						365		

Phe Val Arg Lys Ala Leu Ala Leu Asp Ser Gly Ser Val Leu Tyr Leu  
 370 375 380  
 Asp Ser Leu Ala Trp Gly Tyr Tyr Lys Leu Gly Asn Cys Leu Glu Ala  
 385 390 395 400  
 Lys Lys Ile Phe Ser Ser Ile Ala Lys Glu Ser Ile Gln Ala Glu Pro  
 405 410 415  
 Glu Leu Lys Glu His Asn Lys Ile Ile Gln Glu Cys Lys Lys  
 420 425 430

<210> 255  
 <211> 1090  
 <212> DNA  
 <213> *Helicobacter pylori*

<220>  
 <221> CDS  
 <222> (51)...(1037)  
 <221> misc\_feature  
 <222> 673  
 <223> n = A,T,C or G

<400> 255  
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 Met Lys  
 1  
 aga ttt gtt ttg ttt tta ttg ttc atg tgc gtt tgc gtt caa gct tac 104  
 Arg Phe Val Leu Phe Leu Leu Phe Met Cys Val Cys Val Gln Ala Tyr  
 5 10 15  
 gcc gag caa gat tac ttt ttt agg gat ttt aaa tct aga gat ttg ccc 152  
 Ala Glu Gln Asp Tyr Phe Phe Arg Asp Phe Lys Ser Arg Asp Leu Pro  
 20 25 30  
 caa aaa ctc cat ctt gat aaa aag ctc tcc caa aca ata cag cca tgc 200  
 Gln Lys Leu His Leu Asp Lys Lys Leu Ser Gln Thr Ile Gln Pro Cys  
 35 40 45 50  
 atg caa ctt aac gca tca aaa cac tac act tct acc ggg gtt aga gag 248  
 Met Gln Leu Asn Ala Ser Lys His Tyr Thr Ser Thr Gly Val Arg Glu  
 55 60 65  
 cct gat aaa tgc aca aag agt ttt aaa aaa tcc gct ctc atg tcc tat 296  
 Pro Asp Lys Cys Thr Lys Ser Phe Lys Lys Ser Ala Leu Met Ser Tyr  
 70 75 80  
 gac tta gcg cta ggt tat ttg gtg agt aag aat aag caa tac ggc tta 344  
 Asp Leu Ala Leu Gly Tyr Leu Val Ser Lys Asn Lys Gln Tyr Gly Leu  
 85 90 95  
 aag gct ata gaa att tta aac gct tgg gct aaa gag ctt caa agc gtg 392  
 Lys Ala Ile Glu Ile Leu Asn Ala Trp Ala Lys Glu Leu Gln Ser Val  
 100 105 110

gat act tat cag agc gag gat aat atc aat ttt tac atg cct tat atg	440
Asp Thr Tyr Gln Ser Glu Asp Asn Ile Asn Phe Tyr Met Pro Tyr Met	
115 120 125 130	
aac atg gct tat tgg ttt gtc aaa aag gcg ttt cct agc cca gaa tat	488
Asn Met Ala Tyr Trp Phe Val Lys Lys Ala Phe Pro Ser Pro Glu Tyr	
135 140 145	
gaa gat ttc att aag cgg atg cgc cag tat tct caa tca gct ctt aac	536
Glu Asp Phe Ile Lys Arg Met Arg Gln Tyr Ser Gln Ser Ala Leu Asn	
150 155 160	
act aac cat ggg gcg tgg ggc att ctt ttt gat gtg agt tct gcg cta	584
Thr Asn His Gly Ala Trp Gly Ile Leu Phe Asp Val Ser Ser Ala Leu	
165 170 175	
gcg tta gac gat aat gcc ctt ttg cac aat agc gct aat cgg tgg cag	632
Ala Leu Asp Asp Asn Ala Leu Leu His Asn Ser Ala Asn Arg Trp Gln	
180 185 190	
gag tgg gtg ttt aaa gcc ata gat gag aat ggg gtt att gnt agc gcg	680
Glu Trp Val Phe Lys Ala Ile Asp Glu Asn Gly Val Ile Xaa Ser Ala	
195 200 205 210	
atc act agg agc gat acg agc gat tat cat gcc gcc cct aca aag gcc	728
Ile Thr Arg Ser Asp Thr Ser Asp Tyr His Gly Gly Pro Thr Lys Gly	
215 220 225	
att aag ggg ata gct tat acc aat ttc gcg ctt ctt gcg cta acc ata	776
Ile Lys Gly Ile Ala Tyr Thr Asn Phe Ala Leu Leu Ala Leu Thr Ile	
230 235 240	
tca gcc gaa ttg ctt ttt gag aac ggg tat gat ttg tgg ggt agt gga	824
Ser Gly Glu Leu Leu Phe Glu Asn Gly Tyr Asp Leu Trp Gly Ser Gly	
245 250 255	
gct ggg aaa agg ctc tct gtg gcg tat aac aaa gtt gca aca tgg att	872
Ala Gly Lys Arg Leu Ser Val Ala Tyr Asn Lys Val Ala Thr Trp Ile	
260 265 270	
tta aac cct gaa act ttc cct tat ttc cag cct aac ctt atc ggg gtg	920
Leu Asn Pro Glu Thr Phe Pro Tyr Phe Gln Pro Asn Leu Ile Gly Val	
275 280 285 290	
cat aac aac gcc tat ttc att att tta gcc aag cat tat tct agc cct	968
His Asn Asn Ala Tyr Phe Ile Ile Leu Ala Lys His Tyr Ser Ser Pro	
295 300 305	
agt gca aat gag ctt tta aag caa gcc gat tta cac gaa gat ggt ttc	1016
Ser Ala Asn Glu Leu Leu Lys Gln Gly Asp Leu His Glu Asp Gly Phe	
310 315 320	
agg ctg aaa ctc cga tcg cca tgaatttttc tgtatccaag gttagcctta	1067
Arg Leu Lys Leu Arg Ser Pro	

aggatggcca tgcgctttaa cct

1090

&lt;210&gt; 256

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Helicobacter pylori

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 208

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 256

Met	Lys	Arg	Phe	Val	Leu	Phe	Leu	Leu	Phe	Met	Cys	Val	Cys	Val	Gln
1				5					10					15	
Ala	Tyr	Ala	Glu	Gln	Asp	Tyr	Phe	Phe	Arg	Asp	Phe	Lys	Ser	Arg	Asp
			20					25					30		
Leu	Pro	Gln	Lys	Leu	His	Leu	Asp	Lys	Lys	Leu	Ser	Gln	Thr	Ile	Gln
		35				40						45			
Pro	Cys	Met	Gln	Leu	Asn	Ala	Ser	Lys	His	Tyr	Thr	Ser	Thr	Gly	Val
	50				55						60				
Arg	Glu	Pro	Asp	Lys	Cys	Thr	Lys	Ser	Phe	Lys	Lys	Ser	Ala	Leu	Met
65					70					75					80
Ser	Tyr	Asp	Leu	Ala	Leu	Gly	Tyr	Leu	Val	Ser	Lys	Asn	Lys	Gln	Tyr
			85					90						95	
Gly	Leu	Lys	Ala	Ile	Glu	Ile	Leu	Asn	Ala	Trp	Ala	Lys	Glu	Leu	Gln
		100					105						110		
Ser	Val	Asp	Thr	Tyr	Gln	Ser	Glu	Asp	Asn	Ile	Asn	Phe	Tyr	Met	Pro
	115					120						125			
Tyr	Met	Asn	Met	Ala	Tyr	Trp	Phe	Val	Lys	Lys	Ala	Phe	Pro	Ser	Pro
	130					135					140				
Glu	Tyr	Glu	Asp	Phe	Ile	Lys	Arg	Met	Arg	Gln	Tyr	Ser	Gln	Ser	Ala
145					150					155					160
Leu	Asn	Thr	Asn	His	Gly	Ala	Trp	Gly	Ile	Leu	Phe	Asp	Val	Ser	Ser
			165					170						175	
Ala	Leu	Ala	Leu	Asp	Asp	Asn	Ala	Leu	Leu	His	Asn	Ser	Ala	Asn	Arg
		180					185						190		
Trp	Gln	Glu	Trp	Val	Phe	Lys	Ala	Ile	Asp	Glu	Asn	Gly	Val	Ile	Xaa
	195					200						205			
Ser	Ala	Ile	Thr	Arg	Ser	Asp	Thr	Ser	Asp	Tyr	His	Gly	Gly	Pro	Thr
	210					215					220				
Lys	Gly	Ile	Lys	Gly	Ile	Ala	Tyr	Thr	Asn	Phe	Ala	Leu	Leu	Ala	Leu
225				230						235					240
Thr	Ile	Ser	Gly	Glu	Leu	Leu	Phe	Glu	Asn	Gly	Tyr	Asp	Leu	Trp	Gly
			245					250						255	
Ser	Gly	Ala	Gly	Lys	Arg	Leu	Ser	Val	Ala	Tyr	Asn	Lys	Val	Ala	Thr
		260					265						270		
Trp	Ile	Leu	Asn	Pro	Glu	Thr	Phe	Pro	Tyr	Phe	Gln	Pro	Asn	Leu	Ile
	275					280						285			
Gly	Val	His	Asn	Asn	Ala	Tyr	Phe	Ile	Ile	Leu	Ala	Lys	His	Tyr	Ser
	290				295						300				
Ser	Pro	Ser	Ala	Asn	Glu	Leu	Leu	Lys	Gln	Gly	Asp	Leu	His	Glu	Asp
305					310					315					320

Gly Phe Arg Leu Lys Leu Arg Ser Pro  
325

<210> 257  
<211> 373  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (51)...(320)

<400> 257  
ttaacgatcg caaaagccga tgaaagtttt gatgaaatca taaaagggtgt gtg aat 56  
Val Asn  
1  
  
ttt ttg aaa aag cca aag tat tat aaa ttc ata gag ggg gcg aat tat 104  
Phe Leu Lys Lys Pro Lys Tyr Tyr Lys Phe Ile Glu Gly Ala Asn Tyr  
5 10 15  
  
ttg agc ttg ggg ctt tct atg gtg gta gcg atc ctt atg ggc gtg gct 152  
Leu Ser Leu Gly Leu Ser Met Val Val Ala Ile Leu Met Gly Val Ala  
20 25 30  
  
ata ggc tat ggg ctt aaa aaa ctc act cat att tcg tgg ctt ttt tgg 200  
Ile Gly Tyr Gly Leu Lys Lys Leu Thr His Ile Ser Trp Leu Phe Trp  
35 40 45 50  
  
ctt ggg gtt att tgg ggc gtc tta gcg agc ttt ctc aat gtc tat aaa 248  
Leu Gly Val Ile Trp Gly Val Leu Ala Ser Phe Leu Asn Val Tyr Lys  
55 60 65  
  
gct tat aaa aac atg caa aaa gac tat gaa gaa cta gcc aaa gac cct 296  
Ala Tyr Lys Asn Met Gln Lys Asp Tyr Glu Glu Leu Ala Lys Asp Pro  
70 75 80  
  
aaa tac aca caa aat aaa aca aaa taaatccaat caaatcccat gtgccaaatc 350  
Lys Tyr Thr Gln Asn Lys Thr Lys  
85 90  
  
caatgcttgc ttattttact ttc 373

<210> 258  
<211> 90  
<212> PRT  
<213> Helicobacter pylori

<400> 258  
Val Asn Phe Leu Lys Lys Pro Lys Tyr Tyr Lys Phe Ile Glu Gly Ala  
1 5 10 15  
Asn Tyr Leu Ser Leu Gly Leu Ser Met Val Val Ala Ile Leu Met Gly  
20 25 30  
Val Ala Ile Gly Tyr Gly Leu Lys Lys Leu Thr His Ile Ser Trp Leu

		35					40					45				
Phe	Trp	Leu	Gly	Val	Ile	Trp	Gly	Val	Leu	Ala	Ser	Phe	Leu	Asn	Val	
	50					55					60					
Tyr	Lys	Ala	Tyr	Lys	Asn	Met	Gln	Lys	Asp	Tyr	Glu	Glu	Leu	Ala	Lys	
65					70					75					80	
Asp	Pro	Lys	Tyr	Thr	Gln	Asn	Lys	Thr	Lys							
				85					90							

gat gat aag atc gtg ttt tta ggc tca gcg aat tgg agc aaa aac gct	488
Asp Asp Lys Ile Val Phe Leu Gly Ser Ala Asn Trp Ser Lys Asn Ala	
135 140 145	

ttt gaa aac aat tat gaa gtg ctt tta aaa acc gat gac aca gaa acg	536
Phe Glu Asn Asn Tyr Glu Val Leu Leu Lys Thr Asp Asp Thr Glu Thr	
150 155 160	

atc ctc aaa gcc aag agc tat tac caa aag atg tta ggg agt tgc gtt	584
Ile Leu Lys Ala Lys Ser Tyr Tyr Gln Lys Met Leu Gly Ser Cys Val	
165 170 175	

ggg ttt taaaagccct ttagaagtgg taattatacc ccacataaaa ggcaaagacc	640
Gly Phe	
180	

cta	643
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<210> 260  
 <211> 180  
 <212> PRT  
 <213> Helicobacter pylori

<400> 260	
Met Leu Asn Lys Phe Lys Lys Ile Val Gly Val Ser Val Leu Val Gly	
1 5 10 15	
Cys Leu Gly Val Leu Gln Ala Lys Asn Ser Leu Phe Val Leu Pro Tyr	
20 25 30	
Glu Gln Lys Asp Ala Leu Asn Ser Leu Val Ser Gly Ile Ser Asn Ala	
35 40 45	
Arg Glu Ser Val Lys Ile Ala Ile Tyr Ser Phe Thr His Arg Asp Ile	
50 55 60	
Ala Arg Ala Ile Lys Ser Val Ala Ser Arg Gly Ile Lys Val Gln Ile	
65 70 75 80	
Ile Tyr Asp Tyr Glu Ser Asn His His Asn Lys Gln Ser Thr Ile Gly	
85 90 95	
Tyr Leu Asp Lys Tyr Pro Asn Thr Lys Val Cys Leu Leu Lys Gly Leu	
100 105 110	
Lys Ala Lys Asn Gly Asn Tyr Tyr Gly Ile Met His Gln Lys Val Ala	
115 120 125	
Ile Ile Asp Asp Lys Ile Val Phe Leu Gly Ser Ala Asn Trp Ser Lys	
130 135 140	
Asn Ala Phe Glu Asn Asn Tyr Glu Val Leu Leu Lys Thr Asp Asp Thr	
145 150 155 160	
Glu Thr Ile Leu Lys Ala Lys Ser Tyr Tyr Gln Lys Met Leu Gly Ser	
165 170 175	
Cys Val Gly Phe	
180	

<210> 261  
 <211> 814  
 <212> DNA  
 <213> Helicobacter pylori



<220>

<221> CDS

<222> (51)...(761)

<400> 261

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tataagagag tataattcaa ggcttaaaat aactcaagta aggctagtgg atg aaa 56
                                     Met Lys
                                     1

aaa gcg ctt tat tta ggg gct gtt gcg ttt agc gtt gca ttc agc atg 104
Lys Ala Leu Tyr Leu Gly Ala Val Ala Phe Ser Val Ala Phe Ser Met
      5                      10                      15

gca tca gcc aat gag cca aaa att gat ttt aac cct ccc aat tat gta 152
Ala Ser Ala Asn Glu Pro Lys Ile Asp Phe Asn Pro Pro Asn Tyr Val
      20                      25                      30

gaa gaa acc ccc tct aaa gaa ttt atc cct gaa ttg aac aag tta ggg 200
Glu Glu Thr Pro Ser Lys Glu Phe Ile Pro Glu Leu Asn Lys Leu Gly
      35                      40                      45                      50

agt ttg ttt ggg cag ggt gag cgc ccc ttg ttt gcg gac agg agg gcg 248
Ser Leu Phe Gly Gln Gly Glu Arg Pro Leu Phe Ala Asp Arg Arg Ala
      55                      60                      65

atg aag cct aac gat ttg atc aca atc att gtt tct gaa aaa gcg agc 296
Met Lys Pro Asn Asp Leu Ile Thr Ile Ile Val Ser Glu Lys Ala Ser
      70                      75                      80

gcg aat tat tcc agc tct aaa gat tat aaa agc gct tca ggg ggt aat 344
Ala Asn Tyr Ser Ser Ser Lys Asp Tyr Lys Ser Ala Ser Gly Gly Asn
      85                      90                      95

tcc acg ccc cca aga ctc act tat aac ggg cta gat gaa aga aag aaa 392
Ser Thr Pro Pro Arg Leu Thr Tyr Asn Gly Leu Asp Glu Arg Lys Lys
      100                      105                      110

aaa gaa gcg gag tat tta gac gat aag aat aat tac aat ttc acc aaa 440
Lys Glu Ala Glu Tyr Leu Asp Asp Lys Asn Asn Tyr Asn Phe Thr Lys
      115                      120                      125                      130

tcc agc aat aac acg aat ttt aaa ggc ggt ggc tcg caa aaa aag agc 488
Ser Ser Asn Asn Thr Asn Phe Lys Gly Gly Gly Ser Gln Lys Lys Ser
      135                      140                      145

gaa gat tta gag att gtg ttg agc gct cga atc att aag gtg cta gaa 536
Glu Asp Leu Glu Ile Val Leu Ser Ala Arg Ile Ile Lys Val Leu Glu
      150                      155                      160

aac ggg aat tat ttc atc tat ggg aat aag gaa gtg cta gtg gat ggg 584
Asn Gly Asn Tyr Phe Ile Tyr Gly Asn Lys Lys Glu Val Leu Val Asp Gly
      165                      170                      175

gaa aag caa atc ctt aag gtg agt ggg gtg atc cgc cct tat gat att 632
Glu Lys Gln Ile Leu Lys Val Ser Gly Val Ile Arg Pro Tyr Asp Ile
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180	185	190	
gaa agg aat aac acc atc caa tcc aag ttt tta gcc gac gct aag att			680
Glu Arg Asn Asn Thr Ile Gln Ser Lys Phe Leu Ala Asp Ala Lys Ile			
195	200	205	210
gaa tac acg aat tta ggg cat ttg agc gat tcc aat aag aag aaa ttc			728
Glu Tyr Thr Asn Leu Gly His Leu Ser Asp Ser Asn Lys Lys Lys Phe			
	215	220	225
gct gct gat gcg atg gaa acc caa atg cct tat taaaaagagc aaagcctagc			781
Ala Ala Asp Ala Met Glu Thr Gln Met Pro Tyr			
	230	235	
atgagagcgga tcgctattgt tttagccaga agt			814

<210> 262  
 <211> 237  
 <212> PRT  
 <213> *Helicobacter pylori*

<400> 262

Met Lys Lys Ala Leu Tyr Leu Gly Ala Val Ala Phe Ser Val Ala Phe			
1	5	10	15
Ser Met Ala Ser Ala Asn Glu Pro Lys Ile Asp Phe Asn Pro Pro Asn			
	20	25	30
Tyr Val Glu Glu Thr Pro Ser Lys Glu Phe Ile Pro Glu Leu Asn Lys			
	35	40	45
Leu Gly Ser Leu Phe Gly Gln Gly Glu Arg Pro Leu Phe Ala Asp Arg			
	50	55	60
Arg Ala Met Lys Pro Asn Asp Leu Ile Thr Ile Ile Val Ser Glu Lys			
	65	70	75
Ala Ser Ala Asn Tyr Ser Ser Ser Lys Asp Tyr Lys Ser Ala Ser Gly			
	85	90	95
Gly Asn Ser Thr Pro Pro Arg Leu Thr Tyr Asn Gly Leu Asp Glu Arg			
	100	105	110
Lys Lys Lys Glu Ala Glu Tyr Leu Asp Asp Lys Asn Asn Tyr Asn Phe			
	115	120	125
Thr Lys Ser Ser Asn Asn Thr Asn Phe Lys Gly Gly Gly Ser Gln Lys			
	130	135	140
Lys Ser Glu Asp Leu Glu Ile Val Leu Ser Ala Arg Ile Ile Lys Val			
	145	150	155
Leu Glu Asn Gly Asn Tyr Phe Ile Tyr Gly Asn Lys Glu Val Leu Val			
	165	170	175
Asp Gly Glu Lys Gln Ile Leu Lys Val Ser Gly Val Ile Arg Pro Tyr			
	180	185	190
Asp Ile Glu Arg Asn Asn Thr Ile Gln Ser Lys Phe Leu Ala Asp Ala			
	195	200	205
Lys Ile Glu Tyr Thr Asn Leu Gly His Leu Ser Asp Ser Asn Lys Lys			
	210	215	220
Lys Phe Ala Ala Asp Ala Met Glu Thr Gln Met Pro Tyr			
	225	230	235

<210> 263

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<220>
<221> CDS
<222> (51) ... (797)
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ttgggtaaga ttaggaattg attttaaaga aaaagaaaga aaggaattta atg aaa 56  
Met Lys  
1

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ttt tat acg gct cta gct gat gga atg cct gca aaa cag cag cac aat    152
Phe Tyr Thr Ala Leu Ala Asp Gly Met Pro Ala Lys Gln Gln His Asn
      20                      25                      30

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aag caa gag cct aaa aac agc cat tta gtc gtt ttg atc gaa cct aaa 248  
Lys Gln Glu Pro Lys Asn Ser His Leu Val Val Leu Ile Glu Pro Lys  
55 60 65

aag tct ttg ttt ctc cag ttg agt agt ttt tta gag aga aaa ggc tat 344  
Lys Ser Leu Phe Leu Gln Leu Ser Ser Phe Leu Glu Arg Lys Gly Tyr  
85 90 95

gaa aaa gcg ttg ctc gtt tta cgc atg gat ggg aat gtg gct atc ttg 440  
Glu Lys Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala Ile Leu  
115 120 125 130

gac atg tct tca ggg tat ttg aac ttg aat ttt gtt gag cca aaa agt 536  
Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro Lys Ser  
150 155 160

165	170	175	
gtg att gaa aga gtg gaa ttg cgg cgc acc aat tct gga ggt ttt gtc			632
Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly Phe Val			
180	185	190	
ccc aaa act ttt gtg cat agg att aag gaa acc gat cat gat caa gcc			680
Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp Gln Ala			
195	200	205	210
att aga aaa atc atg aat caa gcc tat cac aaa gtg atg gtg cat att			728
Ile Arg Lys Ile Met Asn Gln Ala Tyr His Lys Val Met Val His Ile			
	215	220	225
acc aaa gag tta agc aaa aaa cac atg gaa cat tat gaa aaa gtt tct			776
Thr Lys Glu Leu Ser Lys Lys His Met Glu His Tyr Glu Lys Val Ser			
	230	235	240
agt gaa atg aaa aaa cga aag tagtttttaa gaaacgaaaa gcttaaaaat			827
Ser Glu Met Lys Lys Arg Lys			
245			
cattgagagc tattttttaa aaa			850
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His Asn Asn Thr Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile			
35 40 45			
Lys Gly Lys Gln Glu Pro Lys Asn Ser His Leu Val Val Leu Ile Glu			
50 55 60			
Pro Lys Ile Glu Ile Asn Lys Val Ile Pro Glu Ser Tyr Gln Lys Glu			
65 70 75 80			
Phe Glu Lys Ser Leu Phe Leu Gln Leu Ser Ser Phe Leu Glu Arg Lys			
85 90 95			
Gly Tyr Ser Val Ser Gln Phe Lys Asp Ala Ser Glu Ile Pro Gln Asp			
100 105 110			
Ile Lys Glu Lys Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala			
115 120 125			
Ile Leu Glu Asp Ile Val Glu Glu Ser Asp Ala Leu Ser Glu Glu Lys			
130 135 140			
Val Ile Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro			
145 150 155 160			
Lys Ser Glu Asp Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile			
165 170 175			
Lys Ala Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly			
180 185 190			
Phe Val Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp			



aat cct aaa cta gcc cct tat gga aaa gcc agc atg gaa gtc tta gag 488  
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 135 140 145

aat tta aaa ctc act ccc agt ctt aaa tct aaa atc gtt tat ggc gct 536  
 Asn Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Val Tyr Gly Ala  
 150 155 160

tct att tct caa gcc cat caa ttt gtc gct act aaa aac gct caa ata 584  
 Ser Ile Ser Gln Ala His Gln Phe Val Ala Thr Lys Asn Ala Gln Ile  
 165 170 175

ggc ttt gga gcg tta tcc ttg atg gat aaa aaa gat aaa aac ctc tct 632  
 Gly Phe Gly Ala Leu Ser Leu Met Asp Lys Lys Asp Lys Asn Leu Ser  
 180 185 190

tat ttc atc att gat aaa gcc ctt tat aac cct att gaa caa gcc ttg 680  
 Tyr Phe Ile Ile Asp Lys Ala Leu Tyr Asn Pro Ile Glu Gln Ala Leu  
 195 200 205 210

att atc act aaa aat ggg gct aac aac cct tta gcc aaa gtc ttt aaa 728  
 Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys Val Phe Lys  
 215 220 225

gat ttt tta ttc agc cct aaa gcc aga gct att ttt aaa gaa tac ggc 776  
 Asp Phe Leu Phe Ser Pro Lys Ala Arg Ala Ile Phe Lys Glu Tyr Gly  
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 Tyr Ile Val Asp  
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tgattaccat gcg 841

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 Thr Arg Ala Leu Lys Ala Leu Val Lys Glu Phe Gln Lys Glu His Pro  
 35 40 45  
 Lys Asp Thr Val Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr Ala  
 50 55 60  
 Gln Ile Ile Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp Met  
 65 70 75 80  
 Ile Arg Pro Lys Lys Leu Tyr Asp Lys Lys Ile Thr Pro Phe Lys Glu  
 85 90 95  
 Glu Val Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Glu Asp Leu Lys  
 100 105 110  
 Met Asp Ser Leu Glu Ile Leu Lys Asn Pro Lys Ile Lys Arg Ile Ala



85	90	95	
gtc gct aga aag ggt gat tta gtc tat ttt agg caa ttc aac aac caa			392
Val Ala Arg Lys Gly Asp Leu Val Tyr Phe Arg Gln Phe Asn Asn Gln			
100	105	110	
gcg ttt tta atc gct cct aat gat gaa ctc tat gag caa atc aga gcg			440
Ala Phe Leu Ile Ala Pro Asn Asp Glu Leu Tyr Glu Gln Ile Arg Ala			
115	120	125	130
act aac acc gat att aat ttt att agt tct gat ttg ttg gtt act ttt			488
Thr Asn Thr Asp Ile Asn Phe Ile Ser Ser Asp Leu Leu Val Thr Phe			
	135	140	145
ttg aat ggg ttt gac cca aaa atc gct aat tta agg aaa gcg tgc aac			536
Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu Arg Lys Ala Cys Asn			
	150	155	160
gtt tat agc gtg ggg gtg att tat att gta acc acc aac acg ctc aat			584
Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr Thr Asn Thr Leu Asn			
	165	170	175
att tta agt tgt gag agt ttt gaa att tta gaa aaa aga gag ctg gat			632
Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu Lys Arg Glu Leu Asp			
	180	185	190
aca agc ggc gtt act aaa act tcc acg ccg ttt ttt tct agg gtt gag			680
Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe Phe Ser Arg Val Glu			
195	200	205	210
ggt att gat gca ggc acg cta ggg aaa ctt ttt tca ggc agt cag tct			728
Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe Ser Gly Ser Gln Ser			
	215	220	225
aaa aat tac ttc gct tac tat gac gct tta gtg aag aaa gaa aaa cgc			776
Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val Lys Lys Glu Lys Arg			
	230	235	240
aaa gaa gtg agg att aaa aag agg gaa gaa aag att gat tct aga gaa			824
Lys Glu Val Arg Ile Lys Lys Arg Glu Glu Lys Ile Asp Ser Arg Glu			
	245	250	255
att aaa cga gaa atc aag caa gag gcc att aaa gag cct aaa aaa gcc			872
Ile Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys Glu Pro Lys Lys Ala			
	260	265	270
aat caa ggc aca caa aac gct cct act tta gaa gag aaa aac tac caa			920
Asn Gln Gly Thr Gln Asn Ala Pro Thr Leu Glu Glu Lys Asn Tyr Gln			
275	280	285	290
aaa gca gag cgc aaa ctt gat gct aaa gaa gaa agg cgt tat ttg aga			968
Lys Ala Glu Arg Lys Leu Asp Ala Lys Glu Glu Arg Arg Tyr Leu Arg			
	295	300	305
gat gaa agg aaa aaa gcc aaa gcc acc aaa aag gct atg gaa ttt gaa			1016



Asp	Glu	Arg	Lys	Lys	Ala	Lys	Ala	Thr	Lys	Lys	Ala	Met	Glu	Phe	Glu		
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Glu	Arg	Glu	Lys	Glu	His	Asp	Glu	Arg	Asp	Glu	Gln	Glu	Thr	Glu	Gly		
			325				330					335					
aga	aga	aaa	gct	tta	gaa	atg	gat	aaa	ggc	gat	aaa	aaa	gaa	gaa	aga	1112	
Arg	Arg	Lys	Ala	Leu	Glu	Met	Asp	Lys	Gly	Asp	Lys	Lys	Glu	Glu	Arg		
			340				345					350					
gtc	aaa	ccc	aaa	gaa	aat	gag	cga	gaa	atc	aag	caa	gaa	gcc	att	aaa	1160	
Val	Lys	Pro	Lys	Glu	Asn	Glu	Arg	Glu	Ile	Lys	Gln	Glu	Ala	Ile	Lys		
					360					365					370		
gag	cca	agt	gat	gga	aat	aac	gcc	acc	caa	caa	ggc	gaa	aaa	caa	aac	1208	
Glu	Pro	Ser	Asp	Gly	Asn	Asn	Ala	Thr	Gln	Gln	Gly	Glu	Lys	Gln	Asn		
				375					380						385		
gct	cct	aaa	gag	aac	aac	gct	caa	aaa	gaa	gag	aat	aaa	cca	aat	tct	1256	
Ala	Pro	Lys	Glu	Asn	Asn	Ala	Gln	Lys	Glu	Glu	Asn	Lys	Pro	Asn	Ser		
			390					395						400			
aaa	gaa	gaa	aaa	cgc	cgc	ttg	aaa	gaa	gaa	aag	aaa	aaa	gcc	aaa	gcc	1304	
Lys	Glu	Glu	Lys	Arg	Arg	Leu	Lys	Glu	Glu	Lys	Lys	Lys	Ala	Lys	Ala		
			405				410					415					
gaa	caa	aga	gcg	aga	gaa	ttt	gaa	caa	aga	gcg	aga	gag	cat	caa	gaa	1352	
Glu	Gln	Arg	Ala	Arg	Glu	Phe	Glu	Gln	Arg	Ala	Arg	Glu	His	Gln	Glu		
			420				425				430						
aga	gat	gaa	aaa	gag	ctt	gaa	gag	cga	aga	aag	gcg	cta	gaa	gcg	ggt	1400	
Arg	Asp	Glu	Lys	Glu	Leu	Glu	Arg	Arg	Lys	Ala	Leu	Glu	Ala	Gly			
					440				445					450			
aaa	aaa	taacatgtta	gaccaacaac	acatccaata	ctttaaaaac	ctagtagggg	1456										
Lys	Lys																
gag																1459	

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 <213> Helicobacter pylori

<400> 268  
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 20 25 30  
 Asp Leu Pro Lys Lys Ile Ile Arg Phe Pro Ala His Asp Leu Gln Val  
 35 40 45  
 Gly Glu Phe Gly Phe Val Val Thr Lys Leu Ser Asp Tyr Glu Ile Val  
 50 55 60

Asn	Ser	Glu	Val	Val	Ile	Ile	Ala	Val	Glu	Asn	Gly	Val	Ala	Thr	Ala	
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Lys	Phe	Arg	Ala	Phe	Glu	Ser	Met	Lys	Gln	Arg	His	Leu	Pro	Thr	Pro	
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Arg	Met	Val	Ala	Arg	Lys	Gly	Asp	Leu	Val	Tyr	Phe	Arg	Gln	Phe	Asn	
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Asn	Gln	Ala	Phe	Leu	Ile	Ala	Pro	Asn	Asp	Glu	Leu	Tyr	Glu	Gln	Ile	
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Thr	Phe	Leu	Asn	Gly	Phe	Asp	Pro	Lys	Ile	Ala	Asn	Leu	Arg	Lys	Ala	
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Cys	Asn	Val	Tyr	Ser	Val	Gly	Val	Ile	Tyr	Ile	Val	Thr	Thr	Asn	Thr	
			165						170					175		
Leu	Asn	Ile	Leu	Ser	Cys	Glu	Ser	Phe	Glu	Ile	Leu	Glu	Lys	Arg	Glu	
		180						185					190			
Leu	Asp	Thr	Ser	Gly	Val	Thr	Lys	Thr	Ser	Thr	Pro	Phe	Phe	Ser	Arg	
		195					200					205				
Val	Glu	Gly	Ile	Asp	Ala	Gly	Thr	Leu	Gly	Lys	Leu	Phe	Ser	Gly	Ser	
	210					215					220					
Gln	Ser	Lys	Asn	Tyr	Phe	Ala	Tyr	Tyr	Asp	Ala	Leu	Val	Lys	Lys	Glu	
225					230					235					240	
Lys	Arg	Lys	Glu	Val	Arg	Ile	Lys	Lys	Arg	Glu	Glu	Lys	Ile	Asp	Ser	
			245						250					255		
Arg	Glu	Ile	Lys	Arg	Glu	Ile	Lys	Gln	Glu	Ala	Ile	Lys	Glu	Pro	Lys	
		260						265					270			
Lys	Ala	Asn	Gln	Gly	Thr	Gln	Asn	Ala	Pro	Thr	Leu	Glu	Glu	Lys	Asn	
	275						280					285				
Tyr	Gln	Lys	Ala	Glu	Arg	Lys	Leu	Asp	Ala	Lys	Glu	Glu	Arg	Arg	Tyr	
	290					295				300						
Leu	Arg	Asp	Glu	Arg	Lys	Lys	Ala	Lys	Ala	Thr	Lys	Lys	Ala	Met	Glu	
305					310					315					320	
Phe	Glu	Glu	Arg	Glu	Lys	Glu	His	Asp	Glu	Arg	Asp	Glu	Gln	Glu	Thr	
			325						330					335		
Glu	Gly	Arg	Arg	Lys	Ala	Leu	Glu	Met	Asp	Lys	Gly	Asp	Lys	Lys	Glu	
		340						345					350			
Glu	Arg	Val	Lys	Pro	Lys	Glu	Asn	Glu	Arg	Glu	Ile	Lys	Gln	Glu	Ala	
	355						360					365				
Ile	Lys	Glu	Pro	Ser	Asp	Gly	Asn	Asn	Ala	Thr	Gln	Gln	Gly	Glu	Lys	
	370					375					380					
Gln	Asn	Ala	Pro	Lys	Glu	Asn	Asn	Ala	Gln	Lys	Glu	Glu	Asn	Lys	Pro	
385					390					395					400	
Asn	Ser	Lys	Glu	Glu	Lys	Arg	Arg	Leu	Lys	Glu	Glu	Lys	Lys	Lys	Ala	
			405						410					415		
Lys	Ala	Glu	Gln	Arg	Ala	Arg	Glu	Phe	Glu	Gln	Arg	Ala	Arg	Glu	His	
		420						425					430			
Gln	Glu	Arg	Asp	Glu	Lys	Glu	Leu	Glu	Glu	Arg	Arg	Lys	Ala	Leu	Glu	
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Ala	Gly	Lys	Lys													
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<213> Helicobacter pylori

<220>

<221> CDS

<222> (74)...(943)

<400> 269

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          Met Lys Phe Leu Arg Ser Val Tyr Ala Phe Cys Ser
              1              5              10

agt tgg gta ggg acg att gtt att gtg ctg ttg gtt atc ttt ttt atc 157
Ser Trp Val Gly Thr Ile Val Ile Val Leu Leu Val Ile Phe Phe Ile
          15              20              25

gcg caa gcc ttt atc att ccc tct cgc tct atg gtt ggc acg ctc tat 205
Ala Gln Ala Phe Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr
          30              35              40

gag ggc gac atg ctc ttt gtc aaa aag ttt tct tac ggc ata ccc att 253
Glu Gly Asp Met Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile
          45              50              55              60

cct aaa atc cca tgg att gag ctt cct gtt atg cct gat ttt aaa aat 301
Pro Lys Ile Pro Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn
          65              70              75

aac gga cat ttg ata gag ggg gat cgc cct aag cgt ggc gaa gtg gtg 349
Asn Gly His Leu Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val
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gtg ttt atc cct ccc cat gaa aaa aag tct tac tat gtt aaa agg aat 397
Val Phe Ile Pro Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn
          95              100              105

ttt gcc att gga ggc gat gag gtg ttg ttc act aat gag ggt ttt tat 445
Phe Ala Ile Gly Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr
          110              115              120

ttg cac cct ttt gag agc gac acg gac aaa aat tac atc gct aaa cat 493
Leu His Pro Phe Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His
          125              130              135              140

tac cct aac gcc atg aca aaa gaa ttt atg ggt aaa att ttt gtt tta 541
Tyr Pro Asn Ala Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu
          145              150              155

aac cct tat aaa aat gag cat ccg ggt atc cat tac caa aaa gac aat 589
Asn Pro Tyr Lys Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn
          160              165              170

gaa acc ttc cac tta atg gag caa tta gcc act caa ggc gca gaa gct 637
Glu Thr Phe His Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala
          175              180              185
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aat atc agc atg caa ctc att caa atg gag ggc gaa aag gtg ttt tat	685
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Lys Lys Ile Asn Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp	
205 210 215 220	
aat tct agc gac tcg cgc ttt tgg ggg agt gtg gct tat aaa aac atc	781
Asn Ser Ser Asp Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile	
225 230 235	
gtg ggt tcg cca tgg ttt gtt tat ttc agt ttg agt tta aaa aat agc	829
Val Gly Ser Pro Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser	
240 245 250	
cta gaa atg gat gca gaa aat aac cct aaa aaa cgc tat ctg gtg cgt	877
Leu Glu Met Asp Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg	
255 260 265	
tgg gaa cgc atg ttt aaa agc gtt gga ggc tta gaa aaa atc att aaa	925
Trp Glu Arg Met Phe Lys Ser Val Gly Gly Leu Glu Lys Ile Ile Lys	
270 275 280	
aaa gaa aac gca acg cat taagggttttt tgtgcaatttt tttgatttct	973
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35 40 45	
Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro Lys Ile Pro	
50 55 60	
Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn Gly His Leu	
65 70 75 80	
Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val Phe Ile Pro	
85 90 95	
Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly	
100 105 110	
Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu His Pro Phe	
115 120 125	
Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr Pro Asn Ala	
130 135 140	

Met	Thr	Lys	Glu	Phe	Met	Gly	Lys	Ile	Phe	Val	Leu	Asn	Pro	Tyr	Lys	
145					150					155					160	
Asn	Glu	His	Pro	Gly	Ile	His	Tyr	Gln	Lys	Asp	Asn	Glu	Thr	Phe	His	
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Leu	Met	Glu	Gln	Leu	Ala	Thr	Gln	Gly	Ala	Glu	Ala	Asn	Ile	Ser	Met	
			180					185					190			
Gln	Leu	Ile	Gln	Met	Glu	Gly	Glu	Lys	Val	Phe	Tyr	Lys	Lys	Ile	Asn	
		195					200					205				
Asp	Asp	Glu	Phe	Phe	Met	Ile	Gly	Asp	Asn	Arg	Asp	Asn	Ser	Ser	Asp	
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Ser	Arg	Phe	Trp	Gly	Ser	Val	Ala	Tyr	Lys	Asn	Ile	Val	Gly	Ser	Pro	
225					230					235					240	
Trp	Phe	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Lys	Asn	Ser	Leu	Glu	Met	Asp	
				245					250					255		
Ala	Glu	Asn	Asn	Pro	Lys	Lys	Arg	Tyr	Leu	Val	Arg	Trp	Glu	Arg	Met	
		260					265						270			
Phe	Lys	Ser	Val	Gly	Gly	Leu	Glu	Lys	Ile	Ile	Lys	Lys	Glu	Asn	Ala	
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Thr	His															
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<220>  
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 gaggttgcaa ttcagggaca agatcactac tgaagaaatc caacaaactt tgattaaaac 240  
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 taaaaccttg tatgatcgct atttggttaa agacgctaac aacaacccta ttgaattgcc 540  
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 Met Phe Met Ser Ile Ala Met Phe Leu Ala Gln Asn Glu Gln  
 1 5 10  
 gaa ccc aat aaa atc gcc tta gaa ttt tat gaa gtt ttg agc aag ttt 637  
 Glu Pro Asn Lys Ile Ala Leu Glu Phe Tyr Glu Val Leu Ser Lys Phe  
 15 20 25 30  
 gaa gcg atg tgc gcg acc ccc act cta gcg aac gcc cgc acc acc aaa 685  
 Glu Ala Met Cys Ala Thr Pro Thr Leu Ala Asn Ala Arg Thr Thr Lys  
 35 40 45  
 cac cag ctc agc tca tgc tat att ggc agc acg ccg gat aat att gag 733  
 His Gln Leu Ser Ser Cys Tyr Ile Gly Ser Thr Pro Asp Asn Ile Glu

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att gat ggg cat aaa aat gcg agc gct ggc acg atc cct ttt tta aaa Ile Asp Gly His Lys Asn Ala Ser Ala Gly Thr Ile Pro Phe Leu Lys 95 100 105 110			877
atc gct aac gat gtg gcg att gcg gtg gat caa tta ggc aca cga aag Ile Ala Asn Asp Val Ala Ile Ala Val Asp Gln Leu Gly Thr Arg Lys 115 120 125			925
ggc gcg att gcg gtg tat ttg gaa att tgg cac att gat gtg atg gag Gly Ala Ile Ala Val Tyr Leu Glu Ile Trp His Ile Asp Val Met Glu 130 135 140			973
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tgg aaa aaa atc tta atg aat tat ttt gaa gcc ggt ttg cct ttc tta Trp Lys Lys Ile Leu Met Asn Tyr Phe Glu Ala Gly Leu Pro Phe Leu 225 230 235			1261
gcc ttt aaa gat aac gcc aat cgg tgc aac cca aac gct cat gca gga Ala Phe Lys Asp Asn Ala Asn Arg Cys Asn Pro Asn Ala His Ala Gly 240 245 250			1309
atc att cga tcc agc aat cta tgc acg gag att ttc caa aat acc gcg Ile Ile Arg Ser Ser Asn Leu Cys Thr Glu Ile Phe Gln Asn Thr Ala 255 260 265 270			1357
cct aac cac tac tac atg caa ata gaa tac acc gac ggc acc ata gag			1405

Pro	Asn	His	Tyr	Tyr	Met	Gln	Ile	Glu	Tyr	Thr	Asp	Gly	Thr	Ile	Glu	
				275					280					285		
ttt	ttt	gaa	gaa	aaa	gag	ttg	gta	acg	aca	gat	agt	aat	atc	act	aaa	1453
Phe	Phe	Glu	Glu	Lys	Glu	Leu	Val	Thr	Thr	Asp	Ser	Asn	Ile	Thr	Lys	
				290				295					300			
tgc	gct	aac	aag	ctc	act	agc	acc	gat	att	cta	aag	ggc	aag	cca	atc	1501
Cys	Ala	Asn	Lys	Leu	Thr	Ser	Thr	Asp	Ile	Leu	Lys	Gly	Lys	Pro	Ile	
				305				310					315			
tat	atc	gct	act	aaa	gtc	gct	aaa	gac	ggg	caa	acg	gcg	gtg	tgc	aat	1549
Tyr	Ile	Ala	Thr	Lys	Val	Ala	Lys	Asp	Gly	Gln	Thr	Ala	Val	Cys	Asn	
				320				325				330				
ctg	gcg	agc	atc	aat	tta	agc	aaa	atc	aac	act	gaa	gaa	gac	att	aaa	1597
Leu	Ala	Ser	Ile	Asn	Leu	Ser	Lys	Ile	Asn	Thr	Glu	Glu	Asp	Ile	Lys	
					340					345					350	
agg	gtt	gtg	ccg	atc	atg	gtc	agg	ctt	tta	gac	aat	gtg	att	gat	ttg	1645
Arg	Val	Val	Pro	Ile	Met	Val	Arg	Leu	Leu	Asp	Asn	Val	Ile	Asp	Leu	
					355					360					365	
aat	ttc	tac	cct	aac	cgc	aaa	gtc	aaa	gcc	act	aat	tta	caa	aat	agg	1693
Asn	Phe	Tyr	Pro	Asn	Arg	Lys	Val	Lys	Ala	Thr	Asn	Leu	Gln	Asn	Arg	
				370				375					380			
gcc	ata	ggg	tta	ggg	gtt	atg	ggt	gaa	gcg	caa	atg	ctc	gca	gaa	cac	1741
Ala	Ile	Gly	Leu	Gly	Val	Met	Gly	Glu	Ala	Gln	Met	Leu	Ala	Glu	His	
				385				390					395			
caa	atc	gct	tgg	ggg	tct	aaa	gag	cat	tta	gaa	aaa	att	gac	gct	tta	1789
Gln	Ile	Ala	Trp	Gly	Ser	Lys	Glu	His	Leu	Glu	Lys	Ile	Asp	Ala	Leu	
			400			405					410					
atg	gag	caa	atc	agc	tac	cat	gcg	att	gac	acg	agc	gcg	aat	tta	gcg	1837
Met	Glu	Gln	Ile	Ser	Tyr	His	Ala	Ile	Asp	Thr	Ser	Ala	Asn	Leu	Ala	
					420					425				430		
aaa	gaa	aaa	ggg	gtt	tat	aag	gat	ttt	gaa	aat	tca	gaa	tgg	agt	aag	1885
Lys	Glu	Lys	Gly	Val	Tyr	Lys	Asp	Phe	Glu	Asn	Ser	Glu	Trp	Ser	Lys	
				435					440					445		
ggg	att	ttc	ccc	att	gat	aaa	gcc	aat	aat	gaa	gcc	tta	aag	ctc	acc	1933
Gly	Ile	Phe	Pro	Ile	Asp	Lys	Ala	Asn	Asn	Glu	Ala	Leu	Lys	Leu	Thr	
				450				455					460			
gaa	aaa	ggg	ctt	ttt	aat	cac	gct	tgc	gat	tgg	caa	ggt	ttg	agg	gaa	1981
Glu	Lys	Gly	Leu	Phe	Asn	His	Ala	Cys	Asp	Trp	Gln	Gly	Leu	Arg	Glu	
				465				470					475			
aaa	gtc	aaa	gcc	aat	ggc	atg	cgt	aat	ggc	tat	tta	atg	gcg	atc	gct	2029
Lys	Val	Lys	Ala	Asn	Gly	Met	Arg	Asn	Gly	Tyr	Leu	Met	Ala	Ile	Ala	
				480				485					490			

ccc aca agc tcc att tct att tta gta ggc aca acc caa acg att gaa 2077  
 Pro Thr Ser Ser Ile Ser Ile Leu Val Gly Thr Thr Gln Thr Ile Glu  
 495 500 505 510

ccc att tat aag aaa aaa tgg ttt gaa gaa aat ttg agc ggg ctt att 2125  
 Pro Ile Tyr Lys Lys Lys Trp Phe Glu Glu Asn Leu Ser Gly Leu Ile  
 515 520 525

cct gtt gtg gtg cct aat ttg aat gta gaa acc tgg aat ttt tac aca 2173  
 Pro Val Val Val Pro Asn Leu Asn Val Glu Thr Trp Asn Phe Tyr Thr  
 530 535 540

tca gcc tat gat att gac gct aaa gat ttg att aaa gca gcg gcc gtg 2221  
 Ser Ala Tyr Asp Ile Asp Ala Lys Asp Leu Ile Lys Ala Ala Ala Val  
 545 550 555

cgc caa aag tgg att gat caa ggc caa agc ctt aat gtg ttt tta cgc 2269  
 Arg Gln Lys Trp Ile Asp Gln Gly Gln Ser Leu Asn Val Phe Leu Arg  
 560 565 570

ata gaa aac gcc agc ggt aaa acc ttg cat gac atc tac acg ctc gct 2317  
 Ile Glu Asn Ala Ser Gly Lys Thr Leu His Asp Ile Tyr Thr Leu Ala  
 575 580 585 590

tgg aaa tta gga ctc aaa tcc act tat tat ttg cgc agc gaa agc cct 2365  
 Trp Lys Leu Gly Leu Lys Ser Thr Tyr Tyr Leu Arg Ser Glu Ser Pro  
 595 600 605

agc ata gat gaa aaa agc gtg ttg gat cga tcg gtg gag tgt ttt aat 2413  
 Ser Ile Asp Glu Lys Ser Val Leu Asp Arg Ser Val Glu Cys Phe Asn  
 610 615 620

tgc caa taatataagc ttaaataagc taatctttgc taaaatgaga tttaaaatta 2469  
 Cys Gln

ttta 2473

<210> 272  
 <211> 624  
 <212> PRT  
 <213> Helicobacter pylori

<400> 272  
 Met Phe Met Ser Ile Ala Met Phe Leu Ala Gln Asn Glu Gln Glu Pro  
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 Asn Lys Ile Ala Leu Glu Phe Tyr Glu Val Leu Ser Lys Phe Glu Ala  
 20 25 30  
 Met Cys Ala Thr Pro Thr Leu Ala Asn Ala Arg Thr Thr Lys His Gln  
 35 40 45  
 Leu Ser Ser Cys Tyr Ile Gly Ser Thr Pro Asp Asn Ile Glu Gly Ile  
 50 55 60  
 Phe Asp Ser Tyr Lys Glu Met Ala Leu Leu Ser Lys Tyr Gly Gly Gly  
 65 70 75 80  
 Ile Gly Trp Asp Phe Ser Leu Val Arg Ser Ile Gly Ser Tyr Ile Asp





Val	Val	Pro	Asn	Leu	Asn	Val	Glu	Thr	Trp	Asn	Phe	Tyr	Thr	Ser	Ala	
530						535					540					
Tyr	Asp	Ile	Asp	Ala	Lys	Asp	Leu	Ile	Lys	Ala	Ala	Ala	Val	Arg	Gln	
545					550					555					560	
Lys	Trp	Ile	Asp	Gln	Gly	Gln	Ser	Leu	Asn	Val	Phe	Leu	Arg	Ile	Glu	
				565					570					575		
Asn	Ala	Ser	Gly	Lys	Thr	Leu	His	Asp	Ile	Tyr	Thr	Leu	Ala	Trp	Lys	
			580					585					590			
Leu	Gly	Leu	Lys	Ser	Thr	Tyr	Tyr	Leu	Arg	Ser	Glu	Ser	Pro	Ser	Ile	
		595					600					605				
Asp	Glu	Lys	Ser	Val	Leu	Asp	Arg	Ser	Val	Glu	Cys	Phe	Asn	Cys	Gln	
610						615					620					

<210> 273  
 <211> 1440  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (56)...(1390)

<400> 273  
 gcaaaattct agccttaaatt ctttgatgaa acgaagtcaa attataagat aaggc atg 58  
 Met  
 1

tta aaa ttc cct aaa atg agt tta agg att tta atg ctt tct gtc atc 106  
 Leu Lys Phe Pro Lys Met Ser Leu Arg Ile Leu Met Leu Ser Val Ile  
 5 10 15

ata ctg gcc gct ggt aaa ggc act cgc atg cgt tct agc ctg cct aaa 154  
 Ile Leu Ala Ala Gly Lys Gly Thr Arg Met Arg Ser Ser Leu Pro Lys  
 20 25 30

act tta cac acc att tgt ggg gag cct atg ttg ttt tac att tta gaa 202  
 Thr Leu His Thr Ile Cys Gly Glu Pro Met Leu Phe Tyr Ile Leu Glu  
 35 40 45

acg gct ttt tca atc agc gat gat gtg cat ctt atc tta cac cac caa 250  
 Thr Ala Phe Ser Ile Ser Asp Asp Val His Leu Ile Leu His His Gln  
 50 55 60 65

caa gaa cgc att aaa gaa gcg gtg ttg gag cgt ttt aag ggc gtc att 298  
 Gln Glu Arg Ile Lys Glu Ala Val Leu Glu Arg Phe Lys Gly Val Ile  
 70 75 80

ttt cac act caa att gtg gaa aaa tat tca ggg aca ggt ggg gct atc 346  
 Phe His Thr Gln Ile Val Glu Lys Tyr Ser Gly Thr Gly Gly Ala Ile  
 85 90 95

atg caa aaa gat aaa acg cct att tct acg aaa cat gag cgg gtt ttg 394  
 Met Gln Lys Asp Lys Thr Pro Ile Ser Thr Lys His Glu Arg Val Leu  
 100 105 110

att ttg aat gcg gac atg cct tta atc act aaa gac gct ctc gcc ccc	442
Ile Leu Asn Ala Asp Met Pro Leu Ile Thr Lys Asp Ala Leu Ala Pro	
115 120 125	
tta tta gaa agc aag aat aac gct ata ggc tta ctc cat tta gct gac	490
Leu Leu Glu Ser Lys Asn Asn Ala Ile Gly Leu Leu His Leu Ala Asp	
130 135 140 145	
cct aaa ggt tat ggg cgc gtt gtt tta gaa aac cat cag gtt aaa aag	538
Pro Lys Gly Tyr Gly Arg Val Val Leu Glu Asn His Gln Val Lys Lys	
150 155 160	
att gta gaa gaa aag gac gct aat gat gaa gaa aaa gaa att aaa agc	586
Ile Val Glu Glu Lys Asp Ala Asn Asp Glu Glu Lys Glu Ile Lys Ser	
165 170 175	
gtg aat gct ggc gtg tat ggg ttt gaa agg gat ttt tta gaa aaa tac	634
Val Asn Ala Gly Val Tyr Gly Phe Glu Arg Asp Phe Leu Glu Lys Tyr	
180 185 190	
tta ccc aag ctc cat gac caa aac gcc caa aaa gaa tac tac ctc acg	682
Leu Pro Lys Leu His Asp Gln Asn Ala Gln Lys Glu Tyr Tyr Leu Thr	
195 200 205	
gat tta atc gct cta ggg atc aat gaa aac gaa aca att gac gct att	730
Asp Leu Ile Ala Leu Gly Ile Asn Glu Asn Glu Thr Ile Asp Ala Ile	
210 215 220 225	
ttc tta aaa gaa gag tgt ttt tta ggg gtg aat agc caa aca gaa agg	778
Phe Leu Lys Glu Glu Cys Phe Leu Gly Val Asn Ser Gln Thr Glu Arg	
230 235 240	
gcg aaa gct gaa gaa atc atg cta gaa aga ctg cgc aaa aac gcc atg	826
Ala Lys Ala Glu Glu Ile Met Leu Glu Arg Leu Arg Lys Asn Ala Met	
245 250 255	
gac ttg ggg gta gtg atg caa ttg cct aat agc att tat tta gaa aaa	874
Asp Leu Gly Val Val Met Gln Leu Pro Asn Ser Ile Tyr Leu Glu Lys	
260 265 270	
ggc gtg agt ttt aag ggg gag tgc gtt tta gag caa ggg gtg cgt ttg	922
Gly Val Ser Phe Lys Gly Glu Cys Val Leu Glu Gln Gly Val Arg Leu	
275 280 285	
att ggg aat tgt ttg ata gaa aac gcg cat att aag gct tat agc gtg	970
Ile Gly Asn Cys Leu Ile Glu Asn Ala His Ile Lys Ala Tyr Ser Val	
290 295 300 305	
ata gaa gag agc cag att gtt aat agc agt gtg ggg ccg ttt gcc cat	1018
Ile Glu Glu Ser Gln Ile Val Asn Ser Ser Val Gly Pro Phe Ala His	
310 315 320	
gcg cgc cct aaa agc gtg att tgt aat agc cat gtg ggg aat ttt gta	1066
Ala Arg Pro Lys Ser Val Ile Cys Asn Ser His Val Gly Asn Phe Val	

325	330	335	
gag act aaa aac gct aaa ctt caa ggc act aaa gca ggg cat ttg agc	1114		
Glu Thr Lys Asn Ala Lys Leu Gln Gly Thr Lys Ala Gly His Leu Ser			
340	345	350	
tat tta ggg gat tgt gag ata ggg aaa aac aca aat gta ggg gct ggc	1162		
Tyr Leu Gly Asp Cys Glu Ile Gly Lys Asn Thr Asn Val Gly Ala Gly			
355	360	365	
gtg atc act tgc aat tac gat ggt aaa aag aaa cac caa aca atc atc	1210		
Val Ile Thr Cys Asn Tyr Asp Gly Lys Lys Lys His Gln Thr Ile Ile			
370	375	380	385
ggg gaa aat gtc ttt ata ggg agc gat agc cag cta gtc gcc ccc ata	1258		
Gly Glu Asn Val Phe Ile Gly Ser Asp Ser Gln Leu Val Ala Pro Ile			
390	395	400	
aat atc ggc tct aat gtc tta atc ggc agc ggc acc act atc act aaa	1306		
Asn Ile Gly Ser Asn Val Leu Ile Gly Ser Gly Thr Thr Ile Thr Lys			
405	410	415	
gac att cct agc ggt tcg ttg agc ctt tca cgc gcc cct caa acc aac	1354		
Asp Ile Pro Ser Gly Ser Leu Ser Leu Ser Arg Ala Pro Gln Thr Asn			
420	425	430	
att gaa aac ggg tat ttt aag ttt ttt aag aaa cct taatttggtt	1400		
Ile Glu Asn Gly Tyr Phe Lys Phe Phe Lys Lys Pro			
435	440	445	
gaataatgaa aaatcctaaa atattaatca tttacttta	1440		
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<211> 445			
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<213> Helicobacter pylori			
<400> 274			
Met Leu Lys Phe Pro Lys Met Ser Leu Arg Ile Leu Met Leu Ser Val			
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Ile Ile Leu Ala Ala Gly Lys Gly Thr Arg Met Arg Ser Ser Leu Pro			
20 25 30			
Lys Thr Leu His Thr Ile Cys Gly Glu Pro Met Leu Phe Tyr Ile Leu			
35 40 45			
Glu Thr Ala Phe Ser Ile Ser Asp Asp Val His Leu Ile Leu His His			
50 55 60			
Gln Gln Glu Arg Ile Lys Glu Ala Val Leu Glu Arg Phe Lys Gly Val			
65 70 75 80			
Ile Phe His Thr Gln Ile Val Glu Lys Tyr Ser Gly Thr Gly Gly Ala			
85 90 95			
Ile Met Gln Lys Asp Lys Thr Pro Ile Ser Thr Lys His Glu Arg Val			
100 105 110			
Leu Ile Leu Asn Ala Asp Met Pro Leu Ile Thr Lys Asp Ala Leu Ala			
115 120 125			
Pro Leu Leu Glu Ser Lys Asn Asn Ala Ile Gly Leu Leu His Leu Ala			

130	135	140
Asp Pro Lys Gly Tyr Gly Arg Val Val Leu Glu Asn His Gln Val Lys		
145	150	155
Lys Ile Val Glu Glu Lys Asp Ala Asn Asp Glu Glu Lys Glu Ile Lys		
	165	170
Ser Val Asn Ala Gly Val Tyr Gly Phe Glu Arg Asp Phe Leu Glu Lys		
	180	185
Tyr Leu Pro Lys Leu His Asp Gln Asn Ala Gln Lys Glu Tyr Tyr Leu		
	195	200
Thr Asp Leu Ile Ala Leu Gly Ile Asn Glu Asn Glu Thr Ile Asp Ala		
	210	215
Ile Phe Leu Lys Glu Glu Cys Phe Leu Gly Val Asn Ser Gln Thr Glu		
225	230	235
Arg Ala Lys Ala Glu Ile Met Leu Glu Arg Leu Arg Lys Asn Ala		
	245	250
Met Asp Leu Gly Val Val Met Gln Leu Pro Asn Ser Ile Tyr Leu Glu		
	260	265
Lys Gly Val Ser Phe Lys Gly Glu Cys Val Leu Glu Gln Gly Val Arg		
	275	280
Leu Ile Gly Asn Cys Leu Ile Glu Asn Ala His Ile Lys Ala Tyr Ser		
	290	295
Val Ile Glu Glu Ser Gln Ile Val Asn Ser Ser Val Gly Pro Phe Ala		
305	310	315
His Ala Arg Pro Lys Ser Val Ile Cys Asn Ser His Val Gly Asn Phe		
	325	330
Val Glu Thr Lys Asn Ala Lys Leu Gln Gly Thr Lys Ala Gly His Leu		
	340	345
Ser Tyr Leu Gly Asp Cys Glu Ile Gly Lys Asn Thr Asn Val Gly Ala		
	355	360
Gly Val Ile Thr Cys Asn Tyr Asp Gly Lys Lys Lys His Gln Thr Ile		
	370	375
Ile Gly Glu Asn Val Phe Ile Gly Ser Asp Ser Gln Leu Val Ala Pro		
385	390	395
Ile Asn Ile Gly Ser Asn Val Leu Ile Gly Ser Gly Thr Thr Ile Thr		
	405	410
Lys Asp Ile Pro Ser Gly Ser Leu Ser Leu Ser Arg Ala Pro Gln Thr		
	420	425
Asn Ile Glu Asn Gly Tyr Phe Lys Phe Phe Lys Lys Pro		
	435	440
		445

<210> 275  
 <211> 771  
 <212> DNA  
 <213> *Helicobacter pylori*

<220>  
 <221> CDS  
 <222> (227)...(715)

<221> misc\_feature  
 <222> 57  
 <223> n = A,T,C or G

<400> 275

gcaaagataa aaaacaaacg gggttttggtg aaattttctg gggaagcggtt agctggngga 60  
 caaccagttt gggattgaca ttcattgtgtt agatcacatc gctaaagaga tcaaaagttt 120  
 agtggaaaac gatattgaag tgggtattgt gattggtgga ggcaatatta ttaggggggt 180  
 tagcgcggtt caagggggga ttattaggcg caccagtggg gattat atg ggc atg 235  
 Met Gly Met

1

tta gcc acc gtg att aat gcg gta gcg atg caa gaa gct tta gag cat 283  
 Leu Ala Thr Val Ile Asn Ala Val Ala Met Gln Glu Ala Leu Glu His  
 5 10 15

atc ggc tta gac aca agg gtg cag agc gcg att gaa atc aaa gag att 331  
 Ile Gly Leu Asp Thr Arg Val Gln Ser Ala Ile Glu Ile Lys Glu Ile  
 20 25 30 35

tgt gaa agt tac att tac aga aaa gcg atc agg cat tta gaa aag ggt 379  
 Cys Glu Ser Tyr Ile Tyr Arg Lys Ala Ile Arg His Leu Glu Lys Gly  
 40 45 50

agg gtg gtg att ttt ggc gca ggc acg gga aac ccg ttt ttc act acg 427  
 Arg Val Val Ile Phe Gly Ala Gly Thr Gly Asn Pro Phe Phe Thr Thr  
 55 60 65

gat acg gct gcc act tta aga gcg att gaa att gga tcg gat tta atc 475  
 Asp Thr Ala Ala Thr Leu Arg Ala Ile Glu Ile Gly Ser Asp Leu Ile  
 70 75 80

att aaa gcg act aaa gtg gat ggc att tac gac aaa gat cct aac aag 523  
 Ile Lys Ala Thr Lys Val Asp Gly Ile Tyr Asp Lys Asp Pro Asn Lys  
 85 90 95

ttt aaa gac gct aaa aaa tta gac act tta agc tat aac gat gcc ttg 571  
 Phe Lys Asp Ala Lys Lys Leu Asp Thr Leu Ser Tyr Asn Asp Ala Leu  
 100 105 110 115

ata ggg gat att gaa gtg atg gac gat acc gct att tct tta gct aaa 619  
 Ile Gly Asp Ile Glu Val Met Asp Asp Thr Ala Ile Ser Leu Ala Lys  
 120 125 130

gac aat aag ctc ccc att gtg gtg tgt aac atg ttc aaa aaa ggg aat 667  
 Asp Asn Lys Leu Pro Ile Val Val Cys Asn Met Phe Lys Lys Gly Asn  
 135 140 145

tta ttg caa gtg atc aag cac caa caa ggc gta ttt tct atg gta aaa 715  
 Leu Leu Gln Val Ile Lys His Gln Gln Gly Val Phe Ser Met Val Lys  
 150 155 160

taagcccttt aacattggat agaactcaaa ataaaaggat cagtttgaaa aaagag 771

<210> 276

<211> 163

<212> PRT

<213> Helicobacter pylori

<400> 276

Met	Gly	Met	Leu	Ala	Thr	Val	Ile	Asn	Ala	Val	Ala	Met	Gln	Glu	Ala
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Leu	Glu	His	Ile	Gly	Leu	Asp	Thr	Arg	Val	Gln	Ser	Ala	Ile	Glu	Ile
			20					25					30		
Lys	Glu	Ile	Cys	Glu	Ser	Tyr	Ile	Tyr	Arg	Lys	Ala	Ile	Arg	His	Leu
		35					40					45			
Glu	Lys	Gly	Arg	Val	Val	Ile	Phe	Gly	Ala	Gly	Thr	Gly	Asn	Pro	Phe
	50					55					60				
Phe	Thr	Thr	Asp	Thr	Ala	Ala	Thr	Leu	Arg	Ala	Ile	Glu	Ile	Gly	Ser
65					70					75					80
Asp	Leu	Ile	Ile	Lys	Ala	Thr	Lys	Val	Asp	Gly	Ile	Tyr	Asp	Lys	Asp
			85						90					95	
Pro	Asn	Lys	Phe	Lys	Asp	Ala	Lys	Lys	Leu	Asp	Thr	Leu	Ser	Tyr	Asn
			100					105					110		
Asp	Ala	Leu	Ile	Gly	Asp	Ile	Glu	Val	Met	Asp	Asp	Thr	Ala	Ile	Ser
		115					120					125			
Leu	Ala	Lys	Asp	Asn	Lys	Leu	Pro	Ile	Val	Val	Cys	Asn	Met	Phe	Lys
	130					135					140				
Lys	Gly	Asn	Leu	Leu	Gln	Val	Ile	Lys	His	Gln	Gln	Gly	Val	Phe	Ser
145					150					155					160
Met	Val	Lys													

<210> 277  
 <211> 659  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (56)...(607)

<400> 277	
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	Met
	1
aga gct ttt tta aag att tta atg gtt ttg att ttt atg agc gtt gct	106
Arg Ala Phe Leu Lys Ile Leu Met Val Leu Ile Phe Met Ser Val Ala	
	5 10 15
tat gct aaa aat cct tca acg ctt tct aaa gaa gaa gag gtt ttg cag	154
Tyr Ala Lys Asn Pro Ser Thr Leu Ser Lys Glu Glu Glu Val Leu Gln	
	20 25 30
cat ttg caa agt ttt agc gcg cat ttc aag cag gtt tta aaa aat gaa	202
His Leu Gln Ser Phe Ser Ala His Phe Lys Gln Val Leu Lys Asn Glu	
	35 40 45
aaa cct tta gtt tat tac ggg gtt tta aag gct aaa gcc cct aat tgg	250
Lys Pro Leu Val Tyr Tyr Gly Val Leu Lys Ala Lys Ala Pro Asn Trp	
	50 55 60 65
gct tta tgg gtt tat gaa aag cct tta aaa aaa gaa att tac atg aac	298

Ala	Leu	Trp	Val	Tyr	Glu	Lys	Pro	Leu	Lys	Lys	Glu	Ile	Tyr	Met	Asn		
				70					75					80			
gat	aaa	gaa	gtg	gta	att	tat	gag	cct	aat	ttg	ttt	caa	gcg	acc	atc	346	
Asp	Lys	Glu	Val	Val	Ile	Tyr	Glu	Pro	Asn	Leu	Phe	Gln	Ala	Thr	Ile		
			85					90				95					
acg	ccc	tta	aaa	gac	aag	acg	gat	ttt	ttc	acc	att	ctc	aag	cgt	tta	394	
Thr	Pro	Leu	Lys	Asp	Lys	Thr	Asp	Phe	Phe	Thr	Ile	Leu	Lys	Arg	Leu		
		100					105					110					
aaa	aag	caa	gat	gac	gga	tct	ttt	aaa	acg	act	atc	aac	aaa	acc	act	442	
Lys	Lys	Gln	Asp	Asp	Gly	Ser	Phe	Lys	Thr	Thr	Ile	Asn	Lys	Thr	Thr		
	115					120					125						
tat	cgt	ttg	gtt	ttt	aaa	gac	ggc	aag	cct	ttt	tca	ttg	gaa	ttt	aaa	490	
Tyr	Arg	Leu	Val	Phe	Lys	Asp	Gly	Lys	Pro	Phe	Ser	Leu	Glu	Phe	Lys		
130					135				140						145		
gat	gga	atg	aac	aat	ctt	gta	acg	atc	act	ttt	tct	caa	gca	gaa	atc	538	
Asp	Gly	Met	Asn	Asn	Leu	Val	Thr	Ile	Thr	Phe	Ser	Gln	Ala	Glu	Ile		
				150				155				160					
aac	ccc	acc	att	gct	aat	gaa	atc	ttt	ggt	ttt	aag	cct	aaa	gat	gaa	586	
Asn	Pro	Thr	Ile	Ala	Asn	Glu	Ile	Phe	Val	Phe	Lys	Pro	Lys	Asp	Glu		
			165				170					175					
aac	att	gat	att	gtg	cgc	caa	tgattttttaa	tgatttcattg	catcttggtta							637	
Asn	Ile	Asp	Ile	Val	Arg	Gln											
			180														
gcaaaaagtta	gctaaaatag	ac														659	
<210>	278																
<211>	184																
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			20					25					30				
Gln	His	Leu	Gln	Ser	Phe	Ser	Ala	His	Phe	Lys	Gln	Val	Leu	Lys	Asn		
	35					40					45						
Glu	Lys	Pro	Leu	Val	Tyr	Tyr	Gly	Val	Leu	Lys	Ala	Lys	Ala	Pro	Asn		
	50				55					60							
Trp	Ala	Leu	Trp	Val	Tyr	Glu	Lys	Pro	Leu	Lys	Glu	Ile	Tyr	Met			
65				70				75					80				
Asn	Asp	Lys	Glu	Val	Ile	Tyr	Glu	Pro	Asn	Leu	Phe	Gln	Ala	Thr			
			85				90					95					
Ile	Thr	Pro	Leu	Lys	Asp	Lys	Thr	Asp	Phe	Phe	Thr	Ile	Leu	Lys	Arg		
		100					105					110					
Leu	Lys	Lys	Gln	Asp	Asp	Gly	Ser	Phe	Lys	Thr	Thr	Ile	Asn	Lys	Thr		
	115						120					125					



Thr Tyr Arg Leu Val Phe Lys Asp Gly Lys Pro Phe Ser Leu Glu Phe  
 130 135 140  
 Lys Asp Gly Met Asn Asn Leu Val Thr Ile Thr Phe Ser Gln Ala Glu  
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 Ile Asn Pro Thr Ile Ala Asn Glu Ile Phe Val Phe Lys Pro Lys Asp  
 165 170 175  
 Glu Asn Ile Asp Ile Val Arg Gln  
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 aacaaggcta tgaattttaa aaaatccaca aagaagaaga attaaaagac aattttaaag 180  
 agcagttaga aaagcttaat gatcattctt tcacgcctaa agaatgggac actctttatt 240  
 ctcaattcat cgctaataaa aacgatgact ataaggctaa aacgaaaaag atccaagaag 300  
 atccgatttt taatctcacg ctagagaacg ggaaaaccaa aaacattaaa atcattgata 360  
 agaaaaatat ccatagaaac gccttgcaag tgatccacca atacagcaat aaagggggga 420  
 agtatcaaaa ccgctatgat gtgagtatcc ttgtgaatgg cttgccttta gtgcatgtgg 480  
 aattgaaaaa aagaggcgtg gcgatcaggg aggcgttcaa ccagatcaag cgctataaaa 540  
 gggatagttt tagcgctgaa gacgggcttt ttgattttgt gcagattttt gtcatcagta 600  
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 ataaagccga tacttttgaa ttcacgaatt attgggcgga tagcaagaat cacaattattg 720  
 aggattha atg gat ttt gct aag gcg ttt ttt gca aag cgc agc ctt ttg 770  
 Met Asp Phe Ala Lys Ala Phe Phe Ala Lys Arg Ser Leu Leu  
 1 5 10  
 aac gtt tta acg tgc tat tgc gtt ttc aca agc gaa gag gtt tta ttg 818  
 Asn Val Leu Thr Cys Tyr Cys Val Phe Thr Ser Glu Glu Val Leu Leu  
 15 20 25 30  
 gtg atg cgg cct tat caa atc gtg gcg gcc gaa agg att ttg gaa aag 866  
 Val Met Arg Pro Tyr Gln Ile Val Ala Ala Glu Arg Ile Leu Glu Lys  
 35 40 45  
 atc aaa acc gcg caa aat agt aaa acg aaa aat caa agc aaa ggc tat 914  
 Ile Lys Thr Ala Gln Asn Ser Lys Thr Lys Asn Gln Ser Lys Gly Tyr  
 50 55 60  
 atc tgg cac acg aca ggg agc ggt aaa acc cta acg agc ttt aaa agc 962  
 Ile Trp His Thr Thr Gly Ser Gly Lys Thr Leu Thr Ser Phe Lys Ser  
 65 70 75  
 gca acg ttg gct aaa gaa tta gag agc gtt tca aaa gtc ttg ttc gtg 1010  
 Ala Thr Leu Ala Lys Glu Leu Glu Ser Val Ser Lys Val Leu Phe Val  
 80 85 90

gtg gac agg aag gat ttg gac tat caa acc atg aaa gaa tac gat aaa	1058
Val Asp Arg Lys Asp Leu Asp Tyr Gln Thr Met Lys Glu Tyr Asp Lys	
95 100 105 110	
ttc caa aaa gat tgc gct aat tcc aac aca agc act aag att tta aaa	1106
Phe Gln Lys Asp Cys Ala Asn Ser Asn Thr Ser Thr Lys Ile Leu Lys	
115 120 125	
gaa cag ctt gaa gat tct aac gct aaa atc att atc acc acg atc caa	1154
Glu Gln Leu Glu Asp Ser Asn Ala Lys Ile Ile Ile Thr Thr Ile Gln	
130 135 140	
aaa tta gac aaa ttc gtt aaa tcc cat aaa ggg cat gcg att ttt aat	1202
Lys Leu Asp Lys Phe Val Lys Ser His Lys Gly His Ala Ile Phe Asn	
145 150 155	
gaa gaa gtt gtg atg att ttt gat gaa tgc cac agg agt cag tta ggc	1250
Glu Glu Val Val Met Ile Phe Asp Glu Cys His Arg Ser Gln Leu Gly	
160 165 170	
tct atg cat caa gcc atc act aaa gcg ttt aaa aaa tac cac ctt ttt	1298
Ser Met His Gln Ala Ile Thr Lys Ala Phe Lys Lys Tyr His Leu Phe	
175 180 185 190	
ggc ttt act ggc acg ccc att ttt gca gct aat tgc gat aaa aac aac	1346
Gly Phe Thr Gly Thr Pro Ile Phe Ala Ala Asn Cys Asp Lys Asn Asn	
195 200 205	
cct tta ggc acg aca gag caa aag ttt ggg aaa tgc ctc cac caa tac	1394
Pro Leu Gly Thr Thr Glu Gln Lys Phe Gly Lys Cys Leu His Gln Tyr	
210 215 220	
acc att att gat gcg atc agg gat aaa aac gtt ttg ccc ttt aga gtg	1442
Thr Ile Ile Asp Ala Ile Arg Asp Lys Asn Val Leu Pro Phe Arg Val	
225 230 235	
gaa tac cac aac acc att aaa gct aaa gag gac att aag gat aat aag	1490
Glu Tyr His Asn Thr Ile Lys Ala Lys Glu Asp Ile Lys Asp Asn Lys	
240 245 250	
gtt aga gcg gtt gat gaa aaa aac gcc ctt ttg gat act agg agg atc	1538
Val Arg Ala Val Asp Glu Lys Asn Ala Leu Leu Asp Thr Arg Arg Ile	
255 260 265 270	
aaa gaa atc act aaa tgc att tta gag cgt ttc aat caa gcc act aaa	1586
Lys Glu Ile Thr Lys Cys Ile Leu Glu Arg Phe Asn Gln Ala Thr Lys	
275 280 285	
aat aaa aaa ttc aat tcc att ctg gca tgc tct agc ata gaa gcg ctg	1634
Asn Lys Lys Phe Asn Ser Ile Leu Ala Cys Ser Ser Ile Glu Ala Leu	
290 295 300	
aaa aaa tac tac caa gcc ttt aaa gaa gaa aaa cac gat ctt aaa atc	1682
Lys Lys Tyr Tyr Gln Ala Phe Lys Glu Glu Lys His Asp Leu Lys Ile	

305	310	315	
gct gcc att ttt agc tat Ala Ala Ile Phe Ser Tyr 320	agc gct aat gag gaa Ser Ala Asn Glu Glu 325	att gac acg cta gaa Ile Asp Thr Leu Glu 330	1730
gat gaa aac aat gaa agc Asp Glu Asn Asn Glu Ser 335	gct tgc cgg cta gac Ala Cys Arg Leu Asp 340	aaa agc tca agg gat Lys Ser Ser Arg Asp 345	1778
ttt tta gag ggc gcg att Phe Leu Glu Gly Ala Ile 355	gcg gat tat aat ggg Ala Asp Tyr Asn Gly 360	atg ttt ggc gtt tct Met Phe Gly Val Ser 365	1826
ttt gac act tcg gat caa Phe Asp Thr Ser Asp 370	aaa ttc caa agt tat Lys Phe Gln Ser Tyr 375	tac aag gat ctt tct Tyr Lys Asp Leu Ser 380	1874
caa aaa atg aaa gag cgt Gln Lys Met Lys Glu Arg 385	aaa atc gat ctt tta Lys Ile Asp Leu Leu 390	atg gtg gtg aac atg Met Val Val Asn Met 395	1922
ttt ttg acc ggg ttt gac Phe Leu Thr Gly Phe Asp 400	gct aca agg ctc aac Ala Thr Arg Leu Asn 405	acc ctt tgg gtg gat Thr Leu Trp Val Asp 410	1970
aaa aat ctc aaa tac cat Lys Asn Leu Lys Tyr His 415	ggg cta att caa gct Gly Leu Ile Gln Ala 420	ttt tca cgc gca aac Phe Ser Arg Ala Asn 425	2018
cgc att tta gat agc gtt Arg Ile Leu Asp Ser 435	aaa acg cat ggg aat Lys Thr His Gly Asn 440	atc gtg tgt ttt agg Ile Val Cys Phe Arg 445	2066
gat tta gaa cag gat ttg Asp Leu Glu Gln Asp 450	aat gac gct ctc atg Asn Asp Ala Leu Met 455	ctt ttt ggc aac aag Leu Phe Gly Asn Lys 460	2114
gac gct caa tct att gcg Asp Ala Gln Ser Ile 465	ctg tta aga aaa tat Ala Leu Arg Lys Tyr 470	gaa gat tat ttg aaa Glu Asp Tyr Leu Lys 475	2162
ggc tac acg gat aac aac Gly Tyr Thr Asp Asn 480	aaa gaa tac gag ggc Lys Glu Tyr Glu Gly 485	tat gag ggt ttg att Tyr Glu Gly Leu Ile 490	2210
aaa agg ctt tta acc gaa Lys Arg Leu Leu Thr 495	ttc cca tta aaa gag Phe Pro Leu Lys Glu 500	cca atc gtt tca gaa Pro Ile Val Ser Glu 505	2258
agc cag aaa aag gat ttt Ser Gln Lys Lys Asp 515	att aag ctt ttt ggc Ile Lys Leu Phe Gly 520	aag att ttg aaa tta Lys Ile Leu Lys Leu 525	2306
gaa aat att tta aac agc gaa aat ttc aaa aaa 530	gac gat tac atc 535		2354

Glu Asn Ile Leu Asn Ser Phe Glu Asn Phe Lys Lys Asp Asp Tyr Ile	
530 535 540	
aat ccc agg gat ttt caa gac tat caa agc aaa tac ctt gat ttt tac	2402
Asn Pro Arg Asp Phe Gln Asp Tyr Gln Ser Lys Tyr Leu Asp Phe Tyr	
545 550 555	
gat gca atg aga tca gaa aaa ggg aag gat aaa gaa gag att aat gat	2450
Asp Ala Met Arg Ser Glu Lys Gly Lys Asp Lys Glu Glu Ile Asn Asp	
560 565 570	
gat ttg att ttt gaa att gaa ctc atc aaa caa gtg gaa gtc aat att	2498
Asp Leu Ile Phe Glu Ile Glu Leu Ile Lys Gln Val Glu Val Asn Ile	
575 580 585 590	
gac tat att ttg aat ttg att gaa gag ttc gct aaa gag cat ggg gtg	2546
Asp Tyr Ile Leu Asn Leu Ile Glu Glu Phe Ala Lys Glu His Gly Val	
595 600 605	
gaa atc caa ggc gtt aaa acc aaa ata gag cca atc atc aac tcc agc	2594
Glu Ile Gln Gly Val Lys Thr Lys Ile Glu Pro Ile Ile Asn Ser Ser	
610 615 620	
ata gag tta agg aat aaa aaa gat ttg atc atg gat ttc att gac aaa	2642
Ile Glu Leu Arg Asn Lys Lys Asp Leu Ile Met Asp Phe Ile Asp Lys	
625 630 635	
tac aac aaa gac caa gaa gtc cat gcg cat ttt caa gat tat atc cac	2690
Tyr Asn Lys Asp Gln Glu Val His Ala His Phe Gln Asp Tyr Ile His	
640 645 650	
caa aaa aga gaa gag gaa ttc caa aat atc ata gaa gaa aac cgc ttg	2738
Gln Lys Arg Glu Glu Phe Gln Asn Ile Ile Glu Glu Asn Arg Leu	
655 660 665 670	
aat gaa gaa aaa gcc tat tcg ttc atg cag cat gcc ttt aaa ggg ggc	2786
Asn Glu Glu Lys Ala Tyr Ser Phe Met Gln His Ala Phe Lys Gly Gly	
675 680 685	
gaa atc agt ttt agt ggg acg gaa ttc cct aaa atc att gaa gaa aaa	2834
Glu Ile Ser Phe Ser Gly Thr Glu Phe Pro Lys Ile Ile Glu Glu Lys	
690 695 700	
ccc tcc atg ttt ggt aaa aat tcg cgc tat caa gag gtg aaa gaa aaa	2882
Pro Ser Met Phe Gly Lys Asn Ser Arg Tyr Gln Glu Val Lys Glu Lys	
705 710 715	
gtc gct gca agc ctt tct cgt ttt ttc cac cgc ttt tgt gat ctc act	2930
Val Ala Ala Ser Leu Ser Arg Phe Phe His Arg Phe Cys Asp Leu Thr	
720 725 730	
agc gct ata ttt aag aaa aat gag gtt aaa aaa gat gag gtt aat gaa	2978
Ser Ala Ile Phe Lys Lys Asn Glu Val Lys Lys Asp Glu Val Asn Glu	
735 740 745 750	

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Lys

gatt 3035

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<213> Helicobacter pylori

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Arg Pro Tyr Gln Ile Val Ala Ala Glu Arg Ile Leu Glu Lys Ile Lys  
35 40 45  
Thr Ala Gln Asn Ser Lys Thr Lys Asn Gln Ser Lys Gly Tyr Ile Trp  
50 55 60  
His Thr Thr Gly Ser Gly Lys Thr Leu Thr Ser Phe Lys Ser Ala Thr  
65 70 75 80  
Leu Ala Lys Glu Leu Glu Ser Val Ser Lys Val Leu Phe Val Val Asp  
85 90 95  
Arg Lys Asp Leu Asp Tyr Gln Thr Met Lys Glu Tyr Asp Lys Phe Gln  
100 105 110  
Lys Asp Cys Ala Asn Ser Asn Thr Ser Thr Lys Ile Leu Lys Glu Gln  
115 120 125  
Leu Glu Asp Ser Asn Ala Lys Ile Ile Ile Thr Thr Ile Gln Lys Leu  
130 135 140  
Asp Lys Phe Val Lys Ser His Lys Gly His Ala Ile Phe Asn Glu Glu  
145 150 155 160  
Val Val Met Ile Phe Asp Glu Cys His Arg Ser Gln Leu Gly Ser Met  
165 170 175  
His Gln Ala Ile Thr Lys Ala Phe Lys Lys Tyr His Leu Phe Gly Phe  
180 185 190  
Thr Gly Thr Pro Ile Phe Ala Ala Asn Cys Asp Lys Asn Asn Pro Leu  
195 200 205  
Gly Thr Thr Glu Gln Lys Phe Gly Lys Cys Leu His Gln Tyr Thr Ile  
210 215 220  
Ile Asp Ala Ile Arg Asp Lys Asn Val Leu Pro Phe Arg Val Glu Tyr  
225 230 235 240  
His Asn Thr Ile Lys Ala Lys Glu Asp Ile Lys Asp Asn Lys Val Arg  
245 250 255  
Ala Val Asp Glu Lys Asn Ala Leu Leu Asp Thr Arg Arg Ile Lys Glu  
260 265 270  
Ile Thr Lys Cys Ile Leu Glu Arg Phe Asn Gln Ala Thr Lys Asn Lys  
275 280 285  
Lys Phe Asn Ser Ile Leu Ala Cys Ser Ser Ile Glu Ala Leu Lys Lys  
290 295 300  
Tyr Tyr Gln Ala Phe Lys Glu Glu Lys His Asp Leu Lys Ile Ala Ala  
305 310 315 320  
Ile Phe Ser Tyr Ser Ala Asn Glu Glu Ile Asp Thr Leu Glu Asp Glu  
325 330 335  
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<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (68)...(799)

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      Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Val Met Ala Ile
        1             5             10

ggt ggt atg agt tta aac gct aaa gat ccg aat gtg ttg cgt aag att 157
Val Val Met Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile
  15             20             25             30

ggt ttt gag aaa tgt ctg cct aat tat gag aaa aat cag aat cct tcg 205
Val Phe Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser
             35             40             45

cca tgc ata gaa gtc aaa ccc gat gcc ggc tat gtg gtt tta aaa gat 253
Pro Cys Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp
             50             55             60

att aac ggc ccg ttg caa tat ttg ttg atg cca aca act cac att agc 301
Ile Asn Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser
             65             70             75

ggt att gaa agc cct ttg tta ctt gat cct tct acg cct aac ttt ttt 349
Gly Ile Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe
  80             85             90

tat tta tcc tgg caa gcg cgt gat ttt atg agt aaa aaa tac ggc caa 397
Tyr Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln
  95             100             105             110

ccc att cct gat tat gcg att tct ttg acg att aac tct agc aaa ggg 445
Pro Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly
             115             120             125

cga tcg caa aac cat ttt cat atc cat atc tct tgc att agt ctt gaa 493
Arg Ser Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu
             130             135             140

gca cgc aaa cag ctg gat aat aac cta aaa aaa atc aac agc cgt tgg 541
Ala Arg Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp
             145             150             155

tcg cca tta ccg ggc ggt ttg aat ggg cat aaa tac ttg gcg cgt cgg 589
Ser Pro Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg
  160             165             170

gta aca gag agc gag tta gtg caa aaa agc ccg ttt gtc atg ctt aat 637
Val Thr Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn
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175	180	185	190	
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Lys Glu Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala				
	195	200	205	
gtg gtg caa caa agc gat aac tcc ttt gtc tta tta gcg aca caa ttt				733
Val Val Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe				
	210	215	220	
aac cca ttg act tta aat cgc gct tca gcc gaa gag att caa gat cat				781
Asn Pro Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His				
	225	230	235	
gaa tgc gcg att ttg cac taaagcgagt tagattctta agcttgagcg				829
Glu Cys Ala Ile Leu His				
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ataaccttta aaaagcgta t				850
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Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser Pro Cys				
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Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp Ile Asn				
	50	55	60	
Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser Gly Ile				
	65	70	75	80
Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe Tyr Leu				
	85	90	95	
Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln Pro Ile				
	100	105	110	
Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly Arg Ser				
	115	120	125	
Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu Ala Arg				
	130	135	140	
Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp Ser Pro				
	145	150	155	160
Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg Val Thr				
	165	170	175	
Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn Lys Glu				
	180	185	190	
Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala Val Val				
	195	200	205	
Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe Asn Pro				
	210	215	220	
Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu Cys				





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Lys Glu Ser Val Arg Asn Phe Tyr Ala Phe Ile Lys His Glu Met Pro	
150 155 160	
aag aga cag aag gct tta gag ggt aaa gaa aat tta cct aag cgt gag	587
Lys Arg Gln Lys Ala Leu Glu Gly Lys Glu Asn Leu Pro Lys Arg Glu	
165 170 175	
agt ttg ccc tgg ttt gca acc att tca aaa gag agc atg ttt gtg tcc	635
Ser Leu Pro Trp Phe Ala Thr Ile Ser Lys Glu Ser Met Phe Val Ser	
180 185 190	
tta tgc cat gcg tgc ggg att aaa agc gct gaa gtg caa ggc ttg aaa	683
Leu Cys His Ala Cys Gly Ile Lys Ser Ala Glu Val Gln Gly Leu Lys	
195 200 205	
ctg ggt caa aac agc gtg gtg aaa aac gct cct aga gtg gaa gtg tat	731
Leu Gly Gln Asn Ser Val Val Lys Asn Ala Pro Arg Val Glu Val Tyr	
210 215 220 225	
ttg aaa gat tca ttt cta gcg ttt gat ttt caa aat aat cac aag gaa	779
Leu Lys Asp Ser Phe Leu Ala Phe Asp Phe Gln Asn Asn His Lys Glu	
230 235 240	
gtt ttt atc ccg ttg aat cgt cat aaa gac atg cag tta gat tct gcc	827
Val Phe Ile Pro Leu Asn Arg His Lys Asp Met Gln Leu Asp Ser Ala	
245 250 255	
tta ttg gcg act ttt ggc gat gct ttt gcc ctt gtg gat ggt agg gat	875
Leu Leu Ala Thr Phe Gly Asp Ala Phe Ala Leu Val Asp Gly Arg Asp	
260 265 270	
tta ggc aat tac gag agc aaa ctt ttt gaa aaa aga gtg tcc tat acg	923
Leu Gly Asn Tyr Glu Ser Lys Leu Phe Glu Lys Arg Val Ser Tyr Thr	
275 280 285	
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Ile Val	
290	
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Val Ala Lys Tyr Lys Ile Glu Ala Gln Tyr Ser Ile Asp Phe Asp Ser	
35 40 45	
Ala Glu His Thr Ser Leu Phe Ile Pro Met Pro Ser Val Val Ala Ser	



gct tgg gtt ttt gaa gac gct aaa gcc ccc tac gaa gaa atg ggc gtg 255  
Ala Trp Val Phe Glu Asp Ala Lys Ala Pro Tyr Glu Glu Met Gly Val  
45 50 55  
  
gcg tat atc cct gtt aat aat aaa tat tta ggg att gag caa gcg acc 303  
Ala Tyr Ile Pro Val Asn Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr  
60 65 70  
  
tta aac gct aaa ttg agt ctg atc gtg gtt ttt cat gaa atc atg atg 351  
Leu Asn Ala Lys Leu Ser Leu Ile Val Val Phe His Glu Ile Met Met  
75 80 85 90  
  
aag tat aaa aaa cgc ttc atg gag caa ttc cat gag tcc gag cag acg 399  
Lys Tyr Lys Lys Arg Phe Met Glu Gln Phe His Glu Ser Glu Gln Thr  
95 100 105  
  
act acg aat atc agt tac gct atc tat aat tat cta gcg act aag atc 447  
Thr Thr Asn Ile Ser Tyr Ala Ile Tyr Asn Tyr Leu Ala Thr Lys Ile  
110 115 120  
  
cag gta tcc aac acc tac acg aat tta aaa tcg gag gtg gcg gtg gtg 495  
Gln Val Ser Asn Thr Tyr Thr Asn Leu Lys Ser Glu Val Ala Val Val  
125 130 135  
  
aaa atc aag cta gtg ggt tgt cag att gag caa atc aaa agg tat tta 543  
Lys Ile Lys Leu Val Gly Cys Gln Ile Glu Gln Ile Lys Arg Tyr Leu  
140 145 150  
  
aaa gcg agc gtt gaa aac ctt aac gat aat gaa atc gct tac atc gct 591  
Lys Ala Ser Val Glu Asn Leu Asn Asp Asn Glu Ile Ala Tyr Ile Ala  
155 160 165 170  
  
aag gtc gct caa aaa gaa ttt ggt agc gtt tgt gcg tta agg 633  
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175 180  
  
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<212> PRT  
<213> Helicobacter pylori

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Gly Met Lys Ser Glu Leu Ser Asp Ala Pro Ala Trp Val Phe Glu Asp  
35 40 45  
Ala Lys Ala Pro Tyr Glu Glu Met Gly Val Ala Tyr Ile Pro Val Asn  
50 55 60  
Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr Leu Asn Ala Lys Leu Ser  
65 70 75 80

Leu	Ile	Val	Val	Phe	His	Glu	Ile	Met	Met	Lys	Tyr	Lys	Lys	Arg	Phe	
				85					90					95		
Met	Glu	Gln	Phe	His	Glu	Ser	Glu	Gln	Thr	Thr	Thr	Asn	Ile	Ser	Tyr	
			100					105					110			
Ala	Ile	Tyr	Asn	Tyr	Leu	Ala	Thr	Lys	Ile	Gln	Val	Ser	Asn	Thr	Tyr	
		115					120					125				
Thr	Asn	Leu	Lys	Ser	Glu	Val	Ala	Val	Val	Lys	Ile	Lys	Leu	Val	Gly	
	130					135					140					
Cys	Gln	Ile	Glu	Gln	Ile	Lys	Arg	Tyr	Leu	Lys	Ala	Ser	Val	Glu	Asn	
145					150					155					160	
Leu	Asn	Asp	Asn	Glu	Ile	Ala	Tyr	Ile	Ala	Lys	Val	Ala	Gln	Lys	Glu	
			165						170					175		
Phe	Gly	Ser	Val	Cys	Ala	Leu	Arg									
			180													

<210> 287  
 <211> 310  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (112)...(252)

<400> 287  
 atgcctgccca tttcatagcc taaatcttct ttagagccga attgataagc ggcttttaag 60  
 acttcttttt gcttagcggt aaaatcttta atattgtcgc aattgggtcat c atg act 117  
 Met Thr  
 1

tta gta acg ggc gat ttg ggc ttg ttt tta acc cct tta gcg ggc tta 165  
 Leu Val Thr Gly Asp Leu Gly Leu Phe Leu Thr Pro Leu Ala Gly Leu  
 5 10 15

ggc tct gtt tta gtg ggg ctt tct gtt gcg gct aaa ctt aaa gat gca 213  
 Gly Ser Val Leu Val Gly Leu Ser Val Ala Ala Lys Leu Lys Asp Ala  
 20 25 30

ctt aag gct gtg cct agc cat aag gct tta aag atg gtg tgagtgagtg 262  
 Leu Lys Ala Val Pro Ser His Lys Ala Leu Lys Met Val  
 35 40 45

gggttaaag tttcaaaacg cctacctttt gtattaagaa ataaacta 310

<210> 288  
 <211> 47  
 <212> PRT  
 <213> Helicobacter pylori

<400> 288  
 Met Thr Leu Val Thr Gly Asp Leu Gly Leu Phe Leu Thr Pro Leu Ala  
 1 5 10 15  
 Gly Leu Gly Ser Val Leu Val Gly Leu Ser Val Ala Ala Lys Leu Lys  
 20 25 30

Asp Ala Leu Lys Ala Val Pro Ser His Lys Ala Leu Lys Met Val  
35 40 45

<210> 289  
<211> 631  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (145)...(579)

<221> misc\_feature  
<222> 48  
<223> n = A,T,C or G

<400> 289  
gcgttcaata gaatgcttta gtttaggaagc tccttgcttt agcaaggngt gggtttcactg 60  
aaagagagta agaaatttga agaaaggggt tatctttttt tagatgaatt tgtgcggttt 120  
ggtaaattgc cttttttatt agaa atg cca gca tta agt agg agc tat ggt 171  
Met Pro Ala Leu Ser Arg Ser Tyr Gly  
1 5

gtg gtt tta att ttt atc acg caa tcc aac gct ctt att gaa aaa tat 219  
Val Val Leu Ile Phe Ile Thr Gln Ser Asn Ala Leu Ile Glu Lys Tyr  
10 15 20 25

tac ggc aga gaa gat gca aga att gtt aat agc acc gtg gct tac aaa 267  
Tyr Gly Arg Glu Asp Ala Arg Ile Val Asn Ser Thr Val Ala Tyr Lys  
30 35 40

ata att ttc aaa atg gat gat tta gaa tac gct aaa cag gtg agc gaa 315  
Ile Ile Phe Lys Met Asp Asp Leu Glu Tyr Ala Lys Gln Val Ser Glu  
45 50 55

gaa gtc ggt aag atg act aga aaa aca cga agc cac tct aca gaa aaa 363  
Glu Val Gly Lys Met Thr Arg Lys Thr Arg Ser His Ser Thr Glu Lys  
60 65 70

gga caa ctc att acc gga ggg act tct agt ata ggt aaa gag gcg tgg 411  
Gly Gln Leu Ile Thr Gly Gly Thr Ser Ser Ile Gly Lys Glu Ala Trp  
75 80 85

gac tta ttg agc gcg caa gat att atg aat att gat aaa gat gaa gtg 459  
Asp Leu Leu Ser Ala Gln Asp Ile Met Asn Ile Asp Lys Asp Glu Val  
90 95 100 105

atc gtt tta gta agc ggt cat aag gct aaa ccc tta aaa tta aaa gcg 507  
Ile Val Leu Val Ser Gly His Lys Ala Lys Pro Leu Lys Leu Lys Ala  
110 115 120

aat tat tat ttc aaa aac aaa gaa tta ctc tct cgt att aac tgg gaa 555  
Asn Tyr Tyr Phe Lys Asn Lys Glu Leu Leu Ser Arg Ile Asn Trp Glu  
125 130 135

gtc aag ccc aat gaa gaa gtg ttt tgatggatta aaaaagtttg catgagtatt 609  
 Val Lys Pro Asn Glu Glu Val Phe  
 140 145

ttttaattgc ttttttaaaa at 631

<210> 290  
 <211> 145  
 <212> PRT  
 <213> Helicobacter pylori

<400> 290  
 Met Pro Ala Leu Ser Arg Ser Tyr Gly Val Val Leu Ile Phe Ile Thr  
 1 5 10 15  
 Gln Ser Asn Ala Leu Ile Glu Lys Tyr Tyr Gly Arg Glu Asp Ala Arg  
 20 25 30  
 Ile Val Asn Ser Thr Val Ala Tyr Lys Ile Ile Phe Lys Met Asp Asp  
 35 40 45  
 Leu Glu Tyr Ala Lys Gln Val Ser Glu Glu Val Gly Lys Met Thr Arg  
 50 55 60  
 Lys Thr Arg Ser His Ser Thr Glu Lys Gly Gln Leu Ile Thr Gly Gly  
 65 70 75 80  
 Thr Ser Ser Ile Gly Lys Glu Ala Trp Asp Leu Leu Ser Ala Gln Asp  
 85 90 95  
 Ile Met Asn Ile Asp Lys Asp Glu Val Ile Val Leu Val Ser Gly His  
 100 105 110  
 Lys Ala Lys Pro Leu Lys Leu Lys Ala Asn Tyr Tyr Phe Lys Asn Lys  
 115 120 125  
 Glu Leu Leu Ser Arg Ile Asn Trp Glu Val Lys Pro Asn Glu Glu Val  
 130 135 140  
 Phe  
 145

<210> 291  
 <211> 290  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (106)...(237)

<400> 291  
 taagggctta cgcataaaat cgcacccgcg ccgatttttt gagcgaactt tgctaaagaa 60  
 agggactcgc tcgtggcggtt actgcccacg ccggctaaca ctttc atg cgc gaa ttt 117  
 Met Arg Glu Phe  
 1

gag ggc gtt tta gtg ttt ttg caa gtt tct atg gcg att tca atg caa 165  
 Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala Ile Ser Met Gln  
 5 10 15 20

cgc atg tgc tct ttg tgg gtg agc gtg gcg gat tct cct gtc gtg cca 213

Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser Pro Val Val Pro  
25 30 35

aca ggc acg cat gcg tcc atg ccc tgaaaaattt ggcgcttgat caaggtttca 267  
Thr Gly Thr His Ala Ser Met Pro  
40

taagcggcct catcaacgct caa 290

<210> 292  
<211> 44  
<212> PRT  
<213> Helicobacter pylori

<400> 292  
Met Arg Glu Phe Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala  
1 5 10 15  
Ile Ser Met Gln Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser  
20 25 30  
Pro Val Val Pro Thr Gly Thr His Ala Ser Met Pro  
35 40

<210> 293  
<211> 421  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (58)...(369)

<400> 293  
aaagaagggtt tgaaaagcctt ttttaaaagg cttttgaagt atttggggta ggcttga atg 60  
Met  
1

aaa gtg caa aat ttt atc cat ttt tct gtt gtg gta ggg ttt ttt ttg 108  
Lys Val Gln Asn Phe Ile His Phe Ser Val Val Val Gly Phe Phe Leu  
5 10 15

ggg tta gtg ttt tcg gtg ttg aaa ttc aat gag cca gag agc att tta 156  
Gly Leu Val Phe Ser Val Leu Lys Phe Asn Glu Pro Glu Ser Ile Leu  
20 25 30

tta tgg acg gtg tta tcc acg ctt ggg ggg tac ttg att gcg ttg ttg 204  
Leu Trp Thr Val Leu Ser Thr Leu Gly Gly Tyr Leu Ile Ala Leu Leu  
35 40 45

ttt gcg tct att ttt atc gct tgc acg gat ttg gat att tgt ctt ttt 252  
Phe Ala Ser Ile Phe Ile Ala Cys Thr Asp Leu Asp Ile Cys Leu Phe  
50 55 60 65

gac aaa aaa ggc act gaa gag agt ttg ctt cgt ttc aac cat gag ttt 300  
Asp Lys Lys Gly Thr Glu Glu Ser Leu Leu Arg Phe Asn His Glu Phe



70	75	80	
aaa aac aga gaa aaa gaa gtg gct agt att tta gaa tac att aga agt			348
Lys Asn Arg Glu Lys Glu Val Ala Ser Ile Leu Glu Tyr Ile Arg Ser			
85	90	95	
tat gat ttt gat gat gga aaa tagaatgccc aaaggaattc aaaaaactga			399
Tyr Asp Phe Asp Asp Gly Lys			
100			
aacaagcgaa aaaaatatag aa			421
<210> 294			
<211> 104			
<212> PRT			
<213> Helicobacter pylori			
<400> 294			
Met Lys Val Gln Asn Phe Ile His Phe Ser Val Val Val Gly Phe Phe			
1	5	10	15
Leu Gly Leu Val Phe Ser Val Leu Lys Phe Asn Glu Pro Glu Ser Ile			
20	25	30	
Leu Leu Trp Thr Val Leu Ser Thr Leu Gly Gly Tyr Leu Ile Ala Leu			
35	40	45	
Leu Phe Ala Ser Ile Phe Ile Ala Cys Thr Asp Leu Asp Ile Cys Leu			
50	55	60	
Phe Asp Lys Lys Gly Thr Glu Glu Ser Leu Leu Arg Phe Asn His Glu			
65	70	75	80
Phe Lys Asn Arg Glu Lys Glu Val Ala Ser Ile Leu Glu Tyr Ile Arg			
85	90	95	
Ser Tyr Asp Phe Asp Asp Gly Lys			
100			
<210> 295			
<211> 670			
<212> DNA			
<213> Helicobacter pylori			
<220>			
<221> CDS			
<222> (51)...(617)			
<400> 295			
gttttagaaaa gcgtttgaac gctataaaaa atgcagagtg gctttaaggc atg aaa			56
		Met Lys	
		1	
aag att gca ttt ttt att ttt gtc att ttg ttt tcg gta ggg att tat			104
Lys Ile Ala Phe Phe Ile Phe Val Ile Leu Phe Ser Val Gly Ile Tyr			
5	10	15	
tta att tgg cat gtt tta ttg gaa aaa gcc cta gaa ttg aaa tta gca			152
Leu Ile Trp His Val Leu Leu Glu Lys Ala Leu Glu Leu Lys Leu Ala			
20	25	30	

acc tca gct aat gat ttg ctt tta aaa ttg ttg gca att ctt ggc gtt 200  
 Thr Ser Ala Asn Asp Leu Leu Leu Lys Leu Leu Ala Ile Leu Gly Val  
 35 40 45 50  
 ttt tca atg tta gtg ctt ttt caa ggc att att tct tcg tat aag aag 248  
 Phe Ser Met Leu Val Leu Phe Gln Gly Ile Ile Ser Ser Tyr Lys Lys  
 55 60 65  
 cgc caa ctc aaa cgc att tta caa aaa ata gac gcc atg aac ggc ttt 296  
 Arg Gln Leu Lys Arg Ile Leu Gln Lys Ile Asp Ala Met Asn Gly Phe  
 70 75 80  
 gaa ttt gaa gaa tat tcc aaa atc ttt ttc act tca aag ggt ttt gaa 344  
 Glu Phe Glu Glu Tyr Ser Lys Ile Phe Phe Thr Ser Lys Gly Phe Glu  
 85 90 95  
 gtg agc atc acg caa aaa agc ggc gat tat gga gcg gat ttg att ata 392  
 Val Ser Ile Thr Gln Lys Ser Gly Asp Tyr Gly Ala Asp Leu Ile Ile  
 100 105 110  
 gaa aaa gac ggc atc aag tgg gcg gtt caa gtc aaa cgc tac tcg cat 440  
 Glu Lys Asp Gly Ile Lys Trp Ala Val Gln Val Lys Arg Tyr Ser His  
 115 120 125 130  
 aaa gtt tcg ccc aaa gcc att caa gag gtg gtc tct tct aaa gct tat 488  
 Lys Val Ser Pro Lys Ala Ile Gln Glu Val Val Ser Ser Lys Ala Tyr  
 135 140 145  
 tac gct tgc gaa aaa gct tgc gtg atc acc aac agc tat ttc acg caa 536  
 Tyr Ala Cys Glu Lys Ala Cys Val Ile Thr Asn Ser Tyr Phe Thr Gln  
 150 155 160  
 gcc gct caa aaa ctg gct caa gct aac gaa gtg ctc ttg att gac aga 584  
 Ala Ala Gln Lys Leu Ala Gln Ala Asn Glu Val Leu Leu Ile Asp Arg  
 165 170 175  
 gac gaa tgg gtc agg ttt ttg aac gaa aag aga tgaaccgatc ccatcagatc 637  
 Asp Glu Trp Val Arg Phe Leu Asn Glu Lys Arg  
 180 185

gtttggttctc aagttctttt aaaattttgt cgt 670

<210> 296

<211> 189

<212> PRT

<213> *Helicobacter pylori*

<400> 296

Met Lys Lys Ile Ala Phe Phe Ile Phe Val Ile Leu Phe Ser Val Gly  
 1 5 10 15  
 Ile Tyr Leu Ile Trp His Val Leu Leu Glu Lys Ala Leu Glu Leu Lys  
 20 25 30  
 Leu Ala Thr Ser Ala Asn Asp Leu Leu Leu Lys Leu Leu Ala Ile Leu  
 35 40 45

Gly	Val	Phe	Ser	Met	Leu	Val	Leu	Phe	Gln	Gly	Ile	Ile	Ser	Ser	Tyr
50						55					60				
Lys	Lys	Arg	Gln	Leu	Lys	Arg	Ile	Leu	Gln	Lys	Ile	Asp	Ala	Met	Asn
65					70					75					80
Gly	Phe	Glu	Phe	Glu	Glu	Tyr	Ser	Lys	Ile	Phe	Phe	Thr	Ser	Lys	Gly
				85					90					95	
Phe	Glu	Val	Ser	Ile	Thr	Gln	Lys	Ser	Gly	Asp	Tyr	Gly	Ala	Asp	Leu
			100					105					110		
Ile	Ile	Glu	Lys	Asp	Gly	Ile	Lys	Trp	Ala	Val	Gln	Val	Lys	Arg	Tyr
		115					120					125			
Ser	His	Lys	Val	Ser	Pro	Lys	Ala	Ile	Gln	Glu	Val	Val	Ser	Ser	Lys
	130					135					140				
Ala	Tyr	Tyr	Ala	Cys	Glu	Lys	Ala	Cys	Val	Ile	Thr	Asn	Ser	Tyr	Phe
145					150					155					160
Thr	Gln	Ala	Ala	Gln	Lys	Leu	Ala	Gln	Ala	Asn	Glu	Val	Leu	Leu	Ile
				165				170						175	
Asp	Arg	Asp	Glu	Trp	Val	Arg	Phe	Leu	Asn	Glu	Lys	Arg			
			180					185							

<210> 297  
 <211> 600  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (125)...(538)

<400> 297  
 caaagagtgg gataaaatca cagaaatttg taagagagcg ctagctttta gataacaaaa 60  
 agatcatggc attttgtatt tgcttaataa cactataata aaatttttaa taaggagata 120  
 catc atg tta gaa aat gtc aaa aag tcc ttt ttt agg gtt ttg tgc ttg 169  
 Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu  
 1 5 10 15  
 ggt gcg ttg tgt tta ggg ggg cta atg gca gag caa gac cct aaa gag 217  
 Gly Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu  
 20 25 30  
 ctt gtg ggt ttg ggg gca aag agc tac aaa gag aaa gat ttc act caa 265  
 Leu Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln  
 35 40 45  
 gcg aag aaa tat ttt gag aaa gcg tgc gat ttg aaa gaa aat agc ggg 313  
 Ala Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly  
 50 55 60  
 tgt ttt aat tta ggg gtg ctt tat tat caa ggg caa ggg gtg gaa aag 361  
 Cys Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys  
 65 70 75  
 aac ttg aaa aaa gcc gcc tcc ttt tac gct aaa gct tgc gat ttg aat 409  
 Asn Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn  
 80 85 90 95

tac agc aat ggg tgt cat ttg cta ggg aat tta tat tac agc ggg caa 457  
Tyr Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln  
100 105 110

ggc gtg tcc caa aac acc aat aaa gcc cta caa tac tac tct aaa gcg 505  
Gly Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala  
115 120 125

tgc gat ttg aaa tac gct gaa ggg tgc gcg act taggggggat ttatcatgat 558  
Cys Asp Leu Lys Tyr Ala Glu Gly Cys Ala Thr  
130 135

ggtaaagtgg taactaggga ttttaaaaaa gcggtggaat at 600

<210> 298  
<211> 138  
<212> PRT  
<213> Helicobacter pylori

<400> 298  
Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu Gly  
1 5 10 15  
Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu Leu  
20 25 30  
Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln Ala  
35 40 45  
Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly Cys  
50 55 60  
Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys Asn  
65 70 75 80  
Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn Tyr  
85 90 95  
Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln Gly  
100 105 110  
Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala Cys  
115 120 125  
Asp Leu Lys Tyr Ala Glu Gly Cys Ala Thr  
130 135

<210> 299  
<211> 879  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (59)...(826)

<400> 299  
ttttaagatt ggtagccatt ggcattatgt ttgatcttat taaagcagag gagtaaca 58  
atg gga tac gca agc aaa tta gcc ttg aag att tgt ttg gca agt tta 106  
Met Gly Tyr Ala Ser Lys Leu Ala Leu Lys Ile Cys Leu Ala Ser Leu  
1 5 10 15

tgt tta ttt agc gct ctt ggt gca gaa cac ctt gaa caa aaa agg aac	154
Cys Leu Phe Ser Ala Leu Gly Ala Glu His Leu Glu Gln Lys Arg Asn	
20 25 30	
tat att tat aam ggg gag gaa gcc tat aat aat aag gaa tat gag cgg	202
Tyr Ile Tyr Xaa Gly Glu Glu Ala Tyr Asn Asn Lys Glu Tyr Glu Arg	
35 40 45	
gcg gct tct ttt tat aag agc gcg att aaa aat ggc gag ccg ctt gct	250
Ala Ala Ser Phe Tyr Lys Ser Ala Ile Lys Asn Gly Glu Pro Leu Ala	
50 55 60	
tat gtt ctt tta ggg atc atg tat gaa aat ggt agg ggt gtg cct aaa	298
Tyr Val Leu Leu Gly Ile Met Tyr Glu Asn Gly Arg Gly Val Pro Lys	
65 70 75 80	
gat gaa aag aaa gcg gct gaa tat ttt caa aaa gcg gtt gat aac gat	346
Asp Glu Lys Lys Ala Ala Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp	
85 90 95	
ata cct aga ggg tat aac aat tta ggc gtg atg tat aaa gag ggt aga	394
Ile Pro Arg Gly Tyr Asn Asn Leu Gly Val Met Tyr Lys Glu Gly Arg	
100 105 110	
ggt gtg cct aaa gat gaa aag aaa gcc gtg gag tat ttt aga ata gct	442
Gly Val Pro Lys Asp Glu Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala	
115 120 125	
acc gag aag ggc tat act aac gcc tat ata aac tta ggc atc atg tat	490
Thr Glu Lys Gly Tyr Thr Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr	
130 135 140	
atg gag ggt agg gga gtt cca agc aac tat gtg aaa gcg aca gag tgc	538
Met Glu Gly Arg Gly Val Pro Ser Asn Tyr Val Lys Ala Thr Glu Cys	
145 150 155 160	
ttt aga aaa gcg atg cat aag ggt aat gta gaa gct tat atc ctt tta	586
Phe Arg Lys Ala Met His Lys Gly Asn Val Glu Ala Tyr Ile Leu Leu	
165 170 175	
ggg gat att tat tat agt ggg aat gat caa ttg ggt att gag cca gac	634
Gly Asp Ile Tyr Tyr Ser Gly Asn Asp Gln Leu Gly Ile Glu Pro Asp	
180 185 190	
aaa gat aag gcg att gtc tat tat aaa atg gcg gct gat atg agc tct	682
Lys Asp Lys Ala Ile Val Tyr Tyr Lys Met Ala Ala Asp Met Ser Ser	
195 200 205	
tct aga gct tat gaa ggg tta gca gag tct tat cag tat ggg tta ggc	730
Ser Arg Ala Tyr Glu Gly Leu Ala Glu Ser Tyr Gln Tyr Gly Leu Gly	
210 215 220	
gtg gaa aaa gat aag aaa aag gct gaa gaa tac atg caa aaa gca tgc	778
Val Glu Lys Asp Lys Lys Lys Ala Glu Glu Tyr Met Gln Lys Ala Cys	

225	230	235	240	
gat ttt gac att gat aaa aat tgt aag aaa aag aac act tca agc cga 826				
Asp Phe Asp Ile Asp Lys Asn Cys Lys Lys Lys Asn Thr Ser Ser Arg				
	245	250	255	

taactctcaa acttgggctt gattaggatt ttgttttat ttttaagtagc atg 879

<210> 300  
 <211> 256  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <221> VARIANT  
 <222> 36  
 <223> Xaa = Any Amino Acid

<400> 300

Met	Gly	Tyr	Ala	Ser	Lys	Leu	Ala	Leu	Lys	Ile	Cys	Leu	Ala	Ser	Leu
1				5				10						15	
Cys	Leu	Phe	Ser	Ala	Leu	Gly	Ala	Glu	His	Leu	Glu	Gln	Lys	Arg	Asn
			20					25					30		
Tyr	Ile	Tyr	Xaa	Gly	Glu	Glu	Ala	Tyr	Asn	Asn	Lys	Glu	Tyr	Glu	Arg
		35					40					45			
Ala	Ala	Ser	Phe	Tyr	Lys	Ser	Ala	Ile	Lys	Asn	Gly	Glu	Pro	Leu	Ala
	50					55					60				
Tyr	Val	Leu	Leu	Gly	Ile	Met	Tyr	Glu	Asn	Gly	Arg	Gly	Val	Pro	Lys
65					70				75					80	
Asp	Glu	Lys	Lys	Ala	Glu	Tyr	Phe	Gln	Lys	Ala	Val	Asp	Asn	Asp	
			85					90					95		
Ile	Pro	Arg	Gly	Tyr	Asn	Asn	Leu	Gly	Val	Met	Tyr	Lys	Glu	Gly	Arg
			100					105					110		
Gly	Val	Pro	Lys	Asp	Glu	Lys	Lys	Ala	Val	Glu	Tyr	Phe	Arg	Ile	Ala
		115					120					125			
Thr	Glu	Lys	Gly	Tyr	Thr	Asn	Ala	Tyr	Ile	Asn	Leu	Gly	Ile	Met	Tyr
	130					135					140				
Met	Glu	Gly	Arg	Gly	Val	Pro	Ser	Asn	Tyr	Val	Lys	Ala	Thr	Glu	Cys
145					150				155					160	
Phe	Arg	Lys	Ala	Met	His	Lys	Gly	Asn	Val	Glu	Ala	Tyr	Ile	Leu	Leu
			165					170					175		
Gly	Asp	Ile	Tyr	Tyr	Ser	Gly	Asn	Asp	Gln	Leu	Gly	Ile	Glu	Pro	Asp
		180					185					190			
Lys	Asp	Lys	Ala	Ile	Val	Tyr	Tyr	Lys	Met	Ala	Ala	Asp	Met	Ser	Ser
	195					200					205				
Ser	Arg	Ala	Tyr	Glu	Gly	Leu	Ala	Glu	Ser	Tyr	Gln	Tyr	Gly	Leu	Gly
	210					215					220				
Val	Glu	Lys	Asp	Lys	Lys	Lys	Ala	Glu	Glu	Tyr	Met	Gln	Lys	Ala	Cys
225				230					235					240	
Asp	Phe	Asp	Ile	Asp	Lys	Asn	Cys	Lys	Lys	Asn	Thr	Ser	Ser	Arg	
			245					250					255		

<210> 301  
 <211> 319

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (66)...(269)

<400> 301

tgggggttgt gggtgctcat gttcgcacatg gtagtaagg ataggagtat ttaaaaggca 60  
aggtc atg aat agt tct aat ctc aaa aat tgg cta ttc cct acc att tgc 110  
Met Asn Ser Ser Asn Leu Lys Asn Trp Leu Phe Pro Thr Ile Cys  
1 5 10 15

ttt ttt tta ttt tgt tat att tta att ttt tta atg ttc ttt atg ttt 158  
Phe Phe Leu Phe Cys Tyr Ile Leu Ile Phe Leu Met Phe Phe Met Phe  
20 25 30

aaa agt ttg caa tcg caa tcg ttt ggc tct gtg gca gaa acc gga aaa 206  
Lys Ser Leu Gln Ser Gln Ser Phe Gly Ser Val Ala Glu Thr Gly Lys  
35 40 45

aaa ccc atc acc acc acc aag aaa ttt ggt aag gaa ttg caa aaa cag 254  
Lys Pro Ile Thr Thr Thr Lys Lys Phe Gly Lys Glu Leu Gln Lys Gln  
50 55 60

att tca aaa atc cat taactttttt tcttttttgc cgataacttgc tgtaatggaa 309  
Ile Ser Lys Ile His  
65

tgaatatcaa 319

<210> 302

<211> 68

<212> PRT

<213> *Helicobacter pylori*

<400> 302

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ctt	atg	aca	aag	ccg	gac	ggc	agt	atc	att	gaa	acg	ccc	att	att	tct	3485	
Leu	Met	Thr	Lys	Pro	Asp	Gly	Ser	Ile	Ile	Glu	Thr	Pro	Ile	Ile	Ser		
		1020					1025					1030					



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Asn Phe Lys Glu Gly Leu Asn Val Leu Glu Tyr Phe Asn Ser Thr His	
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ggc gct aga aag ggc tta gcg gat aca gcg cta aaa aca gcc aat gcg	3581
Gly Ala Arg Lys Gly Leu Ala Asp Thr Ala Leu Lys Thr Ala Asn Ala	
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ggg tat ttg acc aga aag ctc att gat gtt tcg caa aat gtc aag gtg	3629
Gly Tyr Leu Thr Arg Lys Leu Ile Asp Val Ser Gln Asn Val Lys Val	
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gtg tct gat gat tgc ggc acg cat gaa ggg att gaa atc acg gat att	3677
Val Ser Asp Asp Cys Gly Thr His Glu Gly Ile Glu Ile Thr Asp Ile	
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gcg gtg ggg agt gag ctg att gaa cct tta gaa gag cgt att ttt ggg	3725
Ala Val Gly Ser Glu Leu Ile Glu Pro Leu Glu Glu Arg Ile Phe Gly	
1100 1105 1110	
cgc gtt tta tta gaa gat gtg atc gat ccc att acg aat gaa atc ttg	3773
Arg Val Leu Leu Glu Asp Val Ile Asp Pro Ile Thr Asn Glu Ile Leu	
1115 1120 1125	
ctt tat gcg gac act ttg att gat gaa gag ggt gct aaa aag gtg gtt	3821
Leu Tyr Ala Asp Thr Leu Ile Asp Glu Glu Gly Ala Lys Lys Val Val	
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gaa gcc ggg att aaa tcc att acg atc cgc acc cca gta act tgt aaa	3869
Glu Ala Gly Ile Lys Ser Ile Thr Ile Arg Thr Pro Val Thr Cys Lys	
1150 1155 1160	
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Ala Pro Lys Gly Val Cys Ala Lys Cys Tyr Gly Leu Asn Leu Gly Glu	
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Gly Lys Met Ser Tyr Pro Gly Glu Ala Val Gly Val Val Ala Ala Gln	
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Ser Ile Gly Glu Pro Gly Thr Gln Leu Thr Leu Arg Thr Phe His Val	
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Gly Gly Thr Ala Ser Arg Ser Gln Asp Glu Arg Glu Ile Val Ala Ser	
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gag ggt aaa aac att atc gct aac cgc cgt aac gct tct att tta gtg	4157
Glu Gly Lys Asn Ile Ile Ala Asn Arg Arg Asn Ala Ser Ile Leu Val	
1245 1250 1255	

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Val Glu Pro Lys Ile Lys Ala Pro Phe Asp Gly Glu Leu Arg Ile Glu	
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acg gtt tat gaa gaa gtc gtt gtg agc gtg aaa aat ggc gat caa gaa	4253
Thr Val Tyr Glu Glu Val Val Val Ser Val Lys Asn Gly Asp Gln Glu	
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Ala Lys Phe Val Leu Arg Arg Ser Asp Ile Val Lys Pro Ser Glu Leu	
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Ala Gly Val Gly Gly Lys Ile Glu Gly Lys Val Tyr Leu Pro Tyr Ala	
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Ser Gly His Lys Val His Lys Gly Gly Ser Ile Ala Asp Ile Ile Gln	
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Val Lys Asp Asn Asp Pro Ile Ala Gln Asp Val Tyr Ala Lys Glu Lys	
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Gly Val Ile Lys Tyr Tyr Val Leu Glu Ala Asn His Leu Glu Arg Thr	
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His Gly Ile Lys Lys Gly Asp Met Val Ser Glu Lys Gly Leu Phe Ala	
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Val Ile Ala Asp Asp Asn Gly Arg Glu Ala Ala Arg His Tyr Ile Ala	
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Arg Gly Ser Glu Ile Leu Ile Asp Asp Asn Ser Glu Val Ser Thr Asn	
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Trp Asp Pro Tyr Asn Thr Pro Ile Ile Ala Asp Phe Lys Gly Lys Val	
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Gly Phe Val Asp Val Ile Ala Gly Val Thr Val Ala Glu Lys Glu Asp	

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Glu Asn Thr Gly Ile Thr Ser Leu Val	Val Asn Asp Tyr Ile Pro Ser		
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Gly Tyr Lys Pro Ser Leu Phe Leu Glu	Gly Ala Asn Gly Glu Glu Met		
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Arg Tyr Phe Leu Glu Pro Lys Thr Ser	Ile Ala Ile Ser Asp Gly Ser		
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Ser Val Glu Gln Ala Glu Val Leu Ala	Lys Ile Pro Lys Ala Thr Val		
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Lys Ser Arg Asp Ile Thr Gly Gly Leu	Pro Arg Val Ser Glu Leu Phe		
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Glu Ala Arg Lys Pro Lys Pro Lys Asp	Val Ala Ile Leu Ser Glu Val		
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gat ggg att gtg agt ttt ggc aaa ccc	att cgc aat aaa gaa cac atc	5165	
Asp Gly Ile Val Ser Phe Gly Lys Pro	Ile Arg Asn Lys Glu His Ile		
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atc gta act tct aaa gat ggc cgt tcc	atg gat tat ttt gtg gat aaa	5213	
Ile Val Thr Ser Lys Asp Gly Arg Ser	Met Asp Tyr Phe Val Asp Lys		
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ggc aag caa att tta gtg cat gcc gat	gaa ttt gtg cat gcg gga gaa	5261	
Gly Lys Gln Ile Leu Val His Ala Asp	Glu Phe Val His Ala Gly Glu		
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Ala Met Thr Asp Gly Val Ile Ser Ser	His Asp Ile Leu Arg Ile Ser		
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Gly Glu Lys Glu Leu Tyr Lys Tyr Ile	Val Ser Glu Val Gln Gln Val		
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tat cgc agg cag ggg gtg agc att gcg	gac aag cac att gaa atc att	5405	
Tyr Arg Arg Gln Gly Val Ser Ile Ala	Asp Lys His Ile Glu Ile Ile		
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gtt tct caa atg cta aga cag gtg cgt	att tta gac agc ggg gat agc	5453	
Val Ser Gln Met Leu Arg Gln Val Arg	Ile Leu Asp Ser Gly Asp Ser		
1675	1680 1685		
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Lys Phe Ile Glu Gly Asp Leu Val Ser Lys Lys Leu Phe Lys Glu Glu  
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 Asn Ala Arg Val Ile Ala Leu Lys Gly Glu Pro Ala Ile Ala Glu Pro  
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 35 40 45  
 Glu Met His Leu Gly Leu Val Gly Lys Glu Phe Gly Lys Gln Ile Ala  
 50 55 60  
 Arg Met Leu Glu Asp Lys Thr Lys Asp Phe Ala Lys Glu Leu Arg Ala  
 65 70 75 80  
 Lys Met Leu Glu Xaa Ala Asn Ala Ile Asn Glu Lys Asp Pro Leu Thr  
 85 90 95  
 Ile His Ala Leu Glu Asn Cys Ser Asp Glu Glu Leu Leu Glu Tyr Ala  
 100 105 110  
 Lys Asp Trp Ser Lys Gly Val Lys Met Ala Ile Pro Val Phe Glu Gly



Val	Asn	Glu	Leu	Tyr	Arg	Arg	Val	Ile	Asn	Arg	Asn	Gln	Arg	Leu	Lys	565	570	575
Arg	Leu	Met	Glu	Leu	Gly	Ala	Pro	Glu	Ile	Ile	Val	Arg	Asn	Glu	Lys	580	585	590
Arg	Met	Leu	Gln	Glu	Ala	Val	Asp	Val	Leu	Phe	Asp	Asn	Gly	Arg	Ser	595	600	605
Thr	Asn	Ala	Val	Lys	Gly	Ala	Asn	Lys	Arg	Pro	Leu	Lys	Ser	Leu	Ser	610	615	620
Glu	Ile	Ile	Lys	Gly	Lys	Gln	Gly	Arg	Phe	Arg	Gln	Asn	Leu	Leu	Gly	625	630	635
Lys	Arg	Val	Asp	Phe	Ser	Gly	Arg	Ser	Val	Ile	Val	Val	Gly	Pro	Asn	645	650	655
Leu	Lys	Met	Asp	Glu	Cys	Gly	Leu	Pro	Lys	Asn	Met	Ala	Leu	Glu	Leu	660	665	670
Phe	Lys	Pro	His	Leu	Leu	Ser	Lys	Leu	Glu	Glu	Arg	Gly	Tyr	Ala	Thr	675	680	685
Thr	Leu	Lys	Gln	Ala	Lys	Arg	Met	Ile	Glu	Gln	Lys	Ser	Asn	Glu	Val	690	695	700
Trp	Glu	Cys	Leu	Gln	Glu	Ile	Thr	Glu	Gly	Tyr	Pro	Val	Leu	Leu	Asn	705	710	715
Arg	Ala	Pro	Thr	Leu	His	Lys	Gln	Ser	Ile	Gln	Ala	Phe	His	Pro	Lys	725	730	735
Leu	Ile	Asp	Gly	Lys	Ala	Ile	Gln	Leu	His	Pro	Leu	Val	Cys	Ser	Ala	740	745	750
Phe	Asn	Ala	Asp	Phe	Asp	Gly	Asp	Gln	Met	Ala	Val	His	Val	Pro	Leu	755	760	765
Ser	Gln	Glu	Ala	Ile	Ala	Glu	Cys	Lys	Val	Leu	Met	Leu	Ser	Ser	Met	770	775	780
Asn	Ile	Leu	Leu	Pro	Ala	Ser	Gly	Lys	Ala	Val	Ala	Ile	Pro	Ser	Gln	785	790	795
Asp	Met	Val	Leu	Gly	Leu	Tyr	Tyr	Leu	Ser	Leu	Glu	Lys	Ser	Gly	Val	805	810	815
Lys	Gly	Glu	His	Lys	Leu	Phe	Ser	Ser	Val	Asn	Glu	Ile	Ile	Thr	Ala	820	825	830
Ile	Asp	Thr	Lys	Glu	Leu	Asp	Ile	His	Ala	Lys	Ile	Arg	Val	Leu	Asp	835	840	845
Gln	Gly	Asn	Ile	Ile	Ala	Thr	Ser	Ala	Gly	Arg	Met	Ile	Ile	Lys	Ser	850	855	860
Ile	Leu	Pro	Asp	Phe	Ile	Pro	Thr	Asp	Leu	Trp	Asn	Arg	Pro	Met	Lys	865	870	875
Lys	Lys	Asp	Ile	Gly	Val	Leu	Val	Asp	Tyr	Val	His	Lys	Val	Gly	Gly	885	890	895
Ile	Gly	Ile	Thr	Ala	Thr	Phe	Leu	Asp	Asn	Leu	Lys	Thr	Leu	Gly	Phe	900	905	910
Arg	Tyr	Ala	Thr	Lys	Ala	Gly	Ile	Ser	Ile	Ser	Met	Glu	Asp	Ile	Ile	915	920	925
Thr	Pro	Lys	Asp	Lys	Gln	Lys	Met	Val	Glu	Lys	Ala	Lys	Val	Glu	Val	930	935	940
Lys	Lys	Ile	Gln	Gln	Gln	Tyr	Asp	Gln	Gly	Leu	Leu	Thr	Asp	Gln	Glu	945	950	955
Arg	Tyr	Asn	Lys	Ile	Ile	Asp	Thr	Trp	Thr	Glu	Val	Asn	Asp	Lys	Met	965	970	975
Ser	Lys	Glu	Met	Met	Thr	Ala	Ile	Ala	Gln	Asp	Lys	Glu	Gly	Phe	Asn	980	985	990
Ser	Ile	Tyr	Met	Met	Ala	Asp	Ser	Gly	Ala	Arg	Gly	Ser	Ala	Ala	Gln			

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Thr Asn Thr Phe Lys Thr Ile Ala Thr Trp Asp Pro Tyr Asn Thr Pro  
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 1475 1480 1485  
 Leu Val Val Asn Asp Tyr Ile Pro Ser Gly Tyr Lys Pro Ser Leu Phe  
 1490 1495 1500  
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 Thr Ser Ile Ala Ile Ser Asp Gly Ser Ser Val Glu Gln Ala Glu Val  
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agga atg aaa act gag atg aaa tct tct tta aaa ctt ttt atg cgg cct 109
    Met Lys Thr Glu Met Lys Ser Ser Leu Lys Leu Phe Met Arg Pro
      1             5             10             15

ttg ttg gtg gtt tta gcg ttc atg ttg ttg tat gct tta gtg cat gct 157
Leu Leu Val Val Leu Ala Phe Met Leu Leu Tyr Ala Leu Val His Ala
      20             25             30

gcg ctt ggt ttt tat gta aaa aaa gac agc gct cca ata agc cca aat 205
Ala Leu Gly Phe Tyr Val Lys Lys Asp Ser Ala Pro Ile Ser Pro Asn
      35             40             45

gta gaa aaa acc gag aca gag cgt caa aac ggc gtg ctt tcg ccc aaa 253
Val Glu Lys Thr Glu Thr Glu Arg Gln Asn Gly Val Leu Ser Pro Lys
      50             55             60

caa gaa gaa gcc aac gca acc aca act gcc aca gaa gaa agc ccc acc 301
Gln Glu Glu Ala Asn Ala Thr Thr Thr Ala Thr Glu Glu Ser Pro Thr
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aaa gac aca gcg ccg cct tta gac aca gcc gcg caa aaa caa gaa act 349
Lys Asp Thr Ala Pro Pro Leu Asp Thr Ala Ala Gln Lys Gln Glu Thr
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aaa caa gag caa gaa aaa gaa aac gag cct aaa caa gat agc gtc ccg 397
Lys Gln Glu Gln Glu Lys Glu Asn Glu Pro Lys Gln Asp Ser Val Pro
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ccc gtt caa aac aat caa aaa acc cct aca acc ccc tta atg gga aaa 445
Pro Val Gln Asn Asn Gln Lys Thr Pro Thr Thr Pro Leu Met Gly Lys
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aaa cct tta gag tat aaa gtc gca gtc agt ggc gtg aat gtg cgc gct 493
Lys Pro Leu Glu Tyr Lys Val Ala Val Ser Gly Val Asn Val Arg Ala
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ttt ccc agc aca aaa ggt aaa atc ttg gga ttg ctt tta aaa aat aaa 541
Phe Pro Ser Thr Lys Gly Lys Ile Leu Gly Leu Leu Leu Lys Asn Lys
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agc gtg aaa gtt tta gaa atc caa aac gat tgg gct gaa att gaa ttt 589
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tct cac gaa aca aag ggc tat gtg ttt tta aaa ctt tta aaa aag gct 637
Ser His Glu Thr Lys Gly Tyr Val Phe Leu Lys Leu Leu Lys Lys Ala
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 Glu Lys Thr Glu Thr Glu Arg Gln Asn Gly Val Leu Ser Pro Lys Gln  
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 65 70 75 80  
 Asp Thr Ala Pro Pro Leu Asp Thr Ala Ala Gln Lys Gln Glu Thr Lys  
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 Gln Glu Gln Glu Lys Glu Asn Glu Pro Lys Gln Asp Ser Val Pro Pro  
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 115 120 125  
 Pro Leu Glu Tyr Lys Val Ala Val Ser Gly Val Asn Val Arg Ala Phe  
 130 135 140  
 Pro Ser Thr Lys Gly Lys Ile Leu Gly Leu Leu Lys Asn Lys Ser  
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 1 5 10 15  
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Pro	His	Lys	Gly	Thr	Phe	Lys	Ala	Lys	Val	Leu	Asp	Ser	Lys	Lys	Pro		
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aga	caa	gtt	tta	ggc	gtt	tat	aat	atc	tcc	cca	cac	aaa	aaa	ctc	acg	254	
Arg	Gln	Val	Leu	Gly	Val	Tyr	Asn	Ile	Ser	Pro	His	Lys	Lys	Leu	Thr		
		50					55					60					
ctc	act	atc	acc	cac	ata	tcc	act	gca	atc	gtc	tat	caa	ccc	ctt	gat	302	
Leu	Thr	Ile	Thr	His	Ile	Ser	Thr	Ala	Ile	Val	Tyr	Gln	Pro	Leu	Asp		
	65					70					75						
gaa	aaa	ctt	tct	tta	gaa	aca	acc	tta	aac	cct	aac	cgc	cct	act	atc	350	
Glu	Lys	Leu	Ser	Leu	Glu	Thr	Thr	Leu	Asn	Pro	Asn	Arg	Pro	Thr	Ile		
80					85				90						95		
cct	aga	aac	acc	cag	att	gtt	ttt	tct	tca	aaa	gaa	ttg	aaa	gag	tcg	398	
Pro	Arg	Asn	Thr	Gln	Ile	Val	Phe	Ser	Ser	Lys	Glu	Leu	Lys	Glu	Ser		
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cac	ccg	cac	caa	atg	cct	tct	tta	aac	gcg	ccc	atg	caa	aaa	cca	caa	446	
His	Pro	His	Gln	Met	Pro	Ser	Leu	Asn	Ala	Pro	Met	Gln	Lys	Pro	Gln		
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Asn	Lys	Pro	His	Ser	Ser	Gln	Gln	Pro	Ser	Gln	Asn	Phe	Ser	Tyr	Pro		
		130					135					140					
gag	ccc	aaa	cta	ggc	tct	aaa	aac	tct	aaa	aac	agc	ctt	tta	cag	cct	542	
Glu	Pro	Lys	Leu	Gly	Ser	Lys	Asn	Ser	Lys	Asn	Ser	Leu	Leu	Gln	Pro		
	145				150					155							
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Leu	Ala	Ile	Pro	Ser	Lys	Ile	Ser	Pro	Thr	Asn	Glu	Thr	Gln	Thr	Pro		
160					165				170						175		
aca	aac	gac	act	aaa	ccc	cct	tta	aag	cat	tct	tca	gaa	gat	caa	gaa	638	
Thr	Asn	Asp	Thr	Lys	Pro	Pro	Leu	Lys	His	Ser	Ser	Glu	Asp	Gln	Glu		
			180					185					190				
agc	aac	ctc	ttt	ata	acg	cca	ccc	act	gaa	aaa	acg	ctc	cct	aac	aac	686	
Ser	Asn	Leu	Phe	Ile	Thr	Pro	Pro	Thr	Glu	Lys	Thr	Leu	Pro	Asn	Asn		
		195						200					205				
acc	tct	aac	gct	gat	att	agt	gaa	aac	aat	gaa	agc	aat	gag	aat	aaa	734	
Thr	Ser	Asn	Ala	Asp	Ile	Ser	Glu	Asn	Asn	Glu	Ser	Asn	Glu	Asn	Lys		
		210					215					220					
gat	aat	gtg	gaa	aaa	caa	gcc	att	aga	gat	gct	aat	att	aaa	gaa	ttt	782	
Asp	Asn	Val	Glu	Lys	Gln	Ala	Ile	Arg	Asp	Ala	Asn	Ile	Lys	Glu	Phe		
	225				230						235						
gca	tgc	ggg	aag	tgg	gtc	tat	gac	gat	gaa	aat	tta	caa	gcc	tac	cgc	830	
Ala	Cys	Gly	Lys	Trp	Val	Tyr	Asp	Asp	Glu	Asn	Leu	Gln	Ala	Tyr	Arg		
240					245				250						255		

cca agc att tta aaa cgc gtt gat gaa gac aaa caa act gca aca gat	878
Pro Ser Ile Leu Lys Arg Val Asp Glu Asp Lys Gln Thr Ala Thr Asp	
260 265 270	
att acc cct tgc gat tac agc acc gct gaa aat aaa agc ggt aaa atc	926
Ile Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn Lys Ser Gly Lys Ile	
275 280 285	
att acc ccc tat act aaa atc tcc gtt cat aaa aca gag cct tta gaa	974
Ile Thr Pro Tyr Thr Lys Ile Ser Val His Lys Thr Glu Pro Leu Glu	
290 295 300	
gag cca caa act ttt gaa gct aaa aat aat ttc gcc att ctt caa gcc	1022
Glu Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe Ala Ile Leu Gln Ala	
305 310 315	
aga agc tct aca gaa aaa tgc aaa agg gct aga gca aga aaa gac ggc	1070
Arg Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg Ala Arg Lys Asp Gly	
320 325 330 335	
acg act agg caa tgc tat cta ata gaa gag cct tta aaa caa gca tgg	1118
Thr Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp	
340 345 350	
gag agt gag tat gaa atc acc acg caa tta gtg aaa gcc att tat gag	1166
Glu Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu	
355 360 365	
cgc ccc aaa caa gac gat caa gta gag ccg act ttt tat gaa acc agc	1214
Arg Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser	
370 375 380	
gaa ttg gct tat tct tcc aca cga aaa agc gaa ata acg cac aat gaa	1262
Glu Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr His Asn Glu	
385 390 395	
ttg aat ttg aat gaa aaa ttc atg gaa ttt gtg gaa gtg tat gag ggg	1310
Leu Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly	
400 405 410 415	
cat tat tta aac gat ata att aaa gag agc agt gaa tat aaa gaa tgg	1358
His Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp	
420 425 430	
gtt aaa aac cat gtg cgc ttt aaa gaa ggg gtg tgc atg gct tta gaa	1406
Val Lys Asn His Val Arg Phe Lys Glu Gly Val Cys Met Ala Leu Glu	
435 440 445	
ata gaa gaa cag cca cga gct aaa agc acg cct ttg agt att gaa aac	1454
Ile Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro Leu Ser Ile Glu Asn	
450 455 460	
tct cgt gtg gta tgt gtc aaa aag ggg aat tat tta ttc aac gaa gtt	1502
Ser Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val	
465 470 475	

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1550

<210> 312

<211> 479

<212> PRT

<213> Helicobacter pylori

<400> 312

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Leu	Gln	Ala	Leu	Val	Ile	Glu	Leu	Leu	Glu	Glu	Ile	Lys	Thr	Ser	Pro
			20					25					30		
His	Lys	Gly	Thr	Phe	Lys	Ala	Lys	Val	Leu	Asp	Ser	Lys	Lys	Pro	Arg
		35					40					45			
Gln	Val	Leu	Gly	Val	Tyr	Asn	Ile	Ser	Pro	His	Lys	Lys	Leu	Thr	Leu
	50					55					60				
Thr	Ile	Thr	His	Ile	Ser	Thr	Ala	Ile	Val	Tyr	Gln	Pro	Leu	Asp	Glu
65				70						75				80	
Lys	Leu	Ser	Leu	Glu	Thr	Thr	Leu	Asn	Pro	Asn	Arg	Pro	Thr	Ile	Pro
			85					90					95		
Arg	Asn	Thr	Gln	Ile	Val	Phe	Ser	Ser	Lys	Glu	Leu	Lys	Glu	Ser	His
			100					105					110		
Pro	His	Gln	Met	Pro	Ser	Leu	Asn	Ala	Pro	Met	Gln	Lys	Pro	Gln	Asn
		115					120					125			
Lys	Pro	His	Ser	Ser	Gln	Gln	Pro	Ser	Gln	Asn	Phe	Ser	Tyr	Pro	Glu
	130					135					140				
Pro	Lys	Leu	Gly	Ser	Lys	Asn	Ser	Lys	Asn	Ser	Leu	Leu	Gln	Pro	Leu
145				150						155				160	
Ala	Ile	Pro	Ser	Lys	Ile	Ser	Pro	Thr	Asn	Glu	Thr	Gln	Thr	Pro	Thr
			165					170					175		
Asn	Asp	Thr	Lys	Pro	Pro	Leu	Lys	His	Ser	Ser	Glu	Asp	Gln	Glu	Ser
		180						185					190		
Asn	Leu	Phe	Ile	Thr	Pro	Pro	Thr	Glu	Lys	Thr	Leu	Pro	Asn	Asn	Thr
		195					200					205			
Ser	Asn	Ala	Asp	Ile	Ser	Glu	Asn	Asn	Glu	Ser	Asn	Glu	Asn	Lys	Asp
	210					215					220				
Asn	Val	Glu	Lys	Gln	Ala	Ile	Arg	Asp	Ala	Asn	Ile	Lys	Glu	Phe	Ala
225				230						235				240	
Cys	Gly	Lys	Trp	Val	Tyr	Asp	Asp	Glu	Asn	Leu	Gln	Ala	Tyr	Arg	Pro
			245					250					255		
Ser	Ile	Leu	Lys	Arg	Val	Asp	Glu	Asp	Lys	Gln	Thr	Ala	Thr	Asp	Ile
		260						265					270		
Thr	Pro	Cys	Asp	Tyr	Ser	Thr	Ala	Glu	Asn	Lys	Ser	Gly	Lys	Ile	Ile
	275						280					285			
Thr	Pro	Tyr	Thr	Lys	Ile	Ser	Val	His	Lys	Thr	Glu	Pro	Leu	Glu	Glu
	290					295					300				
Pro	Gln	Thr	Phe	Glu	Ala	Lys	Asn	Asn	Phe	Ala	Ile	Leu	Gln	Ala	Arg
305				310						315				320	
Ser	Ser	Thr	Glu	Lys	Cys	Lys	Arg	Ala	Arg	Ala	Arg	Lys	Asp	Gly	Thr
			325					330					335		
Thr	Arg	Gln	Cys	Tyr	Leu	Ile	Glu	Glu	Pro	Leu	Lys	Gln	Ala	Trp	Glu
		340					345					350			
Ser	Glu	Tyr	Glu	Ile	Thr	Thr	Gln	Leu	Val	Lys	Ala	Ile	Tyr	Glu	Arg
	355						360					365			

Pro	Lys	Gln	Asp	Asp	Gln	Val	Glu	Pro	Thr	Phe	Tyr	Glu	Thr	Ser	Glu
370						375					380				
Leu	Ala	Tyr	Ser	Ser	Thr	Arg	Lys	Ser	Glu	Ile	Thr	His	Asn	Glu	Leu
385						390					395				400
Asn	Leu	Asn	Glu	Lys	Phe	Met	Glu	Phe	Val	Glu	Val	Tyr	Glu	Gly	His
				405					410					415	
Tyr	Leu	Asn	Asp	Ile	Ile	Lys	Glu	Ser	Ser	Glu	Tyr	Lys	Glu	Trp	Val
			420					425					430		
Lys	Asn	His	Val	Arg	Phe	Lys	Glu	Gly	Val	Cys	Met	Ala	Leu	Glu	Ile
		435					440					445			
Glu	Glu	Gln	Pro	Arg	Ala	Lys	Ser	Thr	Pro	Leu	Ser	Ile	Glu	Asn	Ser
	450					455					460				
Arg	Val	Val	Cys	Val	Lys	Lys	Gly	Asn	Tyr	Leu	Phe	Asn	Glu	Val	
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 <213> Helicobacter pylori

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           Met Ala Asp Ile Gln Arg Arg Asp Phe Leu Gly Met Ser Leu  
           1                          5                          10

gct agt gtt aca gct ata ggg gct ata gcg agt ctg gta gcg atg aaa 157  
 Ala Ser Val Thr Ala Ile Gly Ala Ile Ala Ser Leu Val Ala Met Lys  
   15                          20                          25                          30

aag act tgg gat ccg ctt cca agc gtt gtt tca gcc ggt ttt acg acc 205  
 Lys Thr Trp Asp Pro Leu Pro Ser Val Val Ser Ala Gly Phe Thr Thr  
                           35                          40                          45

ata gat gtg gcg aat atg caa gaa ggg cag ttt tcc acc gtg gaa tgg 253  
 Ile Asp Val Ala Asn Met Gln Glu Gly Gln Phe Ser Thr Val Glu Trp  
                           50                          55                          60

cgt ggg aaa ccg gtc tat atc ctc aag cgt tct aaa aaa gag ggc ttt 301  
 Arg Gly Lys Pro Val Tyr Ile Leu Lys Arg Ser Lys Lys Glu Gly Phe  
                           65                          70                          75

aat gaa aag cgc gat ttt aaa gtt ggc gag agc gtt ttt acc aca gcc 349  
 Asn Glu Lys Arg Asp Phe Lys Val Gly Glu Ser Val Phe Thr Thr Ala  
   80                          85                          90

att caa att tgc acg cat tta ggg tgt atc ccc act tat caa gat gaa 397  
 Ile Gln Ile Cys Thr His Leu Gly Cys Ile Pro Thr Tyr Gln Asp Glu  
   95                          100                          105                          110

gaa aaa ggc ttt tta tgc cca tgc cat ggg ggg cgt ttc act tct gat 445  
 Glu Lys Gly Phe Leu Cys Pro Cys His Gly Gly Arg Phe Thr Ser Asp  
                   115                                  120                                  125

ggc gtg aat att gcc ggc act ccc cct cca cgc cct ttt gat atc ccg 493  
 Gly Val Asn Ile Ala Gly Thr Pro Pro Pro Arg Pro Phe Asp Ile Pro  
                   130                                  135                                  140

cct ttt aaa att gaa ggc act aag atc act ttt ggt gaa gcc ggg gct 541  
 Pro Phe Lys Ile Glu Gly Thr Lys Ile Thr Phe Gly Glu Ala Gly Ala  
                   145                                  150                                  155

gaa tac aag aaa atg atg gct aaa gcg taaggagagt ttaatggcag 588  
 Glu Tyr Lys Lys Met Met Ala Lys Ala  
                   160                                  165

agataaaaaa agcgaaaaaat ttaggcgaat gg 620

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                   20                                  25                                  30  
 Trp Asp Pro Leu Pro Ser Val Val Ser Ala Gly Phe Thr Thr Ile Asp  
                   35                                  40                                  45  
 Val Ala Asn Met Gln Glu Gly Gln Phe Ser Thr Val Glu Trp Arg Gly  
                   50                                  55                                  60  
 Lys Pro Val Tyr Ile Leu Lys Arg Ser Lys Lys Glu Gly Phe Asn Glu  
  65                                  70                                  75                                  80  
 Lys Arg Asp Phe Lys Val Gly Glu Ser Val Phe Thr Thr Ala Ile Gln  
                   85                                  90                                  95  
 Ile Cys Thr His Leu Gly Cys Ile Pro Thr Tyr Gln Asp Glu Glu Lys  
                   100                                  105                                  110  
 Gly Phe Leu Cys Pro Cys His Gly Gly Arg Phe Thr Ser Asp Gly Val  
                   115                                  120                                  125  
 Asn Ile Ala Gly Thr Pro Pro Pro Arg Pro Phe Asp Ile Pro Pro Phe  
                   130                                  135                                  140  
 Lys Ile Glu Gly Thr Lys Ile Thr Phe Gly Glu Ala Gly Ala Glu Tyr  
  145                                  150                                  155                                  160  
 Lys Lys Met Met Ala Lys Ala  
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<210> 315  
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<220>  
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<222> (52)...(1167)

<400> 315

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aaa aga atg aag tgt ttt agt caa aaa tgg ttg gtt ttt ttt gtt acc 105
Lys Arg Met Lys Cys Phe Ser Gln Lys Trp Leu Val Phe Phe Val Thr
      5                      10                      15

ctt tta ttg gct tct tta ggc cat gcg aaa atg gct ttt gaa tcc gat 153
Leu Leu Leu Ala Ser Leu Gly His Ala Lys Met Ala Phe Glu Ser Asp
      20                      25                      30

att gac acc aaa gcg cta gag gct ttt ggg gtt aat gcg ggc ttt tta 201
Ile Asp Thr Lys Ala Leu Glu Ala Phe Gly Val Asn Ala Gly Phe Leu
      35                      40                      45                      50

tcc caa atg ccc aac gct tta aaa aaa atg aat aaa gaa gaa gaa tgg 249
Ser Gln Met Pro Asn Ala Leu Lys Lys Met Asn Lys Glu Glu Glu Trp
      55                      60                      65

aag aga ctt gtc aaa aga ttt gat gtg aat tac cag ttc atc ccc atc 297
Lys Arg Leu Val Lys Arg Phe Asp Val Asn Tyr Gln Phe Ile Pro Ile
      70                      75                      80

att aaa aac atg ctc ata gaa gcg agc gtg ccg caa gaa ttt tta ttt 345
Ile Lys Asn Met Leu Ile Glu Ala Ser Val Pro Gln Glu Phe Leu Phe
      85                      90                      95

tta gcc atg gcc gag tct aaa ttt tca tca agg gct tat agc agg aaa 393
Leu Ala Met Ala Glu Ser Lys Phe Ser Ser Arg Ala Tyr Ser Arg Lys
      100                      105                      110

aaa gcg gta ggg att tgg caa ttc atg cca agc acg gct aaa gaa tta 441
Lys Ala Val Gly Ile Trp Gln Phe Met Pro Ser Thr Ala Lys Glu Leu
      115                      120                      125                      130

ggg ctt aag gtc aat cat tac att gat gaa aga aga gat ccc att aaa 489
Gly Leu Lys Val Asn His Tyr Ile Asp Glu Arg Arg Asp Pro Ile Lys
      135                      140                      145

agc act caa gcg gcg atc act tat ttg aaa cgg ctc tac aag caa acc 537
Ser Thr Gln Ala Ala Ile Thr Tyr Leu Lys Arg Leu Tyr Lys Gln Thr
      150                      155                      160

gga gag tgg tat ttg gtc gct atg gcg tat aat tac ggc tta cgc aag 585
Gly Glu Trp Tyr Leu Val Ala Met Ala Tyr Asn Tyr Gly Leu Arg Lys
      165                      170                      175

gtt caa aac gct att aaa gcc gcc ggc act tcg gac att aaa att ttg 633
Val Gln Asn Ala Ile Lys Ala Ala Gly Thr Ser Asp Ile Lys Ile Leu
      180                      185                      190
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ttg gat gaa gat aag aaa tac ctc cct aaa gaa aca cga gag tat atc	681
Leu Asp Glu Asp Lys Lys Tyr Leu Pro Lys Glu Thr Arg Glu Tyr Ile	
195 200 205 210	
cgc tcc att cta agc cta gcg tta aaa ttc aac agc cta gac aac ctc	729
Arg Ser Ile Leu Ser Leu Ala Leu Lys Phe Asn Ser Leu Asp Asn Leu	
215 220 225	
aaa gat aaa gaa tat ctg ctc aat cgt ggg gcg agg gtg agt tta gtg	777
Lys Asp Lys Glu Tyr Leu Leu Asn Arg Gly Ala Arg Val Ser Leu Val	
230 235 240	
ggc gtc ccg ttt aaa agg cgt gct tct tta gtc caa gta gcc aaa aat	825
Gly Val Pro Phe Lys Arg Arg Ala Ser Leu Val Gln Val Ala Lys Asn	
245 250 255	
ttg aat ttg agt ttg gaa acc tta aaa tcc tac aac cac caa ttc cgt	873
Leu Asn Leu Ser Leu Glu Thr Leu Lys Ser Tyr Asn His Gln Phe Arg	
260 265 270	
tat aac att ctg cct tct aaa gac ccc act tat acc att tat atc cct	921
Tyr Asn Ile Leu Pro Ser Lys Asp Pro Thr Tyr Thr Ile Tyr Ile Pro	
275 280 285 290	
tat gaa aaa ctc gct ctt ttc aaa caa cgc cag atc aaa caa aat aaa	969
Tyr Glu Lys Leu Ala Leu Phe Lys Gln Arg Gln Ile Lys Gln Asn Lys	
295 300 305	
aac att caa gcc agt tca aaa agc cct ttt atc acc cat gtg gtc tta	1017
Asn Ile Gln Ala Ser Ser Lys Ser Pro Phe Ile Thr His Val Val Leu	
310 315 320	
cct aaa gaa acc cta tct tct atc gct aaa cgc tat caa gtc agt att	1065
Pro Lys Glu Thr Leu Ser Ser Ile Ala Lys Arg Tyr Gln Val Ser Ile	
325 330 335	
tcc aat atc caa tta gcc aat gat ctc aaa gat tct aat att ttt atc	1113
Ser Asn Ile Gln Leu Ala Asn Asp Leu Lys Asp Ser Asn Ile Phe Ile	
340 345 350	
cac cag cgt tta atc atc ccc acc aac aaa aaa tta ctc gct aca agg	1161
His Gln Arg Leu Ile Ile Pro Thr Asn Lys Lys Leu Leu Ala Thr Arg	
355 360 365 370	
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Glu Phe	
atta	1221
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<213> Helicobacter pylori	

<400> 316

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          20           25           30
Ser Asp Ile Asp Thr Lys Ala Leu Glu Ala Phe Gly Val Asn Ala Gly
          35           40           45
Phe Leu Ser Gln Met Pro Asn Ala Leu Lys Lys Met Asn Lys Glu Glu
          50           55           60
Glu Trp Lys Arg Leu Val Lys Arg Phe Asp Val Asn Tyr Gln Phe Ile
65           70           75           80
Pro Ile Ile Lys Asn Met Leu Ile Glu Ala Ser Val Pro Gln Glu Phe
          85           90           95
Leu Phe Leu Ala Met Ala Glu Ser Lys Phe Ser Ser Arg Ala Tyr Ser
          100          105          110
Arg Lys Lys Ala Val Gly Ile Trp Gln Phe Met Pro Ser Thr Ala Lys
          115          120          125
Glu Leu Gly Leu Lys Val Asn His Tyr Ile Asp Glu Arg Arg Asp Pro
          130          135          140
Ile Lys Ser Thr Gln Ala Ala Ile Thr Tyr Leu Lys Arg Leu Tyr Lys
145          150          155          160
Gln Thr Gly Glu Trp Tyr Leu Val Ala Met Ala Tyr Asn Tyr Gly Leu
          165          170          175
Arg Lys Val Gln Asn Ala Ile Lys Ala Ala Gly Thr Ser Asp Ile Lys
          180          185          190
Ile Leu Leu Asp Glu Asp Lys Lys Tyr Leu Pro Lys Glu Thr Arg Glu
          195          200          205
Tyr Ile Arg Ser Ile Leu Ser Leu Ala Leu Lys Phe Asn Ser Leu Asp
          210          215          220
Asn Leu Lys Asp Lys Glu Tyr Leu Leu Asn Arg Gly Ala Arg Val Ser
225          230          235          240
Leu Val Gly Val Pro Phe Lys Arg Arg Ala Ser Leu Val Gln Val Ala
          245          250          255
Lys Asn Leu Asn Leu Ser Leu Glu Thr Leu Lys Ser Tyr Asn His Gln
          260          265          270
Phe Arg Tyr Asn Ile Leu Pro Ser Lys Asp Pro Thr Tyr Thr Ile Tyr
          275          280          285
Ile Pro Tyr Glu Lys Leu Ala Leu Phe Lys Gln Arg Gln Ile Lys Gln
          290          295          300
Asn Lys Asn Ile Gln Ala Ser Ser Lys Ser Pro Phe Ile Thr His Val
305          310          315          320
Val Leu Pro Lys Glu Thr Leu Ser Ser Ile Ala Lys Arg Tyr Gln Val
          325          330          335
Ser Ile Ser Asn Ile Gln Leu Ala Asn Asp Leu Lys Asp Ser Asn Ile
          340          345          350
Phe Ile His Gln Arg Leu Ile Ile Pro Thr Asn Lys Lys Leu Leu Ala
          355          360          365
Thr Arg Glu Phe
          370
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<211> 561

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (46)...(510)

<400> 317

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Val Val Gln Ile Cys Gly Gly Leu Gly Asn Gln Met Phe Gln Tyr Ala  
5 10 15 20

ttc gct aaa agt ttg caa aaa cac tct aat acg cct gtg ctg tta gat 153  
Phe Ala Lys Ser Leu Gln Lys His Ser Asn Thr Pro Val Leu Leu Asp  
25 30 35

atc act tct ttt gat tgg agc gat agg aaa atg caa tta gaa ctt ttc 201  
Ile Thr Ser Phe Asp Trp Ser Asp Arg Lys Met Gln Leu Glu Leu Phe  
40 45 50

cct att gat ttg ccc tat gcg agc gcg aaa gaa atc gct ata gct aaa 249  
Pro Ile Asp Leu Pro Tyr Ala Ser Ala Lys Glu Ile Ala Ile Ala Lys  
55 60 65

atg caa cac ctc ccc aag cta gta aga gac gcg ctc aaa tgc atg gga 297  
Met Gln His Leu Pro Lys Leu Val Arg Asp Ala Leu Lys Cys Met Gly  
70 75 80

ttt gat agg gtg agt caa gaa atc gtt ttt gaa tac gag cct aaa ttg 345  
Phe Asp Arg Val Ser Gln Glu Ile Val Phe Glu Tyr Glu Pro Lys Leu  
85 90 95 100

cta aag cca agc cgc ttg act tat ttt ttt ggc tat ttc caa gat cca 393  
Leu Lys Pro Ser Arg Leu Thr Tyr Phe Phe Gly Tyr Phe Gln Asp Pro  
105 110 115

cga tac ttt gat gct ata tcc cct tta atc aag caa acc ttc act cta 441  
Arg Tyr Phe Asp Ala Ile Ser Pro Leu Ile Lys Gln Thr Phe Thr Leu  
120 125 130

ccc ccc ccc ccc ccg aaa ata ata aga ata ata aaa aag agg aag 489  
Pro Pro Pro Pro Pro Lys Ile Ile Arg Ile Ile Ile Lys Lys Arg Lys  
135 140 145

aat atc agt gca agc ttt ctt tgatttttagc cgctaaaaac agcgtgtttg 540  
Asn Ile Ser Ala Ser Phe Leu  
150 155

tgcatataag aagaggggat t 561

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<211> 155

<212> PRT

<213> Helicobacter pylori

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Val Leu Leu Asp Ile Thr Ser Phe Asp Trp Ser Asp Arg Lys Met Gln  
35 40 45  
Leu Glu Leu Phe Pro Ile Asp Leu Pro Tyr Ala Ser Ala Lys Glu Ile  
50 55 60  
Ala Ile Ala Lys Met Gln His Leu Pro Lys Leu Val Arg Asp Ala Leu  
65 70 75 80  
Lys Cys Met Gly Phe Asp Arg Val Ser Gln Glu Ile Val Phe Glu Tyr  
85 90 95  
Glu Pro Lys Leu Lys Pro Ser Arg Leu Thr Tyr Phe Phe Gly Tyr  
100 105 110  
Phe Gln Asp Pro Arg Tyr Phe Asp Ala Ile Ser Pro Leu Ile Lys Gln  
115 120 125  
Thr Phe Thr Leu Pro Pro Pro Pro Pro Lys Ile Ile Arg Ile Ile Ile  
130 135 140  
Lys Lys Arg Lys Asn Ile Ser Ala Ser Phe Leu  
145 150 155

<210> 319  
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<220>  
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<222> (86)...(1201)

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Met Ser Ile Ile Ile Pro Ile Val Ile  
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Ala Phe Asp Asn His Tyr Ala Met Pro Ala Gly Val Ser Leu Tyr Ser  
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Met Leu Ala Cys Ala Lys Thr Glu His Pro Gln Ser Gln Asn Asp Ser  
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Glu Lys Leu Phe Tyr Lys Ile His Cys Leu Val Asp Asn Leu Ser Leu  
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Glu Asn Gln Ser Lys Leu Lys Glu Thr Leu Ala Pro Phe Ser Ala Phe  
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tcg agc cta gaa ttt tta gac att tca acc ccc aat ctt cac gcc act 352

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Leu	Asn	Ile	Tyr	Ala	Lys	Thr	Arg	Phe	Ser	Lys	Met	Val	Met	Cys	Arg		
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Leu	Phe	Leu	Ala	Ser	Leu	Phe	Pro	Gln	Tyr	Asp	Lys	Ile	Ile	Met	Phe		
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Gln	Lys	Gly	Gln	Cys	Val	Phe	Tyr	Pro	Glu	Gln	Asp	Leu	Leu	Thr	Leu		
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Ala	Cys	Tyr	Gln	Lys	Val	Leu	Ile	Leu	Pro	Tyr	Ile	Tyr	Asn	Thr	His		
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Pro	Phe	Met	Ala	Asn	Gln	Lys	Arg	Phe	Ile	Pro	Asp	Lys	Lys	Glu	Ile		
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Tyr Ala Glu Tyr Ser Val Lys Phe Leu Lys Gln Met Thr Glu Cys Leu  
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Ser Leu Lys Asp Lys Gln Lys Thr Phe Glu Phe Leu Ala Pro Leu Leu  
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Glu Thr Leu Ala Pro Phe Ser Ala Phe Ser Ser Leu Glu Phe Leu Asp  
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Ile Ser Thr Pro Asn Leu His Ala Thr Pro Ile Glu Pro Ser Ala Ile  
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Pro Gln Tyr Asp Lys Ile Ile Met Phe Asp Ala Asp Thr Leu Phe Leu  
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Gly Ala Ala Lys Asp Phe Ala Ser Asp Lys Ser Pro Lys His Phe Gln  
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Tyr Pro Glu Gln Asp Leu Leu Thr Leu Ala Cys Tyr Gln Lys Val Leu		
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Ile Leu Pro Tyr Ile Tyr Asn Thr His Pro Phe Met Ala Asn Gln Lys		
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Arg Phe Ile Pro Asp Lys Lys Glu Ile Val Met Leu His Phe Tyr Phe		
	275	280
Val Gly Lys Pro Trp Val Leu Pro Thr Phe Ser Tyr Ser Lys Glu Trp		
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His Glu Thr Leu Leu Lys Thr Pro Phe Tyr Ala Glu Tyr Ser Val Lys		
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Phe Leu Lys Gln Met Thr Glu Cys Leu Ser Leu Lys Asp Lys Gln Lys		
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 Arg Ala Ser Ile Ala Cys Lys Gln Lys Gly Leu Asn Thr Ile Val Leu  
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 Ser Leu Val Pro Val Arg Arg Ser His Ser Ala Ala Ala Gln Gly Gly  
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Trp	Arg	Thr	Cys	Phe	Thr	Ala	Asp	Ala	Thr	Gly	His	Thr	Met	Leu	Tyr															
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Glu	Lys	Asn	Leu	Arg	Asp	Val	Arg	Asp	Ile	Ala	Met	Thr	Phe	Ala	Gly		
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Ile	Asp	Pro	Ala	Asp	Ser	Lys	Glu	Gln	Thr	Lys	Asp	Asn	Met	Gln	Gly		
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Ile Cys Val Lys Asn Lys Val Leu His Asn Asn Pro Glu Leu Glu Asp	
535 540 545	
gct tac cgc acc aaa aaa atg ctc aaa ctc gcg ctt tgt atc act caa	1737
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Gly Ala Leu Leu Arg Thr Glu Ser Arg Gly Ala His Thr Arg Ile Asp	
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Tyr Pro Lys Arg Asp Asp Glu Lys Trp Leu Asn Arg Thr Leu Ala Ser	
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Trp Pro Ser Ala Glu Gln Asp Met Pro Thr Ile Glu Tyr Glu Glu Leu	
595 600 605 610	
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Cys	Asp	Gln	Gln	Val	Ala	Arg	Met	Phe	Val	Thr	Thr	Ala	Pro	Lys	Ala
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	370					375					380				
Gln	Lys	Gly	Trp	Ile	Pro	Ile	Lys	Pro	Met	Gln	His	Tyr	Ser	Met	Gly
385					390					395					400

Gly Val Arg Thr Asn Pro Lys Gly Glu Thr His Leu Lys Gly Leu Phe  
                                   405                                  410                                  415  
 Cys Ala Gly Glu Ala Ala Cys Trp Asp Leu His Gly Phe Asn Arg Leu  
                                   420                                  425                                  430  
 Gly Gly Asn Ser Val Ser Glu Ala Val Val Ala Gly Met Ile Ile Gly  
                                   435                                  440                                  445  
 Asp Tyr Phe Ala Ser His Cys Leu Glu Ala Gln Ile Glu Ile Asn Thr  
                                   450                                  455                                  460  
 Gln Lys Val Glu Ala Phe Ile Lys Glu Ser Gln Asp Tyr Met His Phe  
                                   465                                  470                                  475                                  480  
 Leu Leu His Asn Glu Gly Lys Glu Asp Val Tyr Glu Ile Arg Glu Arg  
                                   485                                  490                                  495  
 Met Lys Glu Val Met Asp Glu Lys Val Gly Val Phe Arg Glu Gly Lys  
                                   500                                  505                                  510  
 Arg Leu Glu Glu Ala Leu Lys Glu Leu Gln Glu Leu Tyr Ala Arg Ser  
                                   515                                  520                                  525  
 Lys Asn Ile Cys Val Lys Asn Lys Val Leu His Asn Asn Pro Glu Leu  
                                   530                                  535                                  540  
 Glu Asp Ala Tyr Arg Thr Lys Lys Met Leu Lys Leu Ala Leu Cys Ile  
                                   545                                  550                                  555                                  560  
 Thr Gln Gly Ala Leu Leu Arg Thr Glu Ser Arg Gly Ala His Thr Arg  
                                   565                                  570                                  575  
 Ile Asp Tyr Pro Lys Arg Asp Asp Glu Lys Trp Leu Asn Arg Thr Leu  
                                   580                                  585                                  590  
 Ala Ser Trp Pro Ser Ala Glu Gln Asp Met Pro Thr Ile Glu Tyr Glu  
                                   595                                  600                                  605  
 Glu Leu Asp Val Met Lys Met Glu Ile Ser Pro Asp Phe Arg Gly Tyr  
                                   610                                  615                                  620  
 Gly Lys Lys Gly Asn Phe Ile Pro His Pro Lys Lys Glu Glu Arg Asp  
                                   625                                  630                                  635                                  640  
 Ala Glu Ile Leu Lys Thr Ile Leu Glu Leu Glu Lys Leu Gly Lys Asp  
                                   645                                  650                                  655  
 Arg Ile Glu Val Gln His Ala Leu Met Pro Phe Glu Leu Gln Glu Lys  
                                   660                                  665                                  670  
 Tyr Lys Ala Arg Asn Met Arg Leu Glu Asp Glu Glu Val Arg Ala Arg  
                                   675                                  680                                  685  
 Gly Glu His Leu Tyr Ser Phe Asn Val His Glu Leu Leu Asp Gln His  
                                   690                                  695                                  700  
 Asn Ala Asn Leu Lys Gly Glu His His Glu  
 705                                  710

<210> 323  
 <211> 496  
 <212> DNA  
 <213> *Helicobacter pylori*

<220>  
 <221> CDS  
 <222> (77)...(445)

<400> 323  
 atttagttca agagctttta gaagaatttt tgcaaagcgg ggctaaagag attttagaaa 60  
 aggcgcagtt gtttta atg cgt ttg ttt atc gcg cta gtt ttg ttt tgg tgg 112  
                                   Met Arg Leu Phe Ile Ala Leu Val Leu Phe Trp Trp

	1	5	10	
tgg tta agc ttg aac gct aaa gaa gcg gat ttt atc tct gat tta gaa				160
Trp Leu Ser Leu Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu				
	15	20	25	
tac ggg atg gct ctt tat aaa aac cct agg ggt gtt gcg tgc gcg aaa				208
Tyr Gly Met Ala Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys				
	30	35	40	
tgc cat ggc att aaa ggc gaa caa caa gaa atc acc ttt tat tat gaa				256
Cys His Gly Ile Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu				
	45	50	55	60
aaa ggc gag aaa aaa atc ctc tac gcc cct aaa atc aac cat ttg gat				304
Lys Gly Glu Lys Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp				
	65	70	75	
ttt aaa acc ttt aaa gac gcc ttg agt tta ggc aaa ggc atg atg cct				352
Phe Lys Thr Phe Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro				
	80	85	90	
aaa tac aat ctc aat tta gaa gaa atc caa gcg att tat ctt tat atc				400
Lys Tyr Asn Leu Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile				
	95	100	105	
atc tct tta gag cat aaa gaa gag cgt aag gat tct cct aag cct				445
Ile Ser Leu Glu His Lys Glu Glu Arg Lys Asp Ser Pro Lys Pro				
	110	115	120	
taatcaaagc gcttgattta tgctaaaatg gagcggttgca tttttgtttt g				496

<210> 324

<211> 123

<212> PRT

<213> Helicobacter pylori

<400> 324

Met Arg Leu Phe Ile Ala Leu Val Leu Phe Trp Trp Trp Leu Ser Leu				
1	5	10	15	
Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu Tyr Gly Met Ala				
	20	25	30	
Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys Cys His Gly Ile				
	35	40	45	
Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu Lys Gly Glu Lys				
	50	55	60	
Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp Phe Lys Thr Phe				
	65	70	75	80
Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro Lys Tyr Asn Leu				
	85	90	95	
Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile Ile Ser Leu Glu				
	100	105	110	
His Lys Glu Glu Arg Lys Asp Ser Pro Lys Pro				
	115	120		

<210> 325  
 <211> 521  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (72)...(464)

<400> 325  
 gttgcaacaa aaaatagaga gcaggaaaac agacattgtg atccaatcca tggcgaatat 60  
 tctcagcggg a atg aat gag ctt atc cgc tat ggc ttg ata ttt ctc ttt 110  
                   Met Asn Glu Leu Ile Arg Tyr Gly Leu Ile Phe Leu Phe  
                   1                  5                  10

ttt tta aag gcg ttt ggg ctt gat tat ggg ata gat aaa acg cta gaa 158  
 Phe Leu Lys Ala Phe Gly Leu Asp Tyr Gly Ile Asp Lys Thr Leu Glu  
           15                  20                  25

tta aaa aaa gat gaa gtg ttt aaa gcg atc atc aaa gac act tca aat 206  
 Leu Lys Lys Asp Glu Val Phe Lys Ala Ile Ile Lys Asp Thr Ser Asn  
   30                  35                  40                  45

gaa caa acc aaa gaa atc acg ctc tat tgg acg cta tat gca aat aaa 254  
 Glu Gln Thr Lys Glu Ile Thr Leu Tyr Trp Thr Leu Tyr Ala Asn Lys  
                   50                  55                  60

ggt tta gtc atc aac atg cgt ttt aac cat ttc cct tac cag ttt att 302  
 Gly Leu Val Ile Asn Met Arg Phe Asn His Phe Pro Tyr Gln Phe Ile  
                   65                  70                  75

tta tac acc gat cat gcg aga aac acc tat aat ctc aaa gtt ttt gaa 350  
 Leu Tyr Thr Asp His Ala Arg Asn Thr Tyr Asn Leu Lys Val Phe Glu  
           80                  85                  90

gaa aaa ttt tct tct aac agc act ctg tcg ctt gtg ttt aaa gat ttt 398  
 Glu Lys Phe Ser Ser Asn Ser Thr Leu Ser Leu Val Phe Lys Asp Phe  
   95                  100                  105

aaa gaa gat aaa gcc gct tta agg ctt tta gcc ctt atg ccc ctt gtt 446  
 Lys Glu Asp Lys Ala Ala Leu Arg Leu Leu Ala Leu Met Pro Leu Val  
 110                  115                  120                  125

ttt tct cct aaa gag cct taaggaatgt gcatgcaaga aaaacaactt 494  
 Phe Ser Pro Lys Glu Pro  
                   130

aaaaccattc aaaataagat cgcttcc 521

<210> 326  
 <211> 131  
 <212> PRT  
 <213> Helicobacter pylori

<400> 326



<213> Helicobacter pylori

<400> 328

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Met Leu Ser Lys Leu Pro Phe Thr Gly Val Leu Ala Leu Val Leu Lys
 1          5          10          15
Ala Val His Val Ser Leu Ala Glu Asp Lys Ser Lys Phe Thr Ala Cys
          20          25          30
Lys Asn Pro Ala Ser Lys Thr Asp Thr Lys Thr Ile Phe Phe Ile His
          35          40          45
Tyr Pro Leu Met Trp Ser Tyr Gln
 50          55
```

<210> 329

<211> 671

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (66)...(611)

<400> 329

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aatgacttta ggggatattc ttaaagaaaa actctaaaga gtgattttta aagcatgaga 60
atggc atg aga ttt aag ggt gtt gtt gct ttt att tcc cta gct gtc gct 110
  Met Arg Phe Lys Gly Val Val Ala Phe Ile Ser Leu Ala Val Ala
    1          5          10          15

ctt ggc gtt tta gcc tat ttg ttt tta agc gtt aaa aaa gaa atg ccc 158
Leu Gly Val Leu Ala Tyr Leu Phe Leu Ser Val Lys Lys Glu Met Pro
          20          25          30

gct act tct cat gcg atc tct caa aca cat gcg atc tct caa acc aat 206
Ala Thr Ser His Ala Ile Ser Gln Thr His Ala Ile Ser Gln Thr Asn
          35          40          45

gaa ggc ctc tct caa aca gat gca aaa agc cat gac atc gat cta gaa 254
Glu Gly Leu Ser Gln Thr Asp Ala Lys Ser His Asp Ile Asp Leu Glu
          50          55          60

gaa aat agc ccc act gaa acc tct cat aat gaa aaa gcc tcc cat aac 302
Glu Asn Ser Pro Thr Glu Thr Ser His Asn Glu Lys Ala Ser His Asn
          65          70          75

gaa gaa gat cac aat aac gcc ctt tct caa aat ctt gat gcg caa gaa 350
Glu Glu Asp His Asn Asn Ala Leu Ser Gln Asn Leu Asp Ala Gln Glu
          80          85          90          95

tct atc aat tac ccc gtt gtg gaa cat tat tct gaa atc cct ttt gaa 398
Ser Ile Asn Tyr Pro Val Val Glu His Tyr Ser Glu Ile Pro Phe Glu
          100          105          110

gaa aaa aaa agg gaa tat tca aag ctt atc att aag gat tta aag gac 446
Glu Lys Lys Arg Glu Tyr Ser Lys Leu Ile Ile Lys Asp Leu Lys Asp
          115          120          125
```



tat caa tgg tgg tgc tta aaa gaa atc ctc aaa aaa gaa cag att gat 494  
Tyr Gln Trp Trp Cys Leu Lys Glu Ile Leu Lys Lys Glu Gln Ile Asp  
130 135 140

tac gct tac gat aac acc aaa aac caa cct aac ctc atc atc tat tta 542  
Tyr Ala Tyr Asp Asn Thr Lys Asn Gln Pro Asn Leu Ile Ile Tyr Leu  
145 150 155

gat gaa aat aaa aaa gaa cgc ttg ctg gct gat tta gac tat tat aaa 590  
Asp Glu Asn Lys Lys Glu Arg Leu Leu Ala Asp Leu Asp Tyr Tyr Lys  
160 165 170 175

ata cgc tat cat gct gtt ttt taaattcaaa ggataaaaat gtatcaagta 641  
Ile Arg Tyr His Ala Val Phe  
180

gccatttgcg accccatcca tgctaaaggc 671

<210> 330

<211> 182

<212> PRT

<213> Helicobacter pylori

<400> 330

Met Arg Phe Lys Gly Val Val Ala Phe Ile Ser Leu Ala Val Ala Leu  
1 5 10 15  
Gly Val Leu Ala Tyr Leu Phe Leu Ser Val Lys Lys Glu Met Pro Ala  
20 25 30  
Thr Ser His Ala Ile Ser Gln Thr His Ala Ile Ser Gln Thr Asn Glu  
35 40 45  
Gly Leu Ser Gln Thr Asp Ala Lys Ser His Asp Ile Asp Leu Glu Glu  
50 55 60  
Asn Ser Pro Thr Glu Thr Ser His Asn Glu Lys Ala Ser His Asn Glu  
65 70 75 80  
Glu Asp His Asn Asn Ala Leu Ser Gln Asn Leu Asp Ala Gln Glu Ser  
85 90 95  
Ile Asn Tyr Pro Val Val Glu His Tyr Ser Glu Ile Pro Phe Glu Glu  
100 105 110  
Lys Lys Arg Glu Tyr Ser Lys Leu Ile Ile Lys Asp Leu Lys Asp Tyr  
115 120 125  
Gln Trp Trp Cys Leu Lys Glu Ile Leu Lys Lys Glu Gln Ile Asp Tyr  
130 135 140  
Ala Tyr Asp Asn Thr Lys Asn Gln Pro Asn Leu Ile Ile Tyr Leu Asp  
145 150 155 160  
Glu Asn Lys Lys Glu Arg Leu Leu Ala Asp Leu Asp Tyr Tyr Lys Ile  
165 170 175  
Arg Tyr His Ala Val Phe  
180

<210> 331

<211> 341

<212> DNA

<213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (86)...(295)

<400> 331  
 acccacaataa ctaaaaccca ctaacacaat taaccctaac aacacataaa gattgcccaa 60  
 agacgcgcac aacacgctcg caaca atg gtt gca aaa aca aac aca atc ccc 112  
 Met Val Ala Lys Thr Asn Thr Ile Pro  
 1 5  
 ccc atc gta ggg gta tct ttt tta ttc tgg tgg ctt ggc acg aag cta 160  
 Pro Ile Val Gly Val Ser Phe Leu Phe Trp Trp Leu Gly Thr Lys Leu  
 10 15 20 25  
 gaa atg ggc tgg tta gcc ttt tta gcc ttg gcc cat aga atg aat tta 208  
 Glu Met Gly Trp Leu Ala Phe Leu Ala Leu Ala His Arg Met Asn Leu  
 30 35 40  
 ggc att aaa aaa agc gtg aga aaa aaa gct atg aaa aac cct aac cct 256  
 Gly Ile Lys Lys Ser Val Arg Lys Lys Ala Met Lys Asn Pro Asn Pro  
 45 50 55  
 gct cta aaa gtc aaa tac tgg aaa aga ttg ata ttg aaa tagccatata 305  
 Ala Leu Lys Val Lys Tyr Trp Lys Arg Leu Ile Leu Lys  
 60 65 70  
 gtaaagaata gagcataaaa tcccctaataa tcgcca 341

<210> 332  
 <211> 70  
 <212> PRT  
 <213> Helicobacter pylori

<400> 332  
 Met Val Ala Lys Thr Asn Thr Ile Pro Pro Ile Val Gly Val Ser Phe  
 1 5 10 15  
 Leu Phe Trp Trp Leu Gly Thr Lys Leu Glu Met Gly Trp Leu Ala Phe  
 20 25 30  
 Leu Ala Leu Ala His Arg Met Asn Leu Gly Ile Lys Lys Ser Val Arg  
 35 40 45  
 Lys Lys Ala Met Lys Asn Pro Asn Pro Ala Leu Lys Val Lys Tyr Trp  
 50 55 60  
 Lys Arg Leu Ile Leu Lys  
 65 70

<210> 333  
 <211> 2481  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (58)...(2430)

<400> 333

tttttttttt tttttgattt ttatttttta aattttttaga ttaaggagag ttgttgg atg 60  
Met  
1

ttt tta aga gta tac cca aag ctt aga tac gct tta tgt ttc ccc cta 108  
Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro Leu  
5 10 15

ctc gct gag act tgc tat agc gaa gag cgg act tta aat aag gtt acc 156  
Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val Thr  
20 25 30

acc caa gct aaa agg att ttc act tac aac aat gag ttt aaa gta act 204  
Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val Thr  
35 40 45

tct aaa gaa cta gat caa cgc caa agc aat gaa gtc aag gac ttg ttt 252  
Ser Lys Glu Leu Asp Gln Arg Gln Ser Asn Glu Val Lys Asp Leu Phe  
50 55 60 65

agg act aac cct gat gtg aat gtg ggc gga ggg agc gtg atg ggg cag 300  
Arg Thr Asn Pro Asp Val Asn Val Gly Gly Gly Ser Val Met Gly Gln  
70 75 80

aaa atc tat gtg aga ggc gtt gaa gac agg ctt tta agg gtt aca gtg 348  
Lys Ile Tyr Val Arg Gly Val Glu Asp Arg Leu Leu Arg Val Thr Val  
85 90 95

gat ggg gct gca caa aat ggc aat atc tac cac cac caa ggc aac acc 396  
Asp Gly Ala Ala Gln Asn Gly Asn Ile Tyr His His Gln Gly Asn Thr  
100 105 110

gtg att gac cct ggc atg ctc aaa agc gtg gaa gtt acc aaa ggc gcg 444  
Val Ile Asp Pro Gly Met Leu Lys Ser Val Glu Val Thr Lys Gly Ala  
115 120 125

gcg aat gcg agc gcg ggg cca gga gcg att gcg gga gtg att aaa atg 492  
Ala Asn Ala Ser Ala Gly Pro Gly Ala Ile Ala Gly Val Ile Lys Met  
130 135 140 145

gag act aaa gga gcg gct gat ttt atc cct agg ggg aaa aat tat gct 540  
Glu Thr Lys Gly Ala Ala Asp Phe Ile Pro Arg Gly Lys Asn Tyr Ala  
150 155 160

gcc agt ggg gcg gtg agt ttt tat acc aat ttt ggc gat cga gag act 588  
Ala Ser Gly Ala Val Ser Phe Tyr Thr Asn Phe Gly Asp Arg Glu Thr  
165 170 175

ttc aga tgc gct tat caa aac gcg cat ttt gat att atc gct tac tac 636  
Phe Arg Ser Ala Tyr Gln Asn Ala His Phe Asp Ile Ile Ala Tyr Tyr  
180 185 190

acg cac caa aac atc ttc tat tat aga agc ggc gct aca gcg atg aaa 684  
Thr His Gln Asn Ile Phe Tyr Tyr Arg Ser Gly Ala Thr Ala Met Lys

195	200	205	
aac ctt ttc aat ccc	aca caa gcc gat aaa	gag cca gga act cct agc	732
Asn Leu Phe Asn Pro Thr	Gln Ala Asp Lys Glu	Pro Gly Thr Pro Ser	
210	215	220	225
gag caa aac aac gct	ttg att aaa atg aat	ggt tat ttg agc gac aga	780
Glu Gln Asn Asn Ala	Leu Ile Lys Met Asn	Gly Tyr Leu Ser Asp Arg	
230	235	240	
gac acg ctc act ttc	agc tgg aac atg aca	cga gat aac gct aca cgc	828
Asp Thr Leu Thr Phe	Ser Trp Asn Met Thr	Arg Asp Asn Ala Thr Arg	
245	250	255	
cct tta agg agt aac	gct ata ggg tta gcc	tat cct tgt gaa gcc ccc	876
Pro Leu Arg Ser Asn	Ala Ile Gly Leu Ala	Tyr Pro Cys Glu Ala Pro	
260	265	270	
ttt agt cct gat agt	tct caa ggg tgt cct	aat gtg tta gat agt ttc	924
Phe Ser Pro Asp Ser	Ser Gln Gly Cys Pro	Asn Val Leu Asp Ser Phe	
275	280	285	
aca aga tac atg tat	cac tct att aat agt	gcc aac aat ctt tcc tta	972
Thr Arg Tyr Met Tyr	His Ser Ile Asn Ser	Ala Asn Asn Leu Ser Leu	
290	295	300	305
caa tac aaa agg gaa	gcg gga aat tct ttt	ggc gac cca cga tta gat	1020
Gln Tyr Lys Arg Glu	Ala Gly Asn Ser Phe	Gly Asp Pro Arg Leu Asp	
310	315	320	
ttt acc ctt tat aca	agc atc agg aac gct	cag ttt gat ccc cta ttt	1068
Phe Thr Leu Tyr Thr	Ser Ile Arg Asn Ala	Gln Phe Asp Pro Leu Phe	
325	330	335	
gat cct aat ggc gtt	tat gct aaa ttc ccc	act tct tta gcg agc gca	1116
Asp Pro Asn Gly Val	Tyr Ala Lys Phe Pro	Thr Ser Leu Ala Ser Ala	
340	345	350	
tgg gaa aaa gaa aat	tac cca tgc gtt gaa	ggc gct tat tgc acc cca	1164
Trp Glu Lys Glu Asn	Tyr Pro Cys Val Glu	Gly Ala Tyr Cys Thr Pro	
355	360	365	
agc ttt tca gat gtg	gat aaa cca agc tca	cag cct agg aat ttg ttt	1212
Ser Phe Ser Asp Val	Asp Lys Pro Ser Ser	Gln Pro Arg Asn Leu Phe	
370	375	380	385
tta aac aac acc ggc	tta aac ctt aaa gtc	gcg cat gtg att gat gaa	1260
Leu Asn Asn Thr Gly	Leu Asn Leu Lys Val	Ala His Val Ile Asp Glu	
390	395	400	
gcc aca gac agc ctt	ttt gaa tac gga ttc	aac tac caa aat ttg agc	1308
Ala Thr Asp Ser Leu	Phe Glu Tyr Gly Phe	Asn Tyr Gln Asn Leu Ser	
405	410	415	
gtt ttt gac gct cgc	atc cct aaa tca gaa	tta tac agg cct aat caa	1356

Val	Phe	Asp	Ala	Arg	Ile	Pro	Lys	Ser	Glu	Leu	Tyr	Arg	Pro	Asn	Gln		
		420					425					430					
gtt	tat	act	gat	gat	aaa	gga	caa	aaa	caa	atc	gct	tgc	tct	ctt	gtg	1404	
Val	Tyr	Thr	Asp	Asp	Lys	Gly	Gln	Lys	Gln	Ile	Ala	Cys	Ser	Leu	Val		
	435					440					445						
aat	aat	aac	ccc	aat	gac	ccc	act	ctg	tgc	caa	aga	ggg	aaa	gcg	aac	1452	
Asn	Asn	Asn	Pro	Asn	Asp	Pro	Thr	Leu	Cys	Gln	Arg	Gly	Lys	Ala	Asn		
450					455					460					465		
ggg	aat	att	tat	gga	ggc	tac	gtg	caa	gcg	aat	tac	tcg	cct	cat	aaa	1500	
Gly	Asn	Ile	Tyr	Gly	Gly	Tyr	Val	Gln	Ala	Asn	Tyr	Ser	Pro	His	Lys		
				470					475						480		
atc	atc	act	ttt	gga	gcc	ggg	gta	agg	tgg	gac	gct	tac	acg	ctt	tat	1548	
Ile	Ile	Thr	Phe	Gly	Ala	Gly	Val	Arg	Trp	Asp	Ala	Tyr	Thr	Leu	Tyr		
			485					490					495				
gat	aaa	gac	tgg	aac	cac	cgc	tac	act	caa	ggc	ttt	agc	cct	agc	gcg	1596	
Asp	Lys	Asp	Trp	Asn	His	Arg	Tyr	Thr	Gln	Gly	Phe	Ser	Pro	Ser	Ala		
		500					505					510					
gct	ctt	gtg	cta	agc	ccc	att	gag	cct	tta	tct	tta	aaa	atc	act	tat	1644	
Ala	Leu	Val	Leu	Ser	Pro	Ile	Glu	Pro	Leu	Ser	Leu	Lys	Ile	Thr	Tyr		
	515					520					525						
tct	caa	gtt	aca	aga	ggg	gtg	atg	cca	gga	gat	ggc	gtg	tac	atg	cgt	1692	
Ser	Gln	Val	Thr	Arg	Gly	Val	Met	Pro	Gly	Asp	Gly	Val	Tyr	Met	Arg		
530					535				540						545		
caa	aac	gat	tta	cga	tac	gcc	aaa	aac	atc	aag	cct	gaa	gtg	ggc	tct	1740	
Gln	Asn	Asp	Leu	Arg	Tyr	Ala	Lys	Asn	Ile	Lys	Pro	Glu	Val	Gly	Ser		
				550					555					560			
aac	gct	gaa	ttt	aat	att	gat	tat	tca	agc	cag	tat	ttt	agc	ggg	agg	1788	
Asn	Ala	Glu	Phe	Asn	Ile	Asp	Tyr	Ser	Ser	Gln	Tyr	Phe	Ser	Gly	Arg		
			565					570					575				
gct	gcg	gcg	ttt	tat	cag	gct	ttg	gat	aat	ttc	atc	tca	caa	tac	gca	1836	
Ala	Ala	Ala	Phe	Tyr	Gln	Ala	Leu	Asp	Asn	Phe	Ile	Ser	Gln	Tyr	Ala		
		580					585					590					
caa	aat	ttg	att	gta	acc	aat	ttg	agt	caa	gcg	att	cgt	att	tat	ggc	1884	
Gln	Asn	Leu	Ile	Val	Thr	Asn	Leu	Ser	Gln	Ala	Ile	Arg	Ile	Tyr	Gly		
	595					600					605						
tat	gaa	gtg	ggt	ggg	act	ttc	aga	tac	aag	ggc	gtg	agt	ttg	aat	gta	1932	
Tyr	Glu	Val	Gly	Gly	Thr	Phe	Arg	Tyr	Lys	Gly	Val	Ser	Leu	Asn	Val		
610					615					620					625		
ggg	gtc	tcg	cgc	acc	tgg	ccc	acc	act	agg	ggg	tat	tta	atg	gcg	gat	1980	
Gly	Val	Ser	Arg	Thr	Trp	Pro	Thr	Thr	Arg	Gly	Tyr	Leu	Met	Ala	Asp		
				630					635					640			

agc tat gag ctt gcc gca agc acc ggt aat gtt ttt atc atc aaa ttg 2028  
 Ser Tyr Glu Leu Ala Ala Ser Thr Gly Asn Val Phe Ile Ile Lys Leu  
 645 650 655  
 gat tac acc atc ccc aaa aca ggg atc aat ctt gca tgg ctt agc cgc 2076  
 Asp Tyr Thr Ile Pro Lys Thr Gly Ile Asn Leu Ala Trp Leu Ser Arg  
 660 665 670  
 ttt gtt acc ggt tta gat tat tgc ggg ttt gat att tac ttg cct gat 2124  
 Phe Val Thr Gly Leu Asp Tyr Cys Gly Phe Asp Ile Tyr Leu Pro Asp  
 675 680 685  
 tat ggg acg gct gag aaa ccc aaa acc cct acc gat tta gcc aaa tgc 2172  
 Tyr Gly Thr Ala Glu Lys Pro Lys Thr Pro Thr Asp Leu Ala Lys Cys  
 690 695 700 705  
 gga tct caa tta ggg tta gtg cat atg cat aaa ccg ggc tat ggc gtg 2220  
 Gly Ser Gln Leu Gly Leu Val His Met His Lys Pro Gly Tyr Gly Val  
 710 715 720  
 agt aat ttt tat atc aat tgg agt cct aaa acc aaa agc cgc tgg aag 2268  
 Ser Asn Phe Tyr Ile Asn Trp Ser Pro Lys Thr Lys Ser Arg Trp Lys  
 725 730 735  
 ggt ttg ttg ctt tca gcc gtg ttt aat aat gtt ttc aac aaa ttc tat 2316  
 Gly Leu Leu Leu Ser Ala Val Phe Asn Asn Val Phe Asn Lys Phe Tyr  
 740 745 750  
 gtg gat caa aca agc cct tat gtc atg agc ccg gat atg cca ggc act 2364  
 Val Asp Gln Thr Ser Pro Tyr Val Met Ser Pro Asp Met Pro Gly Thr  
 755 760 765  
 gac gct gtt aaa aga gcg atc gct gag cct ggg ttt aac gcg cgt ttt 2412  
 Asp Ala Val Lys Arg Ala Ile Ala Glu Pro Gly Phe Asn Ala Arg Phe  
 770 775 780 785  
 gaa gtg gct tac aaa tgg tagttaatgg agctttaagc gttgcgcatg 2460  
 Glu Val Ala Tyr Lys Trp  
 790  
 cgtgatagca acggctatcg c 2481

<210> 334

<211> 791

<212> PRT

<213> *Helicobacter pylori*

<400> 334

Met Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro  
 1 5 10 15  
 Leu Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val  
 20 25 30  
 Thr Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val  
 35 40 45  
 Thr Ser Lys Glu Leu Asp Gln Arg Gln Ser Asn Glu Val Lys Asp Leu

50						55					60				
Phe	Arg	Thr	Asn	Pro	Asp	Val	Asn	Val	Gly	Gly	Gly	Ser	Val	Met	Gly
65					70					75					80
Gln	Lys	Ile	Tyr	Val	Arg	Gly	Val	Glu	Asp	Arg	Leu	Leu	Arg	Val	Thr
				85					90					95	
Val	Asp	Gly	Ala	Ala	Gln	Asn	Gly	Asn	Ile	Tyr	His	His	Gln	Gly	Asn
			100					105					110		
Thr	Val	Ile	Asp	Pro	Gly	Met	Leu	Lys	Ser	Val	Glu	Val	Thr	Lys	Gly
			115				120						125		
Ala	Ala	Asn	Ala	Ser	Ala	Gly	Pro	Gly	Ala	Ile	Ala	Gly	Val	Ile	Lys
			130			135					140				
Met	Glu	Thr	Lys	Gly	Ala	Ala	Asp	Phe	Ile	Pro	Arg	Gly	Lys	Asn	Tyr
145					150					155					160
Ala	Ala	Ser	Gly	Ala	Val	Ser	Phe	Tyr	Thr	Asn	Phe	Gly	Asp	Arg	Glu
			165						170					175	
Thr	Phe	Arg	Ser	Ala	Tyr	Gln	Asn	Ala	His	Phe	Asp	Ile	Ile	Ala	Tyr
			180				185						190		
Tyr	Thr	His	Gln	Asn	Ile	Phe	Tyr	Tyr	Arg	Ser	Gly	Ala	Thr	Ala	Met
			195				200					205			
Lys	Asn	Leu	Phe	Asn	Pro	Thr	Gln	Ala	Asp	Lys	Glu	Pro	Gly	Thr	Pro
			210			215					220				
Ser	Glu	Gln	Asn	Asn	Ala	Leu	Ile	Lys	Met	Asn	Gly	Tyr	Leu	Ser	Asp
225					230					235					240
Arg	Asp	Thr	Leu	Thr	Phe	Ser	Trp	Asn	Met	Thr	Arg	Asp	Asn	Ala	Thr
			245						250					255	
Arg	Pro	Leu	Arg	Ser	Asn	Ala	Ile	Gly	Leu	Ala	Tyr	Pro	Cys	Glu	Ala
			260					265					270		
Pro	Phe	Ser	Pro	Asp	Ser	Ser	Gln	Gly	Cys	Pro	Asn	Val	Leu	Asp	Ser
			275				280					285			
Phe	Thr	Arg	Tyr	Met	Tyr	His	Ser	Ile	Asn	Ser	Ala	Asn	Asn	Leu	Ser
			290			295					300				
Leu	Gln	Tyr	Lys	Arg	Glu	Ala	Gly	Asn	Ser	Phe	Gly	Asp	Pro	Arg	Leu
305					310					315					320
Asp	Phe	Thr	Leu	Tyr	Thr	Ser	Ile	Arg	Asn	Ala	Gln	Phe	Asp	Pro	Leu
			325						330					335	
Phe	Asp	Pro	Asn	Gly	Val	Tyr	Ala	Lys	Phe	Pro	Thr	Ser	Leu	Ala	Ser
			340					345					350		
Ala	Trp	Glu	Lys	Glu	Asn	Tyr	Pro	Cys	Val	Glu	Gly	Ala	Tyr	Cys	Thr
			355				360					365			
Pro	Ser	Phe	Ser	Asp	Val	Asp	Lys	Pro	Ser	Ser	Gln	Pro	Arg	Asn	Leu
			370			375					380				
Phe	Leu	Asn	Asn	Thr	Gly	Leu	Asn	Leu	Lys	Val	Ala	His	Val	Ile	Asp
385					390					395					400
Glu	Ala	Thr	Asp	Ser	Leu	Phe	Glu	Tyr	Gly	Phe	Asn	Tyr	Gln	Asn	Leu
			405						410					415	
Ser	Val	Phe	Asp	Ala	Arg	Ile	Pro	Lys	Ser	Glu	Leu	Tyr	Arg	Pro	Asn
			420					425					430		
Gln	Val	Tyr	Thr	Asp	Asp	Lys	Gly	Gln	Lys	Gln	Ile	Ala	Cys	Ser	Leu
			435				440					445			
Val	Asn	Asn	Asn	Pro	Asn	Asp	Pro	Thr	Leu	Cys	Gln	Arg	Gly	Lys	Ala
			450			455					460				
Asn	Gly	Asn	Ile	Tyr	Gly	Gly	Tyr	Val	Gln	Ala	Asn	Tyr	Ser	Pro	His
465					470					475					480
Lys	Ile	Ile	Thr	Phe	Gly	Ala	Gly	Val	Arg	Trp	Asp	Ala	Tyr	Thr	Leu
			485						490					495	

Tyr Asp Lys Asp Trp Asn His Arg Tyr Thr Gln Gly Phe Ser Pro Ser  
500 505 510  
Ala Ala Leu Val Leu Ser Pro Ile Glu Pro Leu Ser Leu Lys Ile Thr  
515 520 525  
Tyr Ser Gln Val Thr Arg Gly Val Met Pro Gly Asp Gly Val Tyr Met  
530 535 540  
Arg Gln Asn Asp Leu Arg Tyr Ala Lys Asn Ile Lys Pro Glu Val Gly  
545 550 555 560  
Ser Asn Ala Glu Phe Asn Ile Asp Tyr Ser Ser Gln Tyr Phe Ser Gly  
565 570 575  
Arg Ala Ala Ala Phe Tyr Gln Ala Leu Asp Asn Phe Ile Ser Gln Tyr  
580 585 590  
Ala Gln Asn Leu Ile Val Thr Asn Leu Ser Gln Ala Ile Arg Ile Tyr  
595 600 605  
Gly Tyr Glu Val Gly Gly Thr Phe Arg Tyr Lys Gly Val Ser Leu Asn  
610 615 620  
Val Gly Val Ser Arg Thr Trp Pro Thr Thr Arg Gly Tyr Leu Met Ala  
625 630 635 640  
Asp Ser Tyr Glu Leu Ala Ala Ser Thr Gly Asn Val Phe Ile Ile Lys  
645 650 655  
Leu Asp Tyr Thr Ile Pro Lys Thr Gly Ile Asn Leu Ala Trp Leu Ser  
660 665 670  
Arg Phe Val Thr Gly Leu Asp Tyr Cys Gly Phe Asp Ile Tyr Leu Pro  
675 680 685  
Asp Tyr Gly Thr Ala Glu Lys Pro Lys Thr Pro Thr Asp Leu Ala Lys  
690 695 700  
Cys Gly Ser Gln Leu Gly Leu Val His Met His Lys Pro Gly Tyr Gly  
705 710 715 720  
Val Ser Asn Phe Tyr Ile Asn Trp Ser Pro Lys Thr Lys Ser Arg Trp  
725 730 735  
Lys Gly Leu Leu Ser Ala Val Phe Asn Asn Val Phe Asn Lys Phe  
740 745 750  
Tyr Val Asp Gln Thr Ser Pro Tyr Val Met Ser Pro Asp Met Pro Gly  
755 760 765  
Thr Asp Ala Val Lys Arg Ala Ile Ala Glu Pro Gly Phe Asn Ala Arg  
770 775 780  
Phe Glu Val Ala Tyr Lys Trp  
785 790

<210> 335  
<211> 477  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (120)...(428)

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gtcggtcggg taatgttcaa attcacaaat gagtctgaag acaaagaagt cttgatctag 60  
aagccgaaat ttcataccg cacttagaat tgcgtcaaaa acaaattgat gcgctgttg 119  
gtg cac gat att acc aag cta tgt tac acc aaa cca cta ggg tgt gtt 167  
Val His Asp Ile Thr Lys Leu Cys Tyr Thr Lys Pro Leu Gly Cys Val  
1 5 10 15



gtg ctg ttc agc aag gat act gat ctt gtg cct gtg tta gaa tcc gct 215  
Val Leu Phe Ser Lys Asp Thr Asp Leu Val Pro Val Leu Glu Ser Ala  
20 25 30

tgg gag aaa ggc ttt gaa gtc ttc att gct aac att caa gaa tgc ccc 263  
Trp Glu Lys Gly Phe Glu Val Phe Ile Ala Asn Ile Gln Glu Cys Pro  
35 40 45

aat tct gtc cct tca gac ttg aag aag tct tgc aat gtg agg gaa cgc 311  
Asn Ser Val Pro Ser Asp Leu Lys Lys Ser Cys Asn Val Arg Glu Arg  
50 55 60

agt gtc gct gaa att gta gat aac ttg ccc aaa aat cag cac act ccc 359  
Ser Val Ala Glu Ile Val Asp Asn Leu Pro Lys Asn Gln His Thr Pro  
65 70 75 80

aag aaa aag aac ttt tcc acc aac gag cct ttt aac aac cca ttt aaa 407  
Lys Lys Lys Asn Phe Ser Thr Asn Glu Pro Phe Asn Asn Pro Phe Lys  
85 90 95

gac caa ctc ttt aag aag aac taacacgatc cccacaccaa ggggacaaaa 458  
Asp Gln Leu Phe Lys Lys Asn  
100

aagcacccat tttaaaagg 477

<210> 336

<211> 103

<212> PRT

<213> Helicobacter pylori

<400> 336

Val His Asp Ile Thr Lys Leu Cys Tyr Thr Lys Pro Leu Gly Cys Val  
1 5 10 15  
Val Leu Phe Ser Lys Asp Thr Asp Leu Val Pro Val Leu Glu Ser Ala  
20 25 30  
Trp Glu Lys Gly Phe Glu Val Phe Ile Ala Asn Ile Gln Glu Cys Pro  
35 40 45  
Asn Ser Val Pro Ser Asp Leu Lys Lys Ser Cys Asn Val Arg Glu Arg  
50 55 60  
Ser Val Ala Glu Ile Val Asp Asn Leu Pro Lys Asn Gln His Thr Pro  
65 70 75 80  
Lys Lys Lys Asn Phe Ser Thr Asn Glu Pro Phe Asn Asn Pro Phe Lys  
85 90 95  
Asp Gln Leu Phe Lys Lys Asn  
100

<210> 337

<211> 685

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS  
 <222> (220)...(624)

<221> misc\_feature  
 <222> 121  
 <223> n = A,T,C or G

<400> 337  
 tcttttgaaa ttgcctgatg tggaaaaaga aatgcccaaa gagacgactc aaaaaagctt 60  
 gttttcgcac aaacactttg tttttggggc ttggggatct ttttttatgt ggggggagaa 120  
 ntggcgattg gctcattctt ggtgctaagc tttgaaaagc ttttgaattt agactctcaa 180  
 tcaagcgcgc attacttggg gtattattgg ggagcgcg atg gtg ggc cgt ttc 234  
 Met Val Gly Arg Phe  
 1 5

tta ggc agt gtg ttg atg aat aaa att gcc cct aat aaa tac ttg gct 282  
 Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro Asn Lys Tyr Leu Ala  
 10 15 20

ttc aac gcc tta agc tct att gtt ctc atc gct tta gcc att atc att 330  
 Phe Asn Ala Leu Ser Ser Ile Val Leu Ile Ala Leu Ala Ile Ile Ile  
 25 30 35

gga ggc aag atc gct tta ttc gct ctg act ttt gtg ggc ttt ttc aac 378  
 Gly Gly Lys Ile Ala Leu Phe Ala Leu Thr Phe Val Gly Phe Phe Asn  
 40 45 50

tct atc atg ttc cct acc atc ttt tct ttg gct acg ctc aat tta ggg 426  
 Ser Ile Met Phe Pro Thr Ile Phe Ser Leu Ala Thr Leu Asn Leu Gly  
 55 60 65

cat ctc act tct aaa gct tct ggg gtg att agc atg gcg att gtg gga 474  
 His Leu Thr Ser Lys Ala Ser Gly Val Ile Ser Met Ala Ile Val Gly  
 70 75 80 85

ggg gcg tta atc ccc ccc att caa ggt gcg gtt aca gac atg cta aca 522  
 Gly Ala Leu Ile Pro Pro Ile Gln Gly Ala Val Thr Asp Met Leu Thr  
 90 95 100

gca acc gaa tca aat ttg ctc tac gct tat ggt gtg ccg ttg ttg tgc 570  
 Ala Thr Glu Ser Asn Leu Leu Tyr Ala Tyr Gly Val Pro Leu Leu Cys  
 105 110 115

tat ttt tat att ctc ttc ttt gcg ctt aaa ggg tat aag caa gaa gaa 618  
 Tyr Phe Tyr Ile Leu Phe Phe Ala Leu Lys Gly Tyr Lys Gln Glu Glu  
 120 125 130

aac tcc taaaaaagg gggggtttct ttcttctttc ctttctttta tcttgtttta 674  
 Asn Ser  
 135

aaaatcagta a 685

<210> 338  
 <211> 135

<212> PRT  
 <213> Helicobacter pylori

<400> 338  
 Met Val Gly Arg Phe Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro  
 1 5 10 15  
 Asn Lys Tyr Leu Ala Phe Asn Ala Leu Ser Ser Ile Val Leu Ile Ala  
 20 25 30  
 Leu Ala Ile Ile Ile Gly Gly Lys Ile Ala Leu Phe Ala Leu Thr Phe  
 35 40 45  
 Val Gly Phe Phe Asn Ser Ile Met Phe Pro Thr Ile Phe Ser Leu Ala  
 50 55 60  
 Thr Leu Asn Leu Gly His Leu Thr Ser Lys Ala Ser Gly Val Ile Ser  
 65 70 75 80  
 Met Ala Ile Val Gly Gly Ala Leu Ile Pro Pro Ile Gln Gly Ala Val  
 85 90 95  
 Thr Asp Met Leu Thr Ala Thr Glu Ser Asn Leu Leu Tyr Ala Tyr Gly  
 100 105 110  
 Val Pro Leu Leu Cys Tyr Phe Tyr Ile Leu Phe Phe Ala Leu Lys Gly  
 115 120 125  
 Tyr Lys Gln Glu Glu Asn Ser  
 130 135

<210> 339  
 <211> 809  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (58)...(765)

<400> 339  
 accgatcact aaaaccaatg taacttaccg ctcttttacag cgtaagtgag aaaagga atg 60  
 Met  
 1  
 cat ttg aat acg gat ttt agc cat atc acc gat ata gag ggc atg cgt 108  
 His Leu Asn Thr Asp Phe Ser His Ile Thr Asp Ile Glu Gly Met Arg  
 5 10 15  
 ttt atc aat gaa gaa gac gct ttg aac aaa ttg att aat gaa atc cac 156  
 Phe Ile Asn Glu Glu Asp Ala Leu Asn Lys Leu Ile Asn Glu Ile His  
 20 25 30  
 acg cgc cac att gat tta aaa gat tcc atc atg ctc gct ttg agt ttt 204  
 Thr Arg His Ile Asp Leu Lys Asp Ser Ile Met Leu Ala Leu Ser Phe  
 35 40 45  
 aac gct ctg tat tta gct cac gct tta gcg caa aaa ttt gga gcg act 252  
 Asn Ala Leu Tyr Leu Ala His Ala Leu Ala Gln Lys Phe Gly Ala Thr  
 50 55 60 65  
 tat gat ata ctt ttt tta gaa cct atc cta gcc cct tta aac tca aaa 300

Tyr	Asp	Ile	Leu	Phe	Leu	Glu	Pro	Ile	Leu	Ala	Pro	Leu	Asn	Ser	Lys	
				70					75					80		
tgc	gag	atc	gct	tta	gtg	agt	gag	agc	atg	gat	ata	gtg	atg	aat	gaa	348
Cys	Glu	Ile	Ala	Leu	Val	Ser	Glu	Ser	Met	Asp	Ile	Val	Met	Asn	Glu	
			85					90					95			
agt	ttg	atc	aat	tcc	ttt	gac	atc	act	tta	gac	tat	gtt	tat	ggg	gaa	396
Ser	Leu	Ile	Asn	Ser	Phe	Asp	Ile	Thr	Leu	Asp	Tyr	Val	Tyr	Gly	Glu	
		100					105					110				
gcc	aag	cga	gct	tat	gaa	gaa	gac	att	ttg	tct	cac	atc	tat	cag	tat	444
Ala	Lys	Arg	Ala	Tyr	Glu	Glu	Asp	Ile	Leu	Ser	His	Ile	Tyr	Gln	Tyr	
	115					120					125					
cgc	aaa	ggc	aat	gcg	atc	aaa	agc	tta	aaa	gat	aaa	aat	att	ttt	atc	492
Arg	Lys	Gly	Asn	Ala	Ile	Lys	Ser	Leu	Lys	Asp	Lys	Asn	Ile	Phe	Ile	
130					135					140					145	
gta	gat	agg	ggg	att	gaa	acc	ggg	ttt	aga	gca	ggg	tta	ggc	gtg	caa	540
Val	Asp	Arg	Gly	Ile	Glu	Thr	Gly	Phe	Arg	Ala	Gly	Leu	Gly	Val	Gln	
				150					155					160		
act	tgc	ttg	aaa	aaa	gaa	tgc	caa	gac	att	tat	att	tta	acc	ccc	att	588
Thr	Cys	Leu	Lys	Lys	Glu	Cys	Gln	Asp	Ile	Tyr	Ile	Leu	Thr	Pro	Ile	
			165					170					175			
gtc	gcg	caa	aat	gtc	gct	caa	ggc	tta	gaa	agt	ttg	tgc	gat	ggg	gtg	636
Val	Ala	Gln	Asn	Val	Ala	Gln	Gly	Leu	Glu	Ser	Leu	Cys	Asp	Gly	Val	
		180					185					190				
att	agt	gtg	tat	cgc	cct	gaa	tgt	ttt	gtc	tct	gtg	gag	cat	cat	tat	684
Ile	Ser	Val	Tyr	Arg	Pro	Glu	Cys	Phe	Val	Ser	Val	Glu	His	His	Tyr	
		195				200					205					
aaa	gaa	ctc	aag	cga	tta	agc	aat	gaa	gaa	gtt	gaa	aaa	tac	ttg	ggc	732
Lys	Glu	Leu	Lys	Arg	Leu	Ser	Asn	Glu	Glu	Val	Glu	Lys	Tyr	Leu	Gly	
210					215					220					225	
gct	aac	aac	atg	cct	aat	tta	aaa	aag	gaa	cat	taa	aat	atgga	ttttat	cacc	785
Ala	Asn	Asn	Met	Pro	Asn	Leu	Lys	Lys	Glu	His						
				230					235							
atcaattcta gtaacaaaac cgaa																809
<210> 340																
<211> 236																
<212> PRT																
<213> Helicobacter pylori																
<400> 340																
Met	His	Leu	Asn	Thr	Asp	Phe	Ser	His	Ile	Thr	Asp	Ile	Glu	Gly	Met	
1				5					10					15		
Arg	Phe	Ile	Asn	Glu	Glu	Asp	Ala	Leu	Asn	Lys	Leu	Ile	Asn	Glu	Ile	
			20					25					30			

His	Thr	Arg	His	Ile	Asp	Leu	Lys	Asp	Ser	Ile	Met	Leu	Ala	Leu	Ser
		35					40					45			
Phe	Asn	Ala	Leu	Tyr	Leu	Ala	His	Ala	Leu	Ala	Gln	Lys	Phe	Gly	Ala
	50					55					60				
Thr	Tyr	Asp	Ile	Leu	Phe	Leu	Glu	Pro	Ile	Leu	Ala	Pro	Leu	Asn	Ser
65					70					75				80	
Lys	Cys	Glu	Ile	Ala	Leu	Val	Ser	Glu	Ser	Met	Asp	Ile	Val	Met	Asn
				85					90					95	
Glu	Ser	Leu	Ile	Asn	Ser	Phe	Asp	Ile	Thr	Leu	Asp	Tyr	Val	Tyr	Gly
			100					105					110		
Glu	Ala	Lys	Arg	Ala	Tyr	Glu	Glu	Asp	Ile	Leu	Ser	His	Ile	Tyr	Gln
		115						120				125			
Tyr	Arg	Lys	Gly	Asn	Ala	Ile	Lys	Ser	Leu	Lys	Asp	Lys	Asn	Ile	Phe
	130					135					140				
Ile	Val	Asp	Arg	Gly	Ile	Glu	Thr	Gly	Phe	Arg	Ala	Gly	Leu	Gly	Val
145					150					155					160
Gln	Thr	Cys	Leu	Lys	Lys	Glu	Cys	Gln	Asp	Ile	Tyr	Ile	Leu	Thr	Pro
				165					170						175
Ile	Val	Ala	Gln	Asn	Val	Ala	Gln	Gly	Leu	Glu	Ser	Leu	Cys	Asp	Gly
			180					185					190		
Val	Ile	Ser	Val	Tyr	Arg	Pro	Glu	Cys	Phe	Val	Ser	Val	Glu	His	His
		195					200					205			
Tyr	Lys	Glu	Leu	Lys	Arg	Leu	Ser	Asn	Glu	Glu	Val	Glu	Lys	Tyr	Leu
	210					215					220				
Gly	Ala	Asn	Asn	Met	Pro	Asn	Leu	Lys	Lys	Glu	His				
225					230					235					

<210> 341

<211> 325

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (70)...(285)

<400> 341

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ggagcgtta atg gca aga gat gat gtt ata gaa gtg gat ggg aaa gtg att 111

Met Ala Arg Asp Asp Val Ile Glu Val Asp Gly Lys Val Ile  
1 5 10

gag gcg ttg cct aac gct act ttt aag gtg gag tta gac aat aag cat 159  
Glu Ala Leu Pro Asn Ala Thr Phe Lys Val Glu Leu Asp Asn Lys His  
15 20 25 30

gtg gtg ttg tgc cgt att tct gga aag atg cgc atg cac tat att agg 207  
Val Val Leu Cys Arg Ile Ser Gly Lys Met Arg Met His Tyr Ile Arg  
35 40 45

att gct tta ggc gat agg gtt aag cta gag ctt acg ccc tat agc tta 255  
Ile Ala Leu Gly Asp Arg Val Lys Leu Glu Leu Thr Pro Tyr Ser Leu  
50 55 60





ttt tgg aat tgc gcg att aaa aag ggc tat tct ggg gtg gta act ttc	249
Phe Trp Asn Cys Ala Ile Lys Lys Gly Tyr Ser Gly Val Val Thr Phe	
55 60 65	
act aaa aaa gag cct tta agc gtg agc tat ggt att aat atg gaa gag	297
Thr Lys Lys Glu Pro Leu Ser Val Ser Tyr Gly Ile Asn Met Glu Glu	
70 75 80	
cat gac aaa gaa ggg cgc gta ata act tgc gaa ttt gag tcg ttt tat	345
His Asp Lys Glu Gly Arg Val Ile Thr Cys Glu Phe Glu Ser Phe Tyr	
85 90 95 100	
ttg gtg aat gtt tat acc cct aat tcc caa caa gcc cta tcc agg ctt	393
Leu Val Asn Val Tyr Thr Pro Asn Ser Gln Gln Ala Leu Ser Arg Leu	
105 110 115	
agt tat cgc atg agt tgg gaa gtg gag ttt aag aaa ttt tta aaa gct	441
Ser Tyr Arg Met Ser Trp Glu Val Glu Phe Lys Lys Phe Leu Lys Ala	
120 125 130	
tta gag ttg aaa aaa ccg gtc att gtg tgt ggg gat ttg aat gtg gct	489
Leu Glu Leu Lys Lys Pro Val Ile Val Cys Gly Asp Leu Asn Val Ala	
135 140 145	
cac aat gaa att gat tta gaa aac ccc aaa acc aac cga aaa aat gcc	537
His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn Arg Lys Asn Ala	
150 155 160	
ggc ttt agc gat gaa gag aga gaa aaa ttc agc gag ctt ttg aac gcc	585
Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu Leu Leu Asn Ala	
165 170 175 180	
ggg ttt att gac act ttc cgt tat ttt tac cct aac aaa gaa aag gct	633
Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn Lys Glu Lys Ala	
185 190 195	
tac acc tgg tgg agt tac atg caa caa gca agg gat aaa aac att ggt	681
Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp Lys Asn Ile Gly	
200 205 210	
tgg cgc att gat tat ttt tta tgc tct aac cct tta aaa acg cgc tta	729
Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu Lys Thr Arg Leu	
215 220 225	
aaa gac gct tta atc tat aaa gat att tta ggg agc gat cat tgc ccg	777
Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser Asp His Cys Pro	
230 235 240	
gta ggg ttg gaa tta gtt taaaggtaga aagtgtgcga aataaagaca	825
Val Gly Leu Glu Leu Val	
245 250	
gaaaaaagcc ttacaa	841
<210> 346	



<211> 250  
 <212> PRT  
 <213> Helicobacter pylori

<400> 346  
 Met Lys Leu Ile Ser Trp Asn Val Asn Gly Leu Arg Ala Cys Met Thr  
 1 5 10 15  
 Lys Gly Phe Met Asp Phe Phe Asn Ser Val Asp Ala Asp Val Phe Cys  
 20 25 30  
 Ile Gln Glu Ser Lys Met Gln Gln Glu Gln Asn Thr Phe Glu Phe Lys  
 35 40 45  
 Gly Tyr Phe Asp Phe Trp Asn Cys Ala Ile Lys Lys Gly Tyr Ser Gly  
 50 55 60  
 Val Val Thr Phe Thr Lys Glu Pro Leu Ser Val Ser Tyr Gly Ile  
 65 70 75 80  
 Asn Met Glu Glu His Asp Lys Glu Gly Arg Val Ile Thr Cys Glu Phe  
 85 90 95  
 Glu Ser Phe Tyr Leu Val Asn Val Tyr Thr Pro Asn Ser Gln Gln Ala  
 100 105 110  
 Leu Ser Arg Leu Ser Tyr Arg Met Ser Trp Glu Val Glu Phe Lys Lys  
 115 120 125  
 Phe Leu Lys Ala Leu Glu Leu Lys Lys Pro Val Ile Val Cys Gly Asp  
 130 135 140  
 Leu Asn Val Ala His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn  
 145 150 155 160  
 Arg Lys Asn Ala Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu  
 165 170 175  
 Leu Leu Asn Ala Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn  
 180 185 190  
 Lys Glu Lys Ala Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp  
 195 200 205  
 Lys Asn Ile Gly Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu  
 210 215 220  
 Lys Thr Arg Leu Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser  
 225 230 235 240  
 Asp His Cys Pro Val Gly Leu Glu Leu Val  
 245 250

<210> 347  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 c atg agg gct tta ctt ttt ttt att ttg tta ctt tgg ttc aag ggt tgt 109  
 Met Arg Ala Leu Leu Phe Phe Ile Leu Leu Leu Trp Phe Lys Gly Cys  
 1 5 10 15  
 ggg tat aag cct att gca gct tac gct caa aac gct tta ggc gat agc 157

Gly Tyr Lys Pro Ile Ala Ala Tyr Ala Gln Asn Ala Leu Gly Asp Ser	
20 25 30	
gta tac gtg aaa ctc att gtg aat ttg cct aac cct gaa aac tct gta	205
Val Tyr Val Lys Leu Ile Val Asn Leu Pro Asn Pro Glu Asn Ser Val	
35 40 45	
gag ttt aag gat ttg atg aat cgt tta gtc gtg caa cgc ttc caa agc	253
Glu Phe Lys Asp Leu Met Asn Arg Leu Val Val Gln Arg Phe Gln Ser	
50 55 60	
cgc tta gcg agt gaa aag gat gcg gat tct atc att att ata gaa atc	301
Arg Leu Ala Ser Glu Lys Asp Ala Asp Ser Ile Ile Ile Ile Glu Ile	
65 70 75 80	
acg aat gta acc gat acg agt atc acg caa aat aaa gaa ggc ttc acg	349
Thr Asn Val Thr Asp Thr Ser Ile Thr Gln Asn Lys Glu Gly Phe Thr	
85 90 95	
act ttc tat cgc gca acc gtg tct gtg aat tac acc tac gat aat aaa	397
Thr Phe Tyr Arg Ala Thr Val Ser Val Asn Tyr Thr Tyr Asp Asn Lys	
100 105 110	
aga ggc aca caa aag act ttt caa gat agc ggg tat tac aat tac gct	445
Arg Gly Thr Gln Lys Thr Phe Gln Asp Ser Gly Tyr Tyr Asn Tyr Ala	
115 120 125	
gtg aat ttg caa gac ccc ctt aat acc tac cag aac cgc tat tat gct	493
Val Asn Leu Gln Asp Pro Leu Asn Thr Tyr Gln Asn Arg Tyr Tyr Ala	
130 135 140	
atc aat cag gct gtg gaa cag act ttg act aaa ttt gtg gct caa atc	541
Ile Asn Gln Ala Val Glu Gln Thr Leu Thr Lys Phe Val Ala Gln Ile	
145 150 155 160	
gct tat gag ggg aaa ttc aat aat gaa aaa tagccctttg aatggattga	591
Ala Tyr Glu Gly Lys Phe Asn Asn Glu Lys	
165 170	
atggactaaa ggcgttttta gaaacaa	618

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<211> 170

<212> PRT

<213> Helicobacter pylori

<400> 348

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20 25 30	
Val Tyr Val Lys Leu Ile Val Asn Leu Pro Asn Pro Glu Asn Ser Val	
35 40 45	
Glu Phe Lys Asp Leu Met Asn Arg Leu Val Val Gln Arg Phe Gln Ser	
50 55 60	

Arg	Leu	Ala	Ser	Glu	Lys	Asp	Ala	Asp	Ser	Ile	Ile	Ile	Ile	Glu	Ile	65	70	75	80
Thr	Asn	Val	Thr	Asp	Thr	Ser	Ile	Thr	Gln	Asn	Lys	Glu	Gly	Phe	Thr	85	90	95	
Thr	Phe	Tyr	Arg	Ala	Thr	Val	Ser	Val	Asn	Tyr	Thr	Tyr	Asp	Asn	Lys	100	105	110	
Arg	Gly	Thr	Gln	Lys	Thr	Phe	Gln	Asp	Ser	Gly	Tyr	Tyr	Asn	Tyr	Ala	115	120	125	
Val	Asn	Leu	Gln	Asp	Pro	Leu	Asn	Thr	Tyr	Gln	Asn	Arg	Tyr	Tyr	Ala	130	135	140	
Ile	Asn	Gln	Ala	Val	Glu	Gln	Thr	Leu	Thr	Lys	Phe	Val	Ala	Gln	Ile	145	150	155	160
Ala	Tyr	Glu	Gly	Lys	Phe	Asn	Asn	Glu	Lys							165	170		

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 <222> (61)...(1224)

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 atg act aca gac aga aat ttg ttt ttt tgc gct tcg cta ttg att ttt 108  
 Met Thr Thr Asp Arg Asn Leu Phe Phe Cys Ala Ser Leu Leu Ile Phe  
 1 5 10 15

ttg ggg gta ttg atg agc tat tcg ctc tca act tac acc aca gtg gtg 156  
 Leu Gly Val Leu Met Ser Tyr Ser Leu Ser Thr Tyr Thr Thr Val Val  
 20 25 30

ctg tat cat tat ggg gag ttc cat ttt ttc ata cgc cag ctt gtg agc 204  
 Leu Tyr His Tyr Gly Glu Phe His Phe Phe Ile Arg Gln Leu Val Ser  
 35 40 45

gcg atc ata ggg att gtt atc atg tgg ggg ttg tct agg gtt gat cct 252  
 Ala Ile Ile Gly Ile Val Ile Met Trp Gly Leu Ser Arg Val Asp Pro  
 50 55 60

agc aag tgg ttt agc cgt ttg ggg ttt ttt ctt ctt ttt gtc cca cca 300  
 Ser Lys Trp Phe Ser Arg Leu Gly Phe Phe Leu Leu Phe Val Pro Pro  
 65 70 75 80

tta ctc att att ggc atg ttt ttt ttg cca gaa agc ctt tct agc agt 348  
 Leu Leu Ile Ile Gly Met Phe Phe Leu Pro Glu Ser Leu Ser Ser Ser  
 85 90 95

gct ggg ggg gcg aag cga tgg att cgt ttg ggg ttt ttt tct cta gcg 396  
 Ala Gly Gly Ala Lys Arg Trp Ile Arg Leu Gly Phe Phe Ser Leu Ala  
 100 105 110

cct ttg gag ttt ttg aag att ggt ttc acc ttt ttt ctt gcg tgg agt	444
Pro Leu Glu Phe Leu Lys Ile Gly Phe Thr Phe Phe Leu Ala Trp Ser	
115 120 125	
ttg tct cgc act ttt gtg gca aaa gaa aag gct aat gtt aaa gaa gaa	492
Leu Ser Arg Thr Phe Val Ala Lys Glu Lys Ala Asn Val Lys Glu Glu	
130 135 140	
ctc atc act ttt gtg cct tat tca gtg gtg ttt gta gcc tta gcg att	540
Leu Ile Thr Phe Val Pro Tyr Ser Val Val Phe Val Ala Leu Ala Ile	
145 150 155 160	
ggg gtg ggg gtt ttg caa aac gat ttg ggg cag att gtt ctt ttg ggg	588
Gly Val Gly Val Leu Gln Asn Asp Leu Gly Gln Ile Val Leu Leu Gly	
165 170 175	
gcg gtt tta gcg gtg ttg ttg gtt ttt tct ggg ggg agc gtg cat ttg	636
Ala Val Leu Ala Val Leu Leu Val Phe Ser Gly Gly Ser Val His Leu	
180 185 190	
ttt ggc ttg att att tca ggg gcg ttt gcg atc agc gtt tta gcg att	684
Phe Gly Leu Ile Ile Ser Gly Ala Phe Ala Ile Ser Val Leu Ala Ile	
195 200 205	
gtt aca agc gag cat agg att ttg cgc ctg aaa ttg tgg tgg tct aat	732
Val Thr Ser Glu His Arg Ile Leu Arg Leu Lys Leu Trp Trp Ser Asn	
210 215 220	
ttg caa aat tcg ctt ttc acg ctc ttg ccg gat aga tta gcg aac gct	780
Leu Gln Asn Ser Leu Phe Thr Leu Leu Pro Asp Arg Leu Ala Asn Ala	
225 230 235 240	
ctt aga ata agc gac ttg ccc gaa tcc tat cag gtc ttt cat gca ggc	828
Leu Arg Ile Ser Asp Leu Pro Glu Ser Tyr Gln Val Phe His Ala Gly	
245 250 255	
aat gcc atg cat aat ggg ggg ttg ttt ggg caa ggg ctt ggg ctt ggg	876
Asn Ala Met His Asn Gly Gly Leu Phe Gly Gln Gly Leu Gly Leu Gly	
260 265 270	
caa atc aag ctt ggg ttt ttg agc gaa gtg cat acg gac atg gtc tta	924
Gln Ile Lys Leu Gly Phe Leu Ser Glu Val His Thr Asp Met Val Leu	
275 280 285	
gct ggg atc gcc gaa gaa tgg ggg ttt ttg ggg cta tgc gtt tgt ttt	972
Ala Gly Ile Ala Glu Glu Trp Gly Phe Leu Gly Leu Cys Val Cys Phe	
290 295 300	
att ttg ttt tct gtt ttg att gtt ttg att ttt agg atc gct aac cgc	1020
Ile Leu Phe Ser Val Leu Ile Val Leu Ile Phe Arg Ile Ala Asn Arg	
305 310 315 320	
ttg aaa gag cca aaa tat tcg cta ttt tgc gtg ggc gtg gtg ctg ctt	1068
Leu Lys Glu Pro Lys Tyr Ser Leu Phe Cys Val Gly Val Val Leu Leu	
325 330 335	

att agt ttt tct ttg gtg atc aac gcc ttt ggg gtg ggc ggg att ctt 1116  
 Ile Ser Phe Ser Leu Val Ile Asn Ala Phe Gly Val Gly Gly Ile Leu  
                   340                                  345                                  350

ccg gtt aaa ggt cta gcg gtg ccg ttt ttg agc tat gga ggg agt tcg 1164  
 Pro Val Lys Gly Leu Ala Val Pro Phe Leu Ser Tyr Gly Gly Ser Ser  
                   355                                  360                                  365

ctt cta gcg aat tgt atc gct ata ggg ctt gtt cta agc cta gcg cga 1212  
 Leu Leu Ala Asn Cys Ile Ala Ile Gly Leu Val Leu Ser Leu Ala Arg  
                   370                                  375                                  380

tac acg aaa ggc taaaaacatc aaccctttt taaaaattaa tgccataaaa 1264  
 Tyr Thr Lys Gly  
 385

agggtcaac ctc 1277

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 <212> PRT  
 <213> Helicobacter pylori

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                   20                                  25                                  30  
 Leu Tyr His Tyr Gly Glu Phe His Phe Phe Ile Arg Gln Leu Val Ser  
                   35                                  40                                  45  
 Ala Ile Ile Gly Ile Val Ile Met Trp Gly Leu Ser Arg Val Asp Pro  
   50                                  55                                  60  
 Ser Lys Trp Phe Ser Arg Leu Gly Phe Phe Leu Leu Phe Val Pro Pro  
  65                                  70                                  75                                  80  
 Leu Leu Ile Ile Gly Met Phe Phe Leu Pro Glu Ser Leu Ser Ser Ser  
                   85                                  90                                  95  
 Ala Gly Gly Ala Lys Arg Trp Ile Arg Leu Gly Phe Phe Ser Leu Ala  
                  100                                 105                                 110  
 Pro Leu Glu Phe Leu Lys Ile Gly Phe Thr Phe Phe Leu Ala Trp Ser  
                  115                                 120                                 125  
 Leu Ser Arg Thr Phe Val Ala Lys Glu Lys Ala Asn Val Lys Glu Glu  
  130                                 135                                 140  
 Leu Ile Thr Phe Val Pro Tyr Ser Val Val Phe Val Ala Leu Ala Ile  
  145                                 150                                 155                                 160  
 Gly Val Gly Val Leu Gln Asn Asp Leu Gly Gln Ile Val Leu Leu Gly  
                  165                                 170                                 175  
 Ala Val Leu Ala Val Leu Leu Val Phe Ser Gly Gly Ser Val His Leu  
                  180                                 185                                 190  
 Phe Gly Leu Ile Ile Ser Gly Ala Phe Ala Ile Ser Val Leu Ala Ile  
                  195                                 200                                 205  
 Val Thr Ser Glu His Arg Ile Leu Arg Leu Lys Leu Trp Trp Ser Asn  
  210                                 215                                 220  
 Leu Gln Asn Ser Leu Phe Thr Leu Leu Pro Asp Arg Leu Ala Asn Ala  
  225                                 230                                 235                                 240



ttc ttt aag ggg agt ttg gaa agt tgt gtg gat caa aag att tgt tat	344
Phe Phe Lys Gly Ser Leu Glu Ser Cys Val Asp Gln Lys Ile Cys Tyr	
85 90 95	
tat gag cat aaa gat ggc aag gtt tct ttt gtg gtg aat gac agg gag	392
Tyr Glu His Lys Asp Gly Lys Val Ser Phe Val Val Asn Asp Arg Glu	
100 105 110	
aag ttt tat aaa cat gtg ctt aaa gac tta ggg aca gag ctt tcg ctc	440
Lys Phe Tyr Lys His Val Leu Lys Asp Leu Gly Thr Glu Leu Ser Leu	
115 120 125 130	
cct ttg ttt aac tgg ctt tac aaa ggc tcg gat ttt ggg gct ttg cat	488
Pro Leu Phe Asn Trp Leu Tyr Lys Gly Ser Asp Phe Gly Ala Leu His	
135 140 145	
gag cag ttt ggg gat atg tat gat ggg tat atc aaa tac ttg atc agt	536
Glu Gln Phe Gly Asp Met Tyr Asp Gly Tyr Ile Lys Tyr Leu Ile Ser	
150 155 160	
atg gtt aga ata agc caa aaa gaa aag gct aga aaa gtg gat gca atc	584
Met Val Arg Ile Ser Gln Lys Glu Lys Ala Arg Lys Val Asp Ala Ile	
165 170 175	
gtt ctt aag aaa atg gaa gaa caa gct gag aaa gac act aag gca gcg	632
Val Leu Lys Lys Met Glu Glu Gln Ala Glu Lys Asp Thr Lys Ala Ala	
180 185 190	
ttt caa aag agg agc agt ggg gag ctt gaa agc cat act gat agc cct	680
Phe Gln Lys Arg Ser Ser Gly Glu Leu Glu Ser His Thr Asp Ser Pro	
195 200 205 210	
gaa ttt ata agc tct tct aag agg aca cag aac gct tct aat tcg gat	728
Glu Phe Ile Ser Ser Ser Lys Arg Thr Gln Asn Ala Ser Asn Ser Asp	
215 220 225	
ctc aat tct atg acc aat gct aac gcg ctc aaa gaa aca gct tca aaa	776
Leu Asn Ser Met Thr Asn Ala Asn Ala Leu Lys Glu Thr Ala Ser Lys	
230 235 240	
gag cca gag gct tct tca aaa aaa gag aaa aag tct aag aaa aaa cgt	824
Glu Pro Glu Ala Ser Ser Lys Lys Glu Lys Lys Ser Lys Lys Lys Arg	
245 250 255	
cgc ctt tca aag aaa gaa aaa caa caa caa gcc ttg caa caa gag ttt	872
Arg Leu Ser Lys Lys Glu Lys Gln Gln Gln Ala Leu Gln Gln Glu Phe	
260 265 270	
gaa aaa caa att agc gac tct agt aag tct gaa aaa tagtaataat	918
Glu Lys Gln Ile Ser Asp Ser Ser Lys Ser Glu Lys	
275 280 285	
agttaagctt accttttttag ggggctttca ataaatctct taa	961

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 <212> PRT  
 <213> Helicobacter pylori

<400> 352  
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 Met Phe Ser Glu Ser Ser Thr Gly Asn Val Lys Lys Asp Arg Lys Arg  
 35 40 45  
 Val Leu Lys Ser Met Val Asn Leu Glu Lys Glu Arg Val Lys Asn Phe  
 50 55 60  
 Asn Arg Tyr Ser Glu Thr Lys Met Ser Lys Gly Asp Leu Ser Ala Phe  
 65 70 75 80  
 Gly Ala Phe Phe Lys Gly Ser Leu Glu Ser Cys Val Asp Gln Lys Ile  
 85 90 95  
 Cys Tyr Tyr Glu His Lys Asp Gly Lys Val Ser Phe Val Val Asn Asp  
 100 105 110  
 Arg Glu Lys Phe Tyr Lys His Val Leu Lys Asp Leu Gly Thr Glu Leu  
 115 120 125  
 Ser Leu Pro Leu Phe Asn Trp Leu Tyr Lys Gly Ser Asp Phe Gly Ala  
 130 135 140  
 Leu His Glu Gln Phe Gly Asp Met Tyr Asp Gly Tyr Ile Lys Tyr Leu  
 145 150 155 160  
 Ile Ser Met Val Arg Ile Ser Gln Lys Glu Lys Ala Arg Lys Val Asp  
 165 170 175  
 Ala Ile Val Leu Lys Lys Met Glu Glu Gln Ala Glu Lys Asp Thr Lys  
 180 185 190  
 Ala Ala Phe Gln Lys Arg Ser Ser Gly Glu Leu Glu Ser His Thr Asp  
 195 200 205  
 Ser Pro Glu Phe Ile Ser Ser Lys Arg Thr Gln Asn Ala Ser Asn  
 210 215 220  
 Ser Asp Leu Asn Ser Met Thr Asn Ala Asn Ala Leu Lys Glu Thr Ala  
 225 230 235 240  
 Ser Lys Glu Pro Glu Ala Ser Ser Lys Lys Glu Lys Lys Ser Lys Lys  
 245 250 255  
 Lys Arg Arg Leu Ser Lys Lys Glu Lys Gln Gln Gln Ala Leu Gln Gln  
 260 265 270  
 Glu Phe Glu Lys Gln Ile Ser Asp Ser Ser Lys Ser Glu Lys  
 275 280 285

<210> 353  
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 <212> DNA  
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 <222> (51)...(1499)

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Met Glu Lys Tyr His Ser Asp Gln Glu Tyr Glu Glu Ile Ile Thr Asp																	
		5					10					15					
caa tta ggc gat atg caa tta agg gaa aat ttg cgt tct gca atg gat	152																
Gln Leu Gly Asp Met Gln Leu Arg Glu Asn Leu Arg Ser Ala Met Asp																	
		20					25				30						
acc tta agg gct aat cgt aag aat ctc ctt aaa aat cgt tac agc gaa	200																
Thr Leu Arg Ala Asn Arg Lys Asn Leu Leu Lys Asn Arg Tyr Ser Glu																	
		35				40				45					50		
tgg gaa aat tta agg gaa tta ggc aaa gaa gtc aag ctt aaa atc tta	248																
Trp Glu Asn Leu Arg Glu Leu Gly Lys Glu Val Lys Leu Lys Ile Leu																	
				55					60						65		
tcc agg ctt gat gaa tat ttg gaa ttg ttt gaa aaa aac gcc act caa	296																
Ser Arg Leu Asp Glu Tyr Leu Glu Leu Phe Glu Lys Asn Ala Thr Gln																	
				70				75					80				
aac ggc ttt aaa atc cat tac gct aaa gac ggc gat gaa gct aat gaa	344																
Asn Gly Phe Lys Ile His Tyr Ala Lys Asp Gly Asp Glu Ala Asn Glu																	
			85				90					95					
atc att tac aac ctc gct aaa gaa aag aat atc aag cgc att tta aag	392																
Ile Ile Tyr Asn Leu Ala Lys Glu Lys Asn Ile Lys Arg Ile Leu Lys																	
		100				105				110							
caa aaa tcc atg gcg agc gaa gaa att ggc ttg aac cat tac ttg aaa	440																
Gln Lys Ser Met Ala Ser Glu Glu Ile Gly Leu Asn His Tyr Leu Lys																	
		115				120			125						130		
gaa aag ggc att caa gca caa gaa acg gat ttg ggc gaa ttg att atc	488																
Glu Lys Gly Ile Gln Ala Gln Glu Thr Asp Leu Gly Glu Leu Ile Ile																	
				135				140						145			
caa ctc atc aat gaa cac cct gtg cat att gtc gtg cca gct atc cat	536																
Gln Leu Ile Asn Glu His Pro Val His Ile Val Val Pro Ala Ile His																	
				150				155						160			
aaa aac cgc aag caa atc ggt aag att ttt gaa gaa aaa ctc aac gcc	584																
Lys Asn Arg Lys Gln Ile Gly Lys Ile Phe Glu Glu Lys Leu Asn Ala																	
			165				170					175					
gct tat gaa gaa gag cct gaa aag ctt aat gcg atc gcc aga aaa cac	632																
Ala Tyr Glu Glu Glu Pro Glu Lys Leu Asn Ala Ile Ala Arg Lys His																	
		180				185				190							
atg cgc aaa gaa ttt gaa agc ttt aaa atg ggg att agt ggg gtt aat	680																
Met Arg Lys Glu Phe Glu Ser Phe Lys Met Gly Ile Ser Gly Val Asn																	
		195				200			205						210		

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Phe Ala Ile Ala Asn Glu Gly Ala Ile Trp Leu Val Glu Asn Glu Gly	
215 220 225	
aat ggc aga atg agc acc act gca tgc gat gtg cat gtc gca att tgt	776
Asn Gly Arg Met Ser Thr Thr Ala Cys Asp Val His Val Ala Ile Cys	
230 235 240	
ggg att gaa aaa tta gta gaa agc ttt gat gat gcg gcg att tta aac	824
Gly Ile Glu Lys Leu Val Glu Ser Phe Asp Asp Ala Ala Ile Leu Asn	
245 250 255	
aat ttg ctc gcc cca agc gct gtg ggt gtg cct atc act tgc tat caa	872
Asn Leu Leu Ala Pro Ser Ala Val Gly Val Pro Ile Thr Cys Tyr Gln	
260 265 270	
aac att atc aca ggc cct aga aaa gag ggc gat tta gac ggc cct aaa	920
Asn Ile Ile Thr Gly Pro Arg Lys Glu Gly Asp Leu Asp Gly Pro Lys	
275 280 285 290	
gaa gcc cac atc att tta tta gac aac aac cgc tct aat att ttg gct	968
Glu Ala His Ile Ile Leu Leu Asp Asn Asn Arg Ser Asn Ile Leu Ala	
295 300 305	
gat gaa aag tat tat cgc gct ctt tca tgc atc cgt tgc ggg act tgt	1016
Asp Glu Lys Tyr Tyr Arg Ala Leu Ser Cys Ile Arg Cys Gly Thr Cys	
310 315 320	
ttg aac cac tgc cct gtg tat gat aaa atc ggt ggg cat gcc tat ctt	1064
Leu Asn His Cys Pro Val Tyr Asp Lys Ile Gly Gly His Ala Tyr Leu	
325 330 335	
tct act tat cct ggc cct ata ggc gtg gtg gta tcc ccc caa ctc ttt	1112
Ser Thr Tyr Pro Gly Pro Ile Gly Val Val Val Ser Pro Gln Leu Phe	
340 345 350	
ggc ttg aat aat tac ggg cat atc cct aat ttg tgc agt ctt tgc ggg	1160
Gly Leu Asn Asn Tyr Gly His Ile Pro Asn Leu Cys Ser Leu Cys Gly	
355 360 365 370	
cgt tgc act gaa gta tgc ccc gta gaa atc cct tta gcc gaa ctc att	1208
Arg Cys Thr Glu Val Cys Pro Val Glu Ile Pro Leu Ala Glu Leu Ile	
375 380 385	
agg gat tta cga tcc gat aaa gtg ggc gag ggc agg ggt gta att aag	1256
Arg Asp Leu Arg Ser Asp Lys Val Gly Glu Gly Arg Gly Val Ile Lys	
390 395 400	
ggg gct aaa agc acc caa cac agc ggg atg gaa aaa ttc tct atg aaa	1304
Gly Ala Lys Ser Thr Gln His Ser Gly Met Glu Lys Phe Ser Met Lys	
405 410 415	
atg ttt gcc aaa atg gca agc gat ggg gct aag tgg cgt ttc caa ttg	1352
Met Phe Ala Lys Met Ala Ser Asp Gly Ala Lys Trp Arg Phe Gln Leu	
420 425 430	

aaa atg gct caa ttt ttc tcg cct tta ggc aag ctt tta gct ccc ata 1400  
Lys Met Ala Gln Phe Phe Ser Pro Leu Gly Lys Leu Leu Ala Pro Ile  
435 440 445 450

gac acg agc ttg cat gca aaa gtc cag cac tta gaa ggg gtg att tat 1496  
Asp Thr Ser Leu His Ala Lys Val Gln His Leu Glu Gly Val Ile Tyr  
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Glu

ttcagg 1555

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<210> 354
<211> 483
<212> PRT
<213> Helicobacter pylori
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Met	Asp	Thr	Leu	Arg	Ala	Asn	Arg	Lys	Asn	Leu	Leu	Lys	Asn	Arg	Tyr
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Ser	Glu	Trp	Glu	Asn	Leu	Arg	Glu	Leu	Gly	Lys	Glu	Val	Lys	Leu	Lys
		50				55					60				
Ile 65	Leu	Ser	Arg	Leu	Asp	Glu	Tyr	Leu	Glu	Leu	Phe	Glu	Lys	Asn	Ala
					70					75					80
Thr	Gln	Asn	Gly	Phe	Lys	Ile	His	Tyr	Ala	Lys	Asp	Gly	Asp	Glu	Ala
				85					90					95	
Asn	Glu	Ile	Ile	Tyr	Asn	Leu	Ala	Lys	Glu	Lys	Asn	Ile	Lys	Arg	Ile
			100					105					110		
Leu	Lys	Gln	Lys	Ser	Met	Ala	Ser	Glu	Glu	Ile	Gly	Leu	Asn	His	Tyr
		115					120					125			
Leu	Lys	Glu	Lys	Gly	Ile	Gln	Ala	Gln	Glu	Thr	Asp	Leu	Gly	Glu	Leu
		130				135					140				
Ile 145	Ile	Gln	Leu	Ile	Asn	Glu	His	Pro	Val	His	Ile	Val	Val	Pro	Ala
					150					155					160
Ile	His	Lys	Asn	Arg	Lys	Gln	Ile	Gly	Lys	Ile	Phe	Glu	Glu	Lys	Leu
				165					170					175	
Asn	Ala	Ala	Tyr	Glu	Glu	Glu	Pro	Glu	Lys	Leu	Asn	Ala	Ile	Ala	Arg
			180					185					190		
Lys	His	Met	Arg	Lys	Glu	Phe	Glu	Ser	Phe	Lys	Met	Gly	Ile	Ser	Gly
		195					200					205			
Val	Asn	Phe	Ala	Ile	Ala	Asn	Glu	Gly	Ala	Ile	Trp	Leu	Val	Glu	Asn
		210				215					220				
Glu 225	Gly	Asn	Gly	Arg	Met	Ser	Thr	Thr	Ala	Cys	Asp	Val	His	Val	Ala
					230					235					240

Ile	Cys	Gly	Ile	Glu	Lys	Leu	Val	Glu	Ser	Phe	Asp	Asp	Ala	Ala	Ile	
				245					250					255		
Leu	Asn	Asn	Leu	Leu	Ala	Pro	Ser	Ala	Val	Gly	Val	Pro	Ile	Thr	Cys	
			260					265					270			
Tyr	Gln	Asn	Ile	Ile	Thr	Gly	Pro	Arg	Lys	Glu	Gly	Asp	Leu	Asp	Gly	
		275					280					285				
Pro	Lys	Glu	Ala	His	Ile	Ile	Leu	Leu	Asp	Asn	Asn	Arg	Ser	Asn	Ile	
		290				295					300					
Leu	Ala	Asp	Glu	Lys	Tyr	Tyr	Arg	Ala	Leu	Ser	Cys	Ile	Arg	Cys	Gly	
305					310					315					320	
Thr	Cys	Leu	Asn	His	Cys	Pro	Val	Tyr	Asp	Lys	Ile	Gly	Gly	His	Ala	
			325						330					335		
Tyr	Leu	Ser	Thr	Tyr	Pro	Gly	Pro	Ile	Gly	Val	Val	Val	Ser	Pro	Gln	
		340					345						350			
Leu	Phe	Gly	Leu	Asn	Asn	Tyr	Gly	His	Ile	Pro	Asn	Leu	Cys	Ser	Leu	
	355					360					365					
Cys	Gly	Arg	Cys	Thr	Glu	Val	Cys	Pro	Val	Glu	Ile	Pro	Leu	Ala	Glu	
	370				375					380						
Leu	Ile	Arg	Asp	Leu	Arg	Ser	Asp	Lys	Val	Gly	Glu	Gly	Arg	Gly	Val	
385				390				395							400	
Ile	Lys	Gly	Ala	Lys	Ser	Thr	Gln	His	Ser	Gly	Met	Glu	Lys	Phe	Ser	
			405					410					415			
Met	Lys	Met	Phe	Ala	Lys	Met	Ala	Ser	Asp	Gly	Ala	Lys	Trp	Arg	Phe	
		420					425					430				
Gln	Leu	Lys	Met	Ala	Gln	Phe	Phe	Ser	Pro	Leu	Gly	Lys	Leu	Leu	Ala	
	435					440					445					
Pro	Ile	Leu	Pro	Leu	Val	Lys	Glu	Trp	Ala	Ser	Val	Arg	Thr	Leu	Pro	
	450				455					460						
Asn	Met	Asp	Thr	Ser	Leu	His	Ala	Lys	Val	Gln	His	Leu	Glu	Gly	Val	
465				470					475					480		
Ile	Tyr	Glu														

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 ttgggttagt ctataagact cccatttcaa gctctcctat ctcttatgat ccctacacta 180  
 cccccattgg gagcttgtat gctgaaaaat taaaagaaaa ccctaaccat agcgcgggcca 240  
 ttcttttaga agatggcttt gacgctctgt tgcataagat gggacttatt aga atg 296  
 Met  
 1  
 agc caa aaa agc att gac atg caa act tat atc tat aaa aac gac ctt 344  
 Ser Gln Lys Ser Ile Asp Met Gln Thr Tyr Ile Tyr Lys Asn Asp Leu  
 5 10 15

tct tct caa gtg att gct aaa gaa ctt tta aat gcg gcc aat cgt ggg	392
Ser Ser Gln Val Ile Ala Lys Glu Leu Leu Asn Ala Ala Asn Arg Gly	
20 25 30	
gta aaa gtg cgc atc ctt tta gac gat aac gga ttg gat tcg gat ttt	440
Val Lys Val Arg Ile Leu Leu Asp Asp Asn Gly Leu Asp Ser Asp Phe	
35 40 45	
tca gat att atg ctc tta aat ttc cat aaa aac att gag gtg aaa att	488
Ser Asp Ile Met Leu Leu Asn Phe His Lys Asn Ile Glu Val Lys Ile	
50 55 60 65	
ttt aac ccc tac tat atc cgc aat aaa ggc ttg cgt tat ttt gaa atg	536
Phe Asn Pro Tyr Tyr Ile Arg Asn Lys Gly Leu Arg Tyr Phe Glu Met	
70 75 80	
ctt gcg gat tat gag cgc att aaa aaa cgc atg cac aac aag ctt ttc	584
Leu Ala Asp Tyr Glu Arg Ile Lys Lys Arg Met His Asn Lys Leu Phe	
85 90 95	
atc gtg gat aat ttc gct gtc att ata ggg ggg cgc aat att ggg gac	632
Ile Val Asp Asn Phe Ala Val Ile Ile Gly Gly Arg Asn Ile Gly Asp	
100 105 110	
aat tat ttt gat aac gat tta gac acg aat ttt tta gat tta gac gct	680
Asn Tyr Phe Asp Asn Asp Leu Asp Thr Asn Phe Leu Asp Leu Asp Ala	
115 120 125	
ttg ttt ttt ggg ggg gtt gct tca aaa gcc aaa gaa agc ttt gaa cgc	728
Leu Phe Phe Gly Gly Val Ala Ser Lys Ala Lys Glu Ser Phe Glu Arg	
130 135 140 145	
tat tgg aga ttc cac cgc tct atc cct gtt tca tta cta aga acc cat	776
Tyr Trp Arg Phe His Arg Ser Ile Pro Val Ser Leu Leu Arg Thr His	
150 155 160	
aaa aga ctc aaa aac aac gct aaa gaa atc gct aaa ctc cat gaa aaa	824
Lys Arg Leu Lys Asn Asn Ala Lys Glu Ile Ala Lys Leu His Glu Lys	
165 170 175	
atc cct atc agc gct gaa gac aaa aac cag ttt gaa aaa aaa gtc aat	872
Ile Pro Ile Ser Ala Glu Asp Lys Asn Gln Phe Glu Lys Lys Val Asn	
180 185 190	
gat ttt ata gat cgt ttc caa aaa tac caa tac ccc att tat tat ggg	920
Asp Phe Ile Asp Arg Phe Gln Lys Tyr Gln Tyr Pro Ile Tyr Tyr Gly	
195 200 205	
aat gcc att ttt tta gcc gat tca ccc aaa aaa att gac acg ccc ttg	968
Asn Ala Ile Phe Leu Ala Asp Ser Pro Lys Lys Ile Asp Thr Pro Leu	
210 215 220 225	
tat tcg cct atc aaa atc gct ttt gag aaa gcc ctt aaa aac gct aag	1016
Tyr Ser Pro Ile Lys Ile Ala Phe Glu Lys Ala Leu Lys Asn Ala Lys	

230	235	240	
gac tcc gtt ttt atc gct tca tcg tat ttt att cca ggc aaa aag atg			1064
Asp Ser Val Phe Ile Ala Ser Ser Tyr Phe Ile Pro Gly Lys Lys Met			
245	250	255	
atg aaa atc ttt aaa aat caa att tct aag ggg att gaa ttg aac atc			1112
Met Lys Ile Phe Lys Asn Gln Ile Ser Lys Gly Ile Glu Leu Asn Ile			
260	265	270	
ctt acc aat tcc ctt tca tct act gat gcg ata gtg gtc tat ggg gca			1160
Leu Thr Asn Ser Leu Ser Ser Thr Asp Ala Ile Val Val Tyr Gly Ala			
275	280	285	
tgg gaa agg tat cgc aac caa tta gtg cga atg ggc gcg aat gtc tat			1208
Trp Glu Arg Tyr Arg Asn Gln Leu Val Arg Met Gly Ala Asn Val Tyr			
290	295	300	305
gaa ata cga aac gat ttt ttc aac cgc cag att aaa ggg cgc ttt agc			1256
Glu Ile Arg Asn Asp Phe Phe Asn Arg Gln Ile Lys Gly Arg Phe Ser			
310	315	320	
acc aaa cat tcc ttg cat ggc aag acg att gtt ttt gat gac aat tta			1304
Thr Lys His Ser Leu His Gly Lys Thr Ile Val Phe Asp Asp Asn Leu			
325	330	335	
acg ctt cta ggg agt ttc aat att gat ccg cgc tct gca tac atc aac			1352
Thr Leu Leu Gly Ser Phe Asn Ile Asp Pro Arg Ser Ala Tyr Ile Asn			
340	345	350	
act gaa agc gcg gtt ttg ttt gac aac ccg tct ttt gct aaa agg gtg			1400
Thr Glu Ser Ala Val Leu Phe Asp Asn Pro Ser Phe Ala Lys Arg Val			
355	360	365	
cgt ttg tcg ctt aaa gat cat gcc caa caa tca tgg cat ttg gtg gtg			1448
Arg Leu Ser Leu Lys Asp His Ala Gln Gln Ser Trp His Leu Val Val			
370	375	380	385
tat cgg cat aga gtg att tgg gaa gcg gtg gaa gaa ggc att tta atc			1496
Tyr Arg His Arg Val Ile Trp Glu Ala Val Glu Glu Gly Ile Leu Ile			
390	395	400	
cat gaa aaa act tcg cct gac act tcc ttc ttt ttg cgc ttg att aaa			1544
His Glu Lys Thr Ser Pro Asp Thr Ser Phe Phe Leu Arg Leu Ile Lys			
405	410	415	
gaa tgg tct aaa gtc ctt cct gaa aga gag ctt taaaactttt aatgcgcttt			1597
Glu Trp Ser Lys Val Leu Pro Glu Arg Glu Leu			
420	425		
atattgcgaa aaagcgatgt tattggtaac ggc			1630
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<211> 428			
<212> PRT			

<213> Helicobacter pylori

<400> 356

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			20					25					30		
Gly	Val	Lys	Val	Arg	Ile	Leu	Leu	Asp	Asp	Asn	Gly	Leu	Asp	Ser	Asp
		35					40					45			
Phe	Ser	Asp	Ile	Met	Leu	Leu	Asn	Phe	His	Lys	Asn	Ile	Glu	Val	Lys
	50					55					60				
Ile	Phe	Asn	Pro	Tyr	Tyr	Ile	Arg	Asn	Lys	Gly	Leu	Arg	Tyr	Phe	Glu
65					70					75					80
Met	Leu	Ala	Asp	Tyr	Glu	Arg	Ile	Lys	Lys	Arg	Met	His	Asn	Lys	Leu
				85					90					95	
Phe	Ile	Val	Asp	Asn	Phe	Ala	Val	Ile	Ile	Gly	Gly	Arg	Asn	Ile	Gly
			100					105						110	
Asp	Asn	Tyr	Phe	Asp	Asn	Asp	Leu	Asp	Thr	Asn	Phe	Leu	Asp	Leu	Asp
		115					120					125			
Ala	Leu	Phe	Phe	Gly	Gly	Val	Ala	Ser	Lys	Ala	Lys	Glu	Ser	Phe	Glu
	130					135					140				
Arg	Tyr	Trp	Arg	Phe	His	Arg	Ser	Ile	Pro	Val	Ser	Leu	Leu	Arg	Thr
145					150					155					160
His	Lys	Arg	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Ala	Lys	Leu	His	Glu
				165					170					175	
Lys	Ile	Pro	Ile	Ser	Ala	Glu	Asp	Lys	Asn	Gln	Phe	Glu	Lys	Lys	Val
		180					185						190		
Asn	Asp	Phe	Ile	Asp	Arg	Phe	Gln	Lys	Tyr	Gln	Tyr	Pro	Ile	Tyr	Tyr
		195					200					205			
Gly	Asn	Ala	Ile	Phe	Leu	Ala	Asp	Ser	Pro	Lys	Lys	Ile	Asp	Thr	Pro
	210					215					220				
Leu	Tyr	Ser	Pro	Ile	Lys	Ile	Ala	Phe	Glu	Lys	Ala	Leu	Lys	Asn	Ala
225					230					235					240
Lys	Asp	Ser	Val	Phe	Ile	Ala	Ser	Ser	Tyr	Phe	Ile	Pro	Gly	Lys	Lys
				245					250					255	
Met	Met	Lys	Ile	Phe	Lys	Asn	Gln	Ile	Ser	Lys	Gly	Ile	Glu	Leu	Asn
			260					265					270		
Ile	Leu	Thr	Asn	Ser	Leu	Ser	Ser	Thr	Asp	Ala	Ile	Val	Val	Tyr	Gly
		275					280					285			
Ala	Trp	Glu	Arg	Tyr	Arg	Asn	Gln	Leu	Val	Arg	Met	Gly	Ala	Asn	Val
	290					295					300				
Tyr	Glu	Ile	Arg	Asn	Asp	Phe	Phe	Asn	Arg	Gln	Ile	Lys	Gly	Arg	Phe
305					310					315					320
Ser	Thr	Lys	His	Ser	Leu	His	Gly	Lys	Thr	Ile	Val	Phe	Asp	Asp	Asn
				325					330					335	
Leu	Thr	Leu	Leu	Gly	Ser	Phe	Asn	Ile	Asp	Pro	Arg	Ser	Ala	Tyr	Ile
		340						345					350		
Asn	Thr	Glu	Ser	Ala	Val	Leu	Phe	Asp	Asn	Pro	Ser	Phe	Ala	Lys	Arg
		355					360					365			
Val	Arg	Leu	Ser	Leu	Lys	Asp	His	Ala	Gln	Gln	Ser	Trp	His	Leu	Val
	370					375					380				
Val	Tyr	Arg	His	Arg	Val	Ile	Trp	Glu	Ala	Val	Glu	Glu	Gly	Ile	Leu
385					390					395					400
Ile	His	Glu	Lys	Thr	Ser	Pro	Asp	Thr	Ser	Phe	Phe	Leu	Arg	Leu	Ile
				405					410					415	

Lys Glu Trp Ser Lys Val Leu Pro Glu Arg Glu Leu  
 420 425

<210> 357  
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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (79)...(510)

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 Met Lys Thr Phe Glu Ile Leu Lys His Leu Gln  
 1 5 10  
 gcg gat gcg atc gtg tta ttt atg aaa gtg cat aac ttc cat tgg aat 159  
 Ala Asp Ala Ile Val Leu Phe Met Lys Val His Asn Phe His Trp Asn  
 15 20 25  
 gtg aaa ggc acc gat ttt ttc aat gtg cat aaa gcc act gaa gaa att 207  
 Val Lys Gly Thr Asp Phe Phe Asn Val His Lys Ala Thr Glu Glu Ile  
 30 35 40  
 tat gaa gag ttt gcg gac atg ttt gac gat ctc gct gaa agg atc gtt 255  
 Tyr Glu Glu Phe Ala Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val  
 45 50 55  
 caa tta ggg cat cac ccc tta gtc act tta tcc gaa gcg atc aaa ctc 303  
 Gln Leu Gly His His Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu  
 60 65 70 75  
 act cgt gtt aaa gaa gaa act aaa acg agc ttc cac tct aaa gac atc 351  
 Thr Arg Val Lys Glu Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile  
 80 85 90  
 ttt aaa gaa att cta gag gac tac aaa tat cta gaa aaa gaa ttt aaa 399  
 Phe Lys Glu Ile Leu Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys  
 95 100 105  
 gag ctc tct aac acc gct gaa aaa gaa ggc gat aaa gtt acc gta act 447  
 Glu Leu Ser Asn Thr Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr  
 110 115 120  
 tat gcg gat gat caa tta gcc aag ttg caa aaa tcc att tgg atg ctg 495  
 Tyr Ala Asp Asp Gln Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu  
 125 130 135  
 caa gcc cat ttg gct taagcgacca aaaagaagcc agcatgagag attacagcga 550  
 Gln Ala His Leu Ala  
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<210> 358  
 <211> 144  
 <212> PRT  
 <213> Helicobacter pylori

<400> 358  
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 Leu Phe Met Lys Val His Asn Phe His Trp Asn Val Lys Gly Thr Asp  
 20 25 30  
 Phe Phe Asn Val His Lys Ala Thr Glu Glu Ile Tyr Glu Glu Phe Ala  
 35 40 45  
 Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His  
 50 55 60  
 Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu  
 65 70 75 80  
 Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu  
 85 90 95  
 Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys Glu Leu Ser Asn Thr  
 100 105 110  
 Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr Tyr Ala Asp Asp Gln  
 115 120 125  
 Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu Gln Ala His Leu Ala  
 130 135 140

<210> 359  
 <211> 376  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 Phe Leu Gly Ser Gly Leu Gly Phe Gly Leu Gly Ser Gly Leu Gly Phe  
 5 10 15  
 tct ata ggt ttt ggc ggg gtt ggc ggg gtt ggc gga gtt ggg ggt gtg 152  
 Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly Gly Val  
 20 25 30  
 gga ggc gtt gga ggt ttt tgg ggg cca gcc agc gtg ggt tta gga gcg 200  
 Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu Gly Ala  
 35 40 45 50  
 ccc tgg gtg ttt tta ctg gga tct tgc gaa tgg cct ctt ttt aaa acc 248  
 Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe Lys Thr

55 60 65  
 aat aaa ttt tca gga ttt aat tta aca agc ttg ggt ttt gaa gga aaa 296  
 Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu Gly Lys  
 70 75 80  
 aaa tct tct ctg tgt tca aat aaa aaa taaatcaacc agtgtaacaa 343  
 Lys Ser Ser Leu Cys Ser Asn Lys Lys  
 85 90  
 tacagacaga atgagagaaa agaaaaaatt cct 376  
 <210> 360  
 <211> 91  
 <212> PRT  
 <213> Helicobacter pylori  
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 1 5 10 15  
 Gly Phe Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly  
 20 25 30  
 Gly Val Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu  
 35 40 45  
 Gly Ala Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe  
 50 55 60  
 Lys Thr Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu  
 65 70 75 80  
 Gly Lys Lys Ser Ser Leu Cys Ser Asn Lys Lys  
 85 90  
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 <212> DNA  
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 <221> CDS  
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 aacgctttga cttttttgtc ttttaactct ttggtgggcg cgaaagaaca gcatcacact 180  
 ttgcaaaaag tgacaaccac tgagcaaaaa ttcaatccaa gcgcgcccgt ttcattggcaa 240  
 agcgaagaga tgcgtaattc cacaagctct cgcacgggtga tttccaacaa ggaactcaaa 300  
 aaaacgggga atttgaatat tgaaaacgcc ttgcaaaacg tgccagggat tcaaatcaga 360  
 gacgctacag gcacaggcgt gctgcctaaa atttcggtgc tcaaaattta agttaatttt 420  
 aataattatt tttatagtat gcatcgggtt gaattaa atg aga aag gtt atc aca 475  
 Met Arg Lys Val Ile Thr  
 1 5  
 atg aat ggt tat ttg aga gta aaa acc tct tat ttt tta gcg ttg aac 523  
 Met Asn Gly Tyr Leu Arg Val Lys Thr Ser Tyr Phe Leu Ala Leu Asn

10										15										20										
gct	ttg	act	ttt	ttg	tct	ttt	aac	tct	ttg	gtg	ggc	gcg	aaa	gaa	cag	571														
Ala	Leu	Thr	Phe	Leu	Ser	Phe	Asn	Ser	Leu	Val	Gly	Ala	Lys	Glu	Gln															
25					30					35																				
cat	cac	act	ttg	caa	aaa	gtg	aca	acc	act	gag	caa	aaa	ttc	aat	cca	619														
His	His	Thr	Leu	Gln	Lys	Val	Thr	Thr	Thr	Glu	Gln	Lys	Phe	Asn	Pro															
40					45					50																				
agc	gcg	ccg	ctt	tca	tgg	caa	agc	gaa	gag	atg	cgt	aat	tcc	aca	agc	667														
Ser	Ala	Pro	Leu	Ser	Trp	Gln	Ser	Glu	Glu	Met	Arg	Asn	Ser	Thr	Ser															
55					60					65					70															
tct	cgc	acg	gtg	att	tcc	aac	aag	gaa	ctc	aaa	aaa	acg	ggg	aat	ttg	715														
Ser	Arg	Thr	Val	Ile	Ser	Asn	Lys	Glu	Leu	Lys	Lys	Thr	Gly	Asn	Leu															
75					80					85																				
aat	att	gaa	aac	gcc	ttg	caa	aac	gtg	cca	ggg	att	caa	atc	aga	gac	763														
Asn	Ile	Glu	Asn	Ala	Leu	Gln	Asn	Val	Pro	Gly	Ile	Gln	Ile	Arg	Asp															
90					95					100																				
gct	aca	ggc	aca	ggc	gtg	ctg	cct	aaa	att	tcg	gtg	cgc	ggt	ttt	ggt	811														
Ala	Thr	Gly	Thr	Gly	Val	Leu	Pro	Lys	Ile	Ser	Val	Arg	Gly	Phe	Gly															
105					110					115																				
ggg	ggc	ggt	aac	ggg	cat	agc	aat	acc	aac	atg	att	tta	gtc	aat	ggt	859														
Gly	Gly	Gly	Asn	Gly	His	Ser	Asn	Thr	Asn	Met	Ile	Leu	Val	Asn	Gly															
120					125					130																				
atc	ccc	att	tat	ggc	gcg	ccg	tat	tcc	aat	att	gaa	ctg	gcg	att	ttc	907														
Ile	Pro	Ile	Tyr	Gly	Ala	Pro	Tyr	Ser	Asn	Ile	Glu	Leu	Ala	Ile	Phe															
135					140					145					150															
cct	gta	act	ttc	cag	tca	gtg	gat	agg	att	gat	gtg	att	aaa	ggg	ggc	955														
Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	Asp	Val	Ile	Lys	Gly	Gly															
155					160					165																				
acg	agc	gtg	caa	tac	ggc	cct	aat	act	ttt	gga	ggc	gtg	gtg	aat	atc	1003														
Thr	Ser	Val	Gln	Tyr	Gly	Pro	Asn	Thr	Phe	Gly	Gly	Val	Val	Asn	Ile															
170					175					180																				
atc	act	aaa	gaa	atc	cct	aaa	gag	tgg	gaa	aat	caa	gcg	gct	gaa	agg	1051														
Ile	Thr	Lys	Glu	Ile	Pro	Lys	Glu	Trp	Glu	Asn	Gln	Ala	Ala	Glu	Arg															
185					190					195																				
atc	act	ttt	tgg	ggg	cga	tcc	tct	aat	ggg	aat	ttt	gta	gat	ccc	aaa	1099														
Ile	Thr	Phe	Trp	Gly	Arg	Ser	Ser	Asn	Gly	Asn	Phe	Val	Asp	Pro	Lys															
200					205					210																				
gaa	aaa	ggc	aag	cct	tta	gcc	caa	act	tta	gga	aac	caa	atg	ctg	ttt	1147														
Glu	Lys	Gly	Lys	Pro	Leu	Ala	Gln	Thr	Leu	Gly	Asn	Gln	Met	Leu	Phe															
215					220					225					230															
aac	act	tac	ggg	cga	acg	gct	gga	atg	ttg	ggt	aag	cat	gta	gga	att	1195														

Asn Thr Tyr Gly Arg Thr Ala Gly Met Leu Gly Lys His Val Gly Ile	
235 240 245	
agc gct caa ggc aat tgg att aac ggg caa ggt ttc agg caa aac agc	1243
Ser Ala Gln Gly Asn Trp Ile Asn Gly Gln Gly Phe Arg Gln Asn Ser	
250 255 260	
ccc aca aag gtg caa aac tac ttg ctt gat gcg gtt tat aag att aat	1291
Pro Thr Lys Val Gln Asn Tyr Leu Leu Asp Ala Val Tyr Lys Ile Asn	
265 270 275	
gcg acc aat act ttt aaa gct tat tac caa tat tat caa tac aac tct	1339
Ala Thr Asn Thr Phe Lys Ala Tyr Tyr Gln Tyr Tyr Gln Tyr Asn Ser	
280 285 290	
tac cat cca ggc act ttg agt gca caa gat tat gct tat aac cgc ttc	1387
Tyr His Pro Gly Thr Leu Ser Ala Gln Asp Tyr Ala Tyr Asn Arg Phe	
295 300 305 310	
att aat gag cgc cct gac aat caa gat gga ggg cga gcc aag cgc ttt	1435
Ile Asn Glu Arg Pro Asp Asn Gln Asp Gly Gly Arg Ala Lys Arg Phe	
315 320 325	
ggg atc gtg tat caa aat tat ttt ggc gat ccg gat agg aaa gtg ggg	1483
Gly Ile Val Tyr Gln Asn Tyr Phe Gly Asp Pro Asp Arg Lys Val Gly	
330 335 340	
gga gat ttt aaa ttc act tat ttc acg cat gac atg agt agg gat ttt	1531
Gly Asp Phe Lys Phe Thr Tyr Phe Thr His Asp Met Ser Arg Asp Phe	
345 350 355	
ggg ttt tcc aac caa tac caa agc gtg tat atg agc agt caa aac aag	1579
Gly Phe Ser Asn Gln Tyr Gln Ser Val Tyr Met Ser Ser Gln Asn Lys	
360 365 370	
att tta cct ttt aaa ggc aag gga aaa att agc gcg act aac cct aat	1627
Ile Leu Pro Phe Lys Gly Lys Gly Lys Ile Ser Ala Thr Asn Pro Asn	
375 380 385 390	
tgc ggt ttg tat tct tat agc gac acg aac agc cct tgt tgg caa ttt	1675
Cys Gly Leu Tyr Ser Tyr Ser Asp Thr Asn Ser Pro Cys Trp Gln Phe	
395 400 405	
ttt gac aat atc cgc cga tcc gtg gtg aat gcc ttt gag cca aaa ctc	1723
Phe Asp Asn Ile Arg Arg Ser Val Val Asn Ala Phe Glu Pro Lys Leu	
410 415 420	
aat ctt atc gtc aat acc ggt aaa gtc aaa caa act ttt aat atg gga	1771
Asn Leu Ile Val Asn Thr Gly Lys Val Lys Gln Thr Phe Asn Met Gly	
425 430 435	
atg cgc ttt tta act gaa gat tta tac cgc cga tcc acc acc agg aaa	1819
Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg Arg Ser Thr Thr Arg Lys	
440 445 450	

aac cct agc atg cct aat aat ggg agt ggt ttt gat gca gga act tca	1867
Asn Pro Ser Met Pro Asn Asn Gly Ser Gly Phe Asp Ala Gly Thr Ser	
455 460 465 470	
ctc aat aat ttc aac aat tat acc gct gtg tat gcc agc gat gag atc	1915
Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val Tyr Ala Ser Asp Glu Ile	
475 480 485	
aat ttc aat aac ggc atg cta acg atc acg ccg ggc ttg aga tac act	1963
Asn Phe Asn Asn Gly Met Leu Thr Ile Thr Pro Gly Leu Arg Tyr Thr	
490 495 500	
ttt tta aat tac gaa aaa aaa gac gct cct cct ttt aaa gca ggc caa	2011
Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro Pro Phe Lys Ala Gly Gln	
505 510 515	
aca gga aaa acc att aaa gat cgt tat aac caa tgg aat cca gca gtg	2059
Thr Gly Lys Thr Ile Lys Asp Arg Tyr Asn Gln Trp Asn Pro Ala Val	
520 525 530	
aat gtc ggc tat aaa ccc att aaa gaa ttg ttg ttt tat ttc aat tac	2107
Asn Val Gly Tyr Lys Pro Ile Lys Glu Leu Leu Phe Tyr Phe Asn Tyr	
535 540 545 550	
caa aga agc tac att ccg cct caa ttc agc aat atc ggt agt ttt gta	2155
Gln Arg Ser Tyr Ile Pro Pro Gln Phe Ser Asn Ile Gly Ser Phe Val	
555 560 565	
ggc aca agc acg gat tat ttt caa atc ttt aat gtc atg gaa ggc ggc	2203
Gly Thr Ser Thr Asp Tyr Phe Gln Ile Phe Asn Val Met Glu Gly Gly	
570 575 580	
tca aga tat tat ttt aac aac caa gtg agt ttt aac gcg aat tat ttt	2251
Ser Arg Tyr Tyr Phe Asn Asn Gln Val Ser Phe Asn Ala Asn Tyr Phe	
585 590 595	
gtg att ttt gcg aat aac tat ttt acc ggg cgc tat ggg gat aat aaa	2299
Val Ile Phe Ala Asn Asn Tyr Phe Thr Gly Arg Tyr Gly Asp Asn Lys	
600 605 610	
gag ccg gtc aat gcg aga tcg caa ggc gtg gag cta gag ttg tat tac	2347
Glu Pro Val Asn Ala Arg Ser Gln Gly Val Glu Leu Glu Leu Tyr Tyr	
615 620 625 630	
acg ccg att aga ggg ctt aat ttc cat gcg gct tac act ttc ata gat	2395
Thr Pro Ile Arg Gly Leu Asn Phe His Ala Ala Tyr Thr Phe Ile Asp	
635 640 645	
gcc aat atc aca agc cac acg atg gtt act aac ccc gct aat cct aaa	2443
Ala Asn Ile Thr Ser His Thr Met Val Thr Asn Pro Ala Asn Pro Lys	
650 655 660	
ggg cct aaa aaa gat att ttt ggc aaa aag ctc cct ttt gta agc ccg	2491
Gly Pro Lys Lys Asp Ile Phe Gly Lys Lys Leu Pro Phe Val Ser Pro	
665 670 675	

cac caa ttc att tta gac gcg agc tac act tac gct aaa acc acg att 2539  
His Gln Phe Ile Leu Asp Ala Ser Tyr Thr Tyr Ala Lys Thr Thr Ile  
680 685 690

ggg ttg agt tct ttc ttt tat agc cga act tat agc gat gtg tta aac 2587  
Gly Leu Ser Ser Phe Phe Tyr Ser Arg Thr Tyr Ser Asp Val Leu Asn  
695 700 705 710

acc gtg cct ttt att caa tac gcg ccc acg atc aaa aat ggt gct atc 2635  
Thr Val Pro Phe Ile Gln Tyr Ala Pro Thr Ile Lys Asn Gly Ala Ile  
715 720 725

act acc aaa aca gcg ggc atg acg cca tgg tat tgg gtg tgg aat ttg 2683  
Thr Thr Lys Thr Ala Gly Met Thr Pro Trp Tyr Trp Val Trp Asn Leu  
730 735 740

caa att tct acc act ttt tgg gaa cgc aaa aag caa agc gtt aat gcg 2731  
Gln Ile Ser Thr Thr Phe Trp Glu Arg Lys Lys Gln Ser Val Asn Ala  
745 750 755

agc ttg caa atc aat aac att ttt aac atg aaa tat tgg ttt agc ggg 2779  
Ser Leu Gln Ile Asn Asn Ile Phe Asn Met Lys Tyr Trp Phe Ser Gly  
760 765 770

ata ggc act agc cta acg gga aag aag ccg cgc ctc cta gga gca tca 2827  
Ile Gly Thr Ser Leu Thr Gly Lys Lys Pro Arg Leu Leu Gly Ala Ser  
775 780 785 790

cag cgt atg tgagctatca tttttaattt taggggttgta atgttttgag 2876  
Gln Arg Met

aagttgggcg taaa 2890

<210> 362  
<211> 793  
<212> PRT  
<213> Helicobacter pylori

<400> 362  
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Tyr Phe Leu Ala Leu Asn Ala Leu Thr Phe Leu Ser Phe Asn Ser Leu  
20 25 30  
Val Gly Ala Lys Glu Gln His His Thr Leu Gln Lys Val Thr Thr Thr  
35 40 45  
Glu Gln Lys Phe Asn Pro Ser Ala Pro Leu Ser Trp Gln Ser Glu Glu  
50 55 60  
Met Arg Asn Ser Thr Ser Ser Arg Thr Val Ile Ser Asn Lys Glu Leu  
65 70 75 80  
Lys Lys Thr Gly Asn Leu Asn Ile Glu Asn Ala Leu Gln Asn Val Pro  
85 90 95  
Gly Ile Gln Ile Arg Asp Ala Thr Gly Thr Gly Val Leu Pro Lys Ile  
100 105 110

Ser	Val	Arg	Gly	Phe	Gly	Gly	Gly	Gly	Asn	Gly	His	Ser	Asn	Thr	Asn		
		115						120				125					
Met	Ile	Leu	Val	Asn	Gly	Ile	Pro	Ile	Tyr	Gly	Ala	Pro	Tyr	Ser	Asn		
		130					135				140						
Ile	Glu	Leu	Ala	Ile	Phe	Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile		
145					150					155					160		
Asp	Val	Ile	Lys	Gly	Gly	Thr	Ser	Val	Gln	Tyr	Gly	Pro	Asn	Thr	Phe		
				165					170					175			
Gly	Gly	Val	Val	Asn	Ile	Ile	Thr	Lys	Glu	Ile	Pro	Lys	Glu	Trp	Glu		
			180					185					190				
Asn	Gln	Ala	Ala	Glu	Arg	Ile	Thr	Phe	Trp	Gly	Arg	Ser	Ser	Asn	Gly		
		195					200					205					
Asn	Phe	Val	Asp	Pro	Lys	Glu	Lys	Gly	Lys	Pro	Leu	Ala	Gln	Thr	Leu		
		210				215					220						
Gly	Asn	Gln	Met	Leu	Phe	Asn	Thr	Tyr	Gly	Arg	Thr	Ala	Gly	Met	Leu		
225					230					235					240		
Gly	Lys	His	Val	Gly	Ile	Ser	Ala	Gln	Gly	Asn	Trp	Ile	Asn	Gly	Gln		
				245					250					255			
Gly	Phe	Arg	Gln	Asn	Ser	Pro	Thr	Lys	Val	Gln	Asn	Tyr	Leu	Leu	Asp		
			260					265					270				
Ala	Val	Tyr	Lys	Ile	Asn	Ala	Thr	Asn	Thr	Phe	Lys	Ala	Tyr	Tyr	Gln		
		275					280					285					
Tyr	Tyr	Gln	Tyr	Asn	Ser	Tyr	His	Pro	Gly	Thr	Leu	Ser	Ala	Gln	Asp		
		290				295					300						
Tyr	Ala	Tyr	Asn	Arg	Phe	Ile	Asn	Glu	Arg	Pro	Asp	Asn	Gln	Asp	Gly		
305					310					315					320		
Gly	Arg	Ala	Lys	Arg	Phe	Gly	Ile	Val	Tyr	Gln	Asn	Tyr	Phe	Gly	Asp		
				325					330					335			
Pro	Asp	Arg	Lys	Val	Gly	Gly	Asp	Phe	Lys	Phe	Thr	Tyr	Phe	Thr	His		
			340					345					350				
Asp	Met	Ser	Arg	Asp	Phe	Gly	Phe	Ser	Asn	Gln	Tyr	Gln	Ser	Val	Tyr		
		355					360					365					
Met	Ser	Ser	Gln	Asn	Lys	Ile	Leu	Pro	Phe	Lys	Gly	Lys	Gly	Lys	Ile		
		370				375					380						
Ser	Ala	Thr	Asn	Pro	Asn	Cys	Gly	Leu	Tyr	Ser	Tyr	Ser	Asp	Thr	Asn		
385					390					395					400		
Ser	Pro	Cys	Trp	Gln	Phe	Phe	Asp	Asn	Ile	Arg	Arg	Ser	Val	Val	Asn		
				405					410					415			
Ala	Phe	Glu	Pro	Lys	Leu	Asn	Leu	Ile	Val	Asn	Thr	Gly	Lys	Val	Lys		
			420					425					430				
Gln	Thr	Phe	Asn	Met	Gly	Met	Arg	Phe	Leu	Thr	Glu	Asp	Leu	Tyr	Arg		
		435					440					445					
Arg	Ser	Thr	Thr	Arg	Lys	Asn	Pro	Ser	Met	Pro	Asn	Asn	Gly	Ser	Gly		
		450				455					460						
Phe	Asp	Ala	Gly	Thr	Ser	Leu	Asn	Asn	Phe	Asn	Asn	Tyr	Thr	Ala	Val		
465					470					475					480		
Tyr	Ala	Ser	Asp	Glu	Ile	Asn	Phe	Asn	Asn	Gly	Met	Leu	Thr	Ile	Thr		
				485					490					495			
Pro	Gly	Leu	Arg	Tyr	Thr	Phe	Leu	Asn	Tyr	Glu	Lys	Lys	Asp	Ala	Pro		
			500					505					510				
Pro	Phe	Lys	Ala	Gly	Gln	Thr	Gly	Lys	Thr	Ile	Lys	Asp	Arg	Tyr	Asn		
		515					520					525					
Gln	Trp	Asn	Pro	Ala	Val	Asn	Val	Gly	Tyr	Lys	Pro	Ile	Lys	Glu	Leu		
		530				535					540						
Leu	Phe	Tyr	Phe	Asn	Tyr	Gln	Arg	Ser	Tyr	Ile	Pro	Pro	Gln	Phe	Ser		

545		550		555		560
Asn Ile Gly Ser Phe Val Gly Thr Ser Thr Asp Tyr Phe Gln Ile Phe						
	565		570			575
Asn Val Met Glu Gly Gly Ser Arg Tyr Tyr Phe Asn Asn Gln Val Ser						
	580		585			590
Phe Asn Ala Asn Tyr Phe Val Ile Phe Ala Asn Asn Tyr Phe Thr Gly						
	595		600			605
Arg Tyr Gly Asp Asn Lys Glu Pro Val Asn Ala Arg Ser Gln Gly Val						
	610		615			620
Glu Leu Glu Leu Tyr Tyr Thr Pro Ile Arg Gly Leu Asn Phe His Ala						
	625		630			635
Ala Tyr Thr Phe Ile Asp Ala Asn Ile Thr Ser His Thr Met Val Thr						
	645		650			655
Asn Pro Ala Asn Pro Lys Gly Pro Lys Lys Asp Ile Phe Gly Lys Lys						
	660		665			670
Leu Pro Phe Val Ser Pro His Gln Phe Ile Leu Asp Ala Ser Tyr Thr						
	675		680			685
Tyr Ala Lys Thr Thr Ile Gly Leu Ser Ser Phe Phe Tyr Ser Arg Thr						
	690		695			700
Tyr Ser Asp Val Leu Asn Thr Val Pro Phe Ile Gln Tyr Ala Pro Thr						
	705		710			715
Ile Lys Asn Gly Ala Ile Thr Thr Lys Thr Ala Gly Met Thr Pro Trp						
	725		730			735
Tyr Trp Val Trp Asn Leu Gln Ile Ser Thr Thr Phe Trp Glu Arg Lys						
	740		745			750
Lys Gln Ser Val Asn Ala Ser Leu Gln Ile Asn Asn Ile Phe Asn Met						
	755		760			765
Lys Tyr Trp Phe Ser Gly Ile Gly Thr Ser Leu Thr Gly Lys Lys Pro						
	770		775			780
Arg Leu Leu Gly Ala Ser Gln Arg Met						
785		790				

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 <211> 406  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
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	Ile Lys
	1
ata atc tat caa atc atc aag ttt ttt cgt tct aag aat ttt att ttg	104
Ile Ile Tyr Gln Ile Ile Lys Phe Phe Arg Ser Lys Asn Phe Ile Leu	
	5 10 15
ttt ttt aga ata gca acg ata aag ttc ttc ttt tat ctc att tgg gaa	152
Phe Phe Arg Ile Ala Thr Ile Lys Phe Phe Phe Tyr Leu Ile Trp Glu	
	20 25 30



ttt ttg aat gtt ata gac aat ttc act atc tct ttg att ttg ttt ata 200  
Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu Phe Ile  
35 40 45 50

ttt ttt agc ccc ata cca aag aaa tat ttg ata aaa aat aag aaa aat 248  
Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys Lys Asn  
55 60 65

agc gta aaa gaa aaa gaa aat aaa gaa aaa aga aag aga aaa aga aag 296  
Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys Arg Lys  
70 75 80

gat ttt gtt ttg ggt gta ttg gaa aat aga ctc aaa aat caa ttg aaa 344  
Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln Leu Lys  
85 90 95

aac ccc ttt tagattaaaa ataaaaacaa taagcgaaac gacaaaagca 393  
Asn Pro Phe  
100

agcagaaaag aag 406

<210> 364  
<211> 101  
<212> PRT  
<213> Helicobacter pylori

<400> 364  
Ile Lys Ile Ile Tyr Gln Ile Ile Lys Phe Phe Arg Ser Lys Asn Phe  
1 5 10 15  
Ile Leu Phe Phe Arg Ile Ala Thr Ile Lys Phe Phe Phe Tyr Leu Ile  
20 25 30  
Trp Glu Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu  
35 40 45  
Phe Ile Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys  
50 55 60  
Lys Asn Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys  
65 70 75 80  
Arg Lys Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln  
85 90 95  
Leu Lys Asn Pro Phe  
100

<210> 365  
<211> 1143  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (89)...(1087)

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ctccataaat catacaaaaa ggatcggtt atg tta gtt act cgc ttt aaa aaa	112
Met Leu Val Thr Arg Phe Lys Lys	
1 5	
gct tta atc tct tat tct tta ggc gcg ctt ctt gtt tca tcg tta ttg	160
Ala Leu Ile Ser Tyr Ser Leu Gly Ala Leu Leu Val Ser Ser Leu Leu	
10 15 20	
ggc gtg gct agt gct tcc aat caa gaa atc caa gtc aaa gat tat ttt	208
Gly Val Ala Ser Ala Ser Asn Gln Glu Ile Gln Val Lys Asp Tyr Phe	
25 30 35 40	
ggg gat caa gcc atc aag ctt cct gtt tct aaa ata atc tac ttg ggt	256
Gly Asp Gln Ala Ile Lys Leu Pro Val Ser Lys Ile Ile Tyr Leu Gly	
45 50 55	
agc ttt gca gaa gtg cct gct atg ttc cat act tgg gat agg gtc gtg	304
Ser Phe Ala Glu Val Pro Ala Met Phe His Thr Trp Asp Arg Val Val	
60 65 70	
gga att tcg gat tac gct ttt aaa tct gat att gtt aaa gct act ctc	352
Gly Ile Ser Asp Tyr Ala Phe Lys Ser Asp Ile Val Lys Ala Thr Leu	
75 80 85	
aaa gat cct aaa cgc att aaa tcc atg agc agt gat cat gtg gcg gcg	400
Lys Asp Pro Lys Arg Ile Lys Ser Met Ser Ser Asp His Val Ala Ala	
90 95 100	
ttg aat gtg gag ctt tta aaa aag ctt ggc ccc gat ctt gtg gta acc	448
Leu Asn Val Glu Leu Leu Lys Lys Leu Gly Pro Asp Leu Val Val Thr	
105 110 115 120	
ttt gtg ggc aac cct aaa gcg gta gag cat gcg aaa aaa ttt ggt ata	496
Phe Val Gly Asn Pro Lys Ala Val Glu His Ala Lys Lys Phe Gly Ile	
125 130 135	
tta ttt ctt tct ttc caa gaa aaa acc att gca gaa gtc atg gaa gat	544
Leu Phe Leu Ser Phe Gln Glu Lys Thr Ile Ala Glu Val Met Glu Asp	
140 145 150	
att gac gct caa gct aaa gcc tta gaa att gat gct tct aaa aaa ctg	592
Ile Asp Ala Gln Ala Lys Ala Leu Glu Ile Asp Ala Ser Lys Lys Leu	
155 160 165	
gcc aaa atg caa gaa act ttg gat ttt att gct gag cgt ttg aaa ggt	640
Ala Lys Met Gln Glu Thr Leu Asp Phe Ile Ala Glu Arg Leu Lys Gly	
170 175 180	
gtc aaa aag aaa aaa ggg gtg gag ctt ttc cat aag gcc aat aag atc	688
Val Lys Lys Lys Lys Gly Val Glu Leu Phe His Lys Ala Asn Lys Ile	
185 190 195 200	
agc ggc cat caa gcc ctt gat tca gac att tta gaa aaa gga ggc ata	736
Ser Gly His Gln Ala Leu Asp Ser Asp Ile Leu Glu Lys Gly Gly Ile	
205 210 215	

gac aat ttt ggc ttg aaa tat gtc aaa ttt ggg cgt gct gac att agc 784  
Asp Asn Phe Gly Leu Lys Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser  
220 225 230

gtg gaa aaa atc gtt aaa gaa aac cct gag att atc ttt att tgg tgg 832  
Val Glu Lys Ile Val Lys Glu Asn Pro Glu Ile Ile Phe Ile Trp Trp  
235 240 245

ata agc cca ctc acg cct gaa gat gtg tta aac aac ccc aaa ttt gct 880  
Ile Ser Pro Leu Thr Pro Glu Asp Val Leu Asn Asn Pro Lys Phe Ala  
250 255 260

acc atc aaa gcc att aaa aac aag cag gtt tat aaa ctc ccc aca atg 928  
Thr Ile Lys Ala Ile Lys Asn Lys Gln Val Tyr Lys Leu Pro Thr Met  
265 270 275 280

gat att ggc ggg cct aga gcc cca ctc ata agt ctt ttt atc gct cta 976  
Asp Ile Gly Gly Pro Arg Ala Pro Leu Ile Ser Leu Phe Ile Ala Leu  
285 290 295

aaa gcc cac cct gaa gcc ttt aag ggc gtg gat att aat gcg att gtt 1024  
Lys Ala His Pro Glu Ala Phe Lys Gly Val Asp Ile Asn Ala Ile Val  
300 305 310

aaa gac tac tat aaa gtg gtt ttt gat ttg aat gat gca gag gtt gaa 1072  
Lys Asp Tyr Tyr Lys Val Val Phe Asp Leu Asn Asp Ala Glu Val Glu  
315 320 325

ccc ttt tta tgg cat taatttttaa aaaagggctg atatttttag ccctttgtgt 1127  
Pro Phe Leu Trp His  
330

atcgcgctag gattag 1143

<210> 366  
<211> 333  
<212> PRT  
<213> Helicobacter pylori

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Ala Leu Leu Val Ser Ser Leu Leu Gly Val Ala Ser Ala Ser Asn Gln  
20 25 30  
Glu Ile Gln Val Lys Asp Tyr Phe Gly Asp Gln Ala Ile Lys Leu Pro  
35 40 45  
Val Ser Lys Ile Ile Tyr Leu Gly Ser Phe Ala Glu Val Pro Ala Met  
50 55 60  
Phe His Thr Trp Asp Arg Val Val Gly Ile Ser Asp Tyr Ala Phe Lys  
65 70 75 80  
Ser Asp Ile Val Lys Ala Thr Leu Lys Asp Pro Lys Arg Ile Lys Ser  
85 90 95  
Met Ser Ser Asp His Val Ala Ala Leu Asn Val Glu Leu Leu Lys Lys  
100 105 110



gac aaa cct aaa ccc cta act att gat aaa aac aat gaa aaa cag caa	248
Asp Lys Pro Lys Pro Leu Thr Ile Asp Lys Asn Asn Glu Lys Gln Gln	
55 60 65	
atc tta gac aaa aac cag caa atc tta aaa agg gct ttg gaa aaa agc	296
Ile Leu Asp Lys Asn Gln Gln Ile Leu Lys Arg Ala Leu Glu Lys Ser	
70 75 80	
ctt aaa ttc ttt ttc att ttt gga tac aac tat tcg caa gcc act ttt	344
Leu Lys Phe Phe Phe Ile Phe Gly Tyr Asn Tyr Ser Gln Ala Thr Phe	
85 90 95	
tca act tct aac caa acc ttg act ttt gta gcc aat agc ata ggg ttt	392
Ser Thr Ser Asn Gln Thr Leu Thr Phe Val Ala Asn Ser Ile Gly Phe	
100 105 110	
aac acc gct acc ggt tta gag cat ttt tta aga aac cac cct aaa gtc	440
Asn Thr Ala Thr Gly Leu Glu His Phe Leu Arg Asn His Pro Lys Val	
115 120 125 130	
ggt ttt aga atc ttt agc gtc tat aac tat ttc cat tct gtt tcc ctc	488
Gly Phe Arg Ile Phe Ser Val Tyr Asn Tyr Phe His Ser Val Ser Leu	
135 140 145	
tcc cag cct caa acc tta atg gtg caa aat tat ggg ggc gcg tta gat	536
Ser Gln Pro Gln Thr Leu Met Val Gln Asn Tyr Gly Gly Ala Leu Asp	
150 155 160	
ttt tct tgg att ttt gta gat aaa aat att tat cgc ttt agg agt tat	584
Phe Ser Trp Ile Phe Val Asp Lys Asn Ile Tyr Arg Phe Arg Ser Tyr	
165 170 175	
tta ggg atc gct tta gaa caa ggg gtg ttg tta gtg gat acg att aaa	632
Leu Gly Ile Ala Leu Glu Gln Gly Val Leu Leu Val Asp Thr Ile Lys	
180 185 190	
cca ggt gct atc aca acg att atc cca aga acc aaa aaa acc ttt ttt	680
Pro Gly Ala Ile Thr Thr Ile Ile Pro Arg Thr Lys Lys Thr Phe Phe	
195 200 205 210	
caa gcc cct ttg cgt ttt ggt ttt atc gtg gat ttt atc ggc tat ttg	728
Gln Ala Pro Leu Arg Phe Gly Phe Ile Val Asp Phe Ile Gly Tyr Leu	
215 220 225	
tct ttg caa tta ggg att gaa atg cct tta gtg agg aat gtt ttt tac	776
Ser Leu Gln Leu Gly Ile Glu Met Pro Leu Val Arg Asn Val Phe Tyr	
230 235 240	
acc tac aac aac cat caa gaa aga ttc aaa cca cga ttt aac gct aat	824
Thr Tyr Asn Asn His Gln Glu Arg Phe Lys Pro Arg Phe Asn Ala Asn	
245 250 255	
ctt tct tta atc gtt tcg ttt tagccccct tttccccctt taaataagcc	875
Leu Ser Leu Ile Val Ser Phe	

260

265

catgattttc ctagggtatt tta

898

&lt;210&gt; 368

&lt;211&gt; 265

&lt;212&gt; PRT

&lt;213&gt; Helicobacter pylori

&lt;400&gt; 368

Leu	Gly	Thr	Ile	Ala	Thr	Lys	Ser	Leu	Arg	Leu	Tyr	Leu	Lys	Thr	Leu
1				5					10					15	
Phe	Ser	Ile	Tyr	Leu	Phe	Leu	Ser	Leu	Asn	Pro	Leu	Phe	Leu	Glu	Ala
		20						25					30		
Asn	Glu	Ile	Thr	Trp	Ser	Lys	Phe	Leu	Glu	Asn	Phe	Lys	Asn	Lys	Asn
		35					40					45			
Asp	Asp	Asp	Lys	Pro	Lys	Pro	Leu	Thr	Ile	Asp	Lys	Asn	Asn	Glu	Lys
	50					55					60				
Gln	Gln	Ile	Leu	Asp	Lys	Asn	Gln	Gln	Ile	Leu	Lys	Arg	Ala	Leu	Glu
65					70					75				80	
Lys	Ser	Leu	Lys	Phe	Phe	Phe	Ile	Phe	Gly	Tyr	Asn	Tyr	Ser	Gln	Ala
				85					90					95	
Thr	Phe	Ser	Thr	Ser	Asn	Gln	Thr	Leu	Thr	Phe	Val	Ala	Asn	Ser	Ile
			100					105					110		
Gly	Phe	Asn	Thr	Ala	Thr	Gly	Leu	Glu	His	Phe	Leu	Arg	Asn	His	Pro
		115				120					125				
Lys	Val	Gly	Phe	Arg	Ile	Phe	Ser	Val	Tyr	Asn	Tyr	Phe	His	Ser	Val
	130					135					140				
Ser	Leu	Ser	Gln	Pro	Gln	Thr	Leu	Met	Val	Gln	Asn	Tyr	Gly	Gly	Ala
145					150					155				160	
Leu	Asp	Phe	Ser	Trp	Ile	Phe	Val	Asp	Lys	Asn	Ile	Tyr	Arg	Phe	Arg
			165					170						175	
Ser	Tyr	Leu	Gly	Ile	Ala	Leu	Glu	Gln	Gly	Val	Leu	Leu	Val	Asp	Thr
		180					185						190		
Ile	Lys	Pro	Gly	Ala	Ile	Thr	Thr	Ile	Ile	Pro	Arg	Thr	Lys	Lys	Thr
		195					200					205			
Phe	Phe	Gln	Ala	Pro	Leu	Arg	Phe	Gly	Phe	Ile	Val	Asp	Phe	Ile	Gly
	210					215					220				
Tyr	Leu	Ser	Leu	Gln	Leu	Gly	Ile	Glu	Met	Pro	Leu	Val	Arg	Asn	Val
225					230					235				240	
Phe	Tyr	Thr	Tyr	Asn	Asn	His	Gln	Glu	Arg	Phe	Lys	Pro	Arg	Phe	Asn
				245				250						255	
Ala	Asn	Leu	Ser	Leu	Ile	Val	Ser	Phe							
		260					265								

&lt;210&gt; 369

&lt;211&gt; 742

&lt;212&gt; DNA

&lt;213&gt; Helicobacter pylori

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (51)...(689)

<400> 369

gcacttcacg cattccataa acgatattga ttatttgcta gacagcttga aaa aag	56
Lys Lys	
1	
cag tta aaa aat tgc gtt aag cta aaa cta ttt tta agg aaa aat ttg	104
Gln Leu Lys Asn Cys Val Lys Leu Lys Leu Phe Leu Arg Lys Asn Leu	
5 10 15	
gat att tta gat ttg aac aaa gcg caa gcg gtg caa caa aat gaa caa	152
Asp Ile Leu Asp Leu Asn Lys Ala Gln Ala Val Gln Gln Asn Glu Gln	
20 25 30	
gag gta gag gat aaa gag cga gag tct aaa gag ccg gtg gtt tta gaa	200
Glu Val Glu Asp Lys Glu Arg Glu Ser Lys Glu Pro Val Val Leu Glu	
35 40 45 50	
gat ttg agc gct tta gcg tgg ctt gaa tta gaa gag ttt agc cgc ctt	248
Asp Leu Ser Ala Leu Ala Trp Leu Glu Leu Glu Glu Phe Ser Arg Leu	
55 60 65	
tca ggg ctt cct aaa gaa agg att ttg gaa tta gtg aat ctt ggt aaa	296
Ser Gly Leu Pro Lys Glu Arg Ile Leu Glu Leu Val Asn Leu Gly Lys	
70 75 80	
atc aag agc aaa ata agc agc aac aag ctt tta att gat gcg agc agc	344
Ile Lys Ser Lys Ile Ser Ser Asn Lys Leu Leu Ile Asp Ala Ser Ser	
85 90 95	
ggg aca aac gct tta atc aaa aag gta gaa aat agt ttg att tct atg	392
Gly Thr Asn Ala Leu Ile Lys Lys Val Glu Asn Ser Leu Ile Ser Met	
100 105 110	
gat atg aac ggg cgt tct tta gaa cct gtg ttt gtg gaa aag acc att	440
Asp Met Asn Gly Arg Ser Leu Glu Pro Val Phe Val Glu Lys Thr Ile	
115 120 125 130	
aac acg att tta aac ttg cat gat aag gtc att ggc gct aaa gat gaa	488
Asn Thr Ile Leu Asn Leu His Asp Lys Val Ile Gly Ala Lys Asp Glu	
135 140 145	
acg att tca gcc ttt aaa aat gaa aac atg ttt tta aaa gac gct tta	536
Thr Ile Ser Ala Phe Lys Asn Glu Asn Met Phe Leu Lys Asp Ala Leu	
150 155 160	
atc tct atg caa gaa gtc tat gaa gaa gat aaa aaa acc att gat ctt	584
Ile Ser Met Gln Glu Val Tyr Glu Glu Asp Lys Lys Thr Ile Asp Leu	
165 170 175	
ttg cgc gat gaa ctc aat caa gcg aga gaa gaa att gaa ttt atg aag	632
Leu Arg Asp Glu Leu Asn Gln Ala Arg Glu Glu Ile Glu Phe Met Lys	
180 185 190	
agg aaa tac cgc ttg atg tgg ggg aaa gtc gct gac atg agc agc gtg	680
Arg Lys Tyr Arg Leu Met Trp Gly Lys Val Ala Asp Met Ser Ser Val	

195

200

205

210

aat aaa aag tagttttaaa ttaacgcca tgctgagggc ttattagcgg  
 Asn Lys Lys

729

taatttttagg tga

742

&lt;210&gt; 370

&lt;211&gt; 213

&lt;212&gt; PRT

&lt;213&gt; Helicobacter pylori

&lt;400&gt; 370

Lys Lys Gln Leu Lys Asn Cys Val Lys Leu Lys Leu Phe Leu Arg Lys  
 1 5 10 15  
 Asn Leu Asp Ile Leu Asp Leu Asn Lys Ala Gln Ala Val Gln Gln Asn  
 20 25 30  
 Glu Gln Glu Val Glu Asp Lys Glu Arg Glu Ser Lys Glu Pro Val Val  
 35 40 45  
 Leu Glu Asp Leu Ser Ala Leu Ala Trp Leu Glu Leu Glu Glu Phe Ser  
 50 55 60  
 Arg Leu Ser Gly Leu Pro Lys Glu Arg Ile Leu Glu Leu Val Asn Leu  
 65 70 75 80  
 Gly Lys Ile Lys Ser Lys Ile Ser Ser Asn Lys Leu Leu Ile Asp Ala  
 85 90 95  
 Ser Ser Gly Thr Asn Ala Leu Ile Lys Lys Val Glu Asn Ser Leu Ile  
 100 105 110  
 Ser Met Asp Met Asn Gly Arg Ser Leu Glu Pro Val Phe Val Glu Lys  
 115 120 125  
 Thr Ile Asn Thr Ile Leu Asn Leu His Asp Lys Val Ile Gly Ala Lys  
 130 135 140  
 Asp Glu Thr Ile Ser Ala Phe Lys Asn Glu Asn Met Phe Leu Lys Asp  
 145 150 155 160  
 Ala Leu Ile Ser Met Gln Glu Val Tyr Glu Glu Asp Lys Lys Thr Ile  
 165 170 175  
 Asp Leu Leu Arg Asp Glu Leu Asn Gln Ala Arg Glu Glu Ile Glu Phe  
 180 185 190  
 Met Lys Arg Lys Tyr Arg Leu Met Trp Gly Lys Val Ala Asp Met Ser  
 195 200 205  
 Ser Val Asn Lys Lys  
 210